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(54) **Staphylococcus aureus polynucleotides and sequences**

(57) The present invention provides polynucleotide sequences of the genome of *Staphylococcus aureus*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynu-

cleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

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D scription

The present invention relates to the field of molecular biology. In particular, it relates to, among other things, nucleotide sequences of *Staphylococcus aureus*, contigs, ORFs, fragments, probes, primers and related polynucleotides thereof, peptides and polypeptides encoded by the sequences, and uses of the polynucleotides and sequences thereof, such as in fermentation, polypeptide production, assays and pharmaceutical development, among others.

The genus *Staphylococcus* includes at least 20 distinct species. (For a review see Novick, R. P., The *Staphylococcus* as a Molecular Genetic System, Chapter 1, pgs. 1-37 in MOLECULAR BIOLOGY OF THE STAPHYLOCOCCI, R. Novick, Ed., VCH Publishers, New York (1990)). Species differ from one another by 80% or more, by hybridization kinetics, whereas strains within a species are at least 90% identical by the same measure.

The species *Staphylococcus aureus*, a gram-positive, facultatively aerobic, clump-forming cocci, is among the most important etiological agents of bacterial infection in humans, as discussed briefly below.

Human Health and *S. Aureus*

Staphylococcus aureus is a ubiquitous pathogen. (See, for instance, Mims *et al.*, MEDICAL MICROBIOLOGY, Mosby-Year Book Europe Limited, London, UK (1993)). It is an etiological agent of a variety of conditions, ranging in severity from mild to fatal. A few of the more common conditions caused by *S. aureus* infection are burns, cellulitis, eyelid infections, food poisoning, joint infections, neonatal conjunctivitis, osteomyelitis, skin infections, surgical wound infection, scalded skin syndrome and toxic shock syndrome, some of which are described further below.

Burns

Burn wounds generally are sterile initially. However, they generally compromise physical and immune barriers to infection, cause loss of fluid and electrolytes and result in local or general physiological dysfunction. After cooling, contact with viable bacteria results in mixed colonization at the injury site. Infection may be restricted to the non-viable debris on the burn surface ("eschar"), it may progress into full skin infection and invade viable tissue below the eschar and it may reach below the skin, enter the lymphatic and blood circulation and develop into septicaemia. *S. aureus* is among the most important pathogens typically found in burn wound infections. It can destroy granulation tissue and produce severe septicaemia.

Cellulitis

Cellulitis, an acute infection of the skin that expands from a typically superficial origin to spread below the cutaneous layer, most commonly is caused by *S. aureus* in conjunction with *S. pyogenes*. Cellulitis can lead to systemic infection. In fact, cellulitis can be one aspect of synergistic bacterial gangrene. This condition typically is caused by a mixture of *S. aureus* and microaerophilic streptococci. It causes necrosis and treatment is limited to excision of the necrotic tissue. The condition often is fatal.

Eyelid infections

S. aureus is the cause of styes and of sticky eye" in neonates, among other eye infections. Typically such infections are limited to the surface of the eye, and may occasionally penetrate the surface with more severe consequences.

Food poisoning

Some strains of *S. aureus* produce one or more of five serologically distinct, heat and acid stable enterotoxins that are not destroyed by digestive process of the stomach and small intestine (enterotoxins A-E). Ingestion of the toxin, in sufficient quantities, typically results in severe vomiting, but not diarrhoea. The effect does not require viable bacteria. Although the toxins are known, their mechanism of action is not understood.

Joint infections

S. aureus infects bone joints causing diseases such osteomyelitis.

Osteomyelitis

S. aureus is the most common causative agent of haematogenous osteomyelitis. The disease tends to occur in

children and adolescents more than adults and it is associated with non-penetrating injuries to bones. Infection typically occurs in the long end of growing bone, hence its occurrence in physically immature populations. Most often, infection is localized in the vicinity of sprouting capillary loops adjacent to epiphysial growth plates in the end of long, growing bones.

Skin infections

S. aureus is the most common pathogen of such minor skin infections as abscesses and boils. Such infections often are resolved by normal host response mechanisms, but they also can develop into severe internal infections. Recurrent infections of the nasal passages plague nasal carriers of *S. aureus*.

Surgical Wound Infections

Surgical wounds often penetrate far into the body. Infection of such wound thus poses a grave risk to the patient. *S. aureus* is the most important causative agent of infections in surgical wounds. *S. aureus* is unusually adept at invading surgical wounds; sutured wounds can be infected by far fewer *S. aureus* cells than are necessary to cause infection in normal skin. Invasion of surgical wound can lead to severe *S. aureus* septicaemia. Invasion of the blood stream by *S. aureus* can lead to seeding and infection of internal organs, particularly heart valves and bone, causing systemic diseases, such as endocarditis and osteomyelitis.

Scalded Skin Syndrome

S. aureus is responsible for "scalded skin syndrome" (also called toxic epidermal necrosis, Ritter's disease and Lyell's disease). This disease occurs in older children, typically in outbreaks caused by flowering of *S. aureus* strains produce exfoliation (also called scalded skin syndrome toxin). Although the bacteria initially may infect only a minor lesion, the toxin destroys intercellular connections, spreads epidermal layers and allows the infection to penetrate the outer layer of the skin, producing the desquamation that typifies the diseases. Shedding of the outer layer of skin generally reveals normal skin below, but fluid lost in the process can produce severe injury in young children if it is not treated properly.

Toxic Shock Syndrome

Toxic shock syndrome is caused by strains of *S. aureus* that produce the so-called toxic shock syndrome toxin. The disease can be caused by *S. aureus* infection at any site, but it is too often erroneously viewed exclusively as a disease solely of women who use tampons. The disease involves toxemia and septicaemia, and can be fatal.

Nocosomal Infections

In the 1984 National Nosocomial Infection Surveillance Study ("NNIS") *S. aureus* was the most prevalent agent of surgical wound infections in many hospital services, including medicine, surgery, obstetrics, pediatrics and newborns.

Resistance to drugs of S. aureus strains

Prior to the introduction of penicillin the prognosis for patients seriously infected with *S. aureus* was unfavorable. Following the introduction of penicillin in the early 1940s even the worst *S. aureus* infections generally could be treated successfully. The emergence of penicillin-resistant strains of *S. aureus* did not take long, however. Most strains of *S. aureus* encountered in hospital infections today do not respond to penicillin; although, fortunately, this is not the case for *S. aureus* encountered in community infections.

It is well known now that penicillin-resistant strains of *S. aureus* produce a lactamase which converts penicillin to penicilloic acid, and thereby destroys antibiotic activity. Furthermore, the lactamase gene often is propagated episomally, typically on a plasmid, and often is only one of several genes on an episomal element that, together, confer multidrug resistance.

Methicillins, introduced in the 1960s, largely overcame the problem of penicillin resistance in *S. aureus*. These compounds conserve the portions of penicillin responsible for antibiotic activity and modify or alter other portions that make penicillin a good substrate for inactivating lactamases. However, methicillin resistance has emerged in *S. aureus*, along with resistance to many other antibiotics effective against this organism, including aminoglycosides, tetracycline, chloramphenicol, macrolides and lincosamides. In fact, methicillin-resistant strains of *S. aureus* generally are multiply drug resistant.

The molecular genetics of most types of drug resistance in *S. aureus* has been elucidated (See Lyon *et al.*, *Microbiology Reviews* 51: 88-134 (1987)). Generally, resistance is mediated by plasmids, as noted above regarding penicillin resistance; however, several stable forms of drug resistance have been observed that apparently involve integration of a resistance element into the *S. aureus* genome itself.

Thus far each new antibiotic gives rise to resistance strains, strains emerge that are resistance to multiple drugs and increasingly persistent forms of resistance begin to emerge. Drug resistance of *S. aureus* infections already poses significant treatment difficulties, which are likely to get much worse unless new therapeutic agents are developed.

Molecular Genetics of *Staphylococcus Aureus*

Despite its importance in, among other things, human disease, relatively little is known about the genome of this organism.

Most genetic studies of *S. aureus* have been carried out using the strain NCTC8325, which contains prophages psi11 psi12 and psi13, and the UV-cured derivative of this strain, 8325-4 (also referred to as RN450), which is free of the prophages.

These studies revealed that the *S. aureus* genome, like that of other *staphylococci*, consists of one circular, covalently closed, double-stranded DNA and a collection of so-called variable accessory genetic elements, such as prophages, plasmids, transposons and the like.

Physical characterization of the genome has not been carried out in any detail. Pattee *et al.* published a low resolution and incomplete genetic and physical map of the chromosome of *S. aureus* strain NCTC 8325. (Pattee *et al.* Genetic and Physical Mapping of Chromosome of *Staphylococcus aureus* NCTC 8325, Chapter 11, pgs. 163-169 in. MOLECULAR BIOLOGY OF THE STAPHYLOCOCCI, R.P. Novick, Ed., VCH Publishers, New York, (1990) The genetic map largely was produced by mapping insertions of Tn551 and Tn4001, which, respectively, confer erythromycin and gentamicin resistance, and by analysis of SmaI-digested DNA by Pulsed Field Gel Electrophoresis ("PFGE").

The map was of low resolution; even estimating the physical size of the genome was difficult, according to the investigators. The size of the largest SmaI chromosome fragment, for instance, was too large for accurate sizing by PFGE. To estimate its size, additional restriction sites had to be introduced into the chromosome using a transposon containing a SmaI recognition sequence.

In sum, most physical characteristics and almost all of the genes of *Staphylococcus aureus* are unknown. Among the few genes that have been identified, most have not been physically mapped or characterized in detail. Only a very few genes of this organism have been sequenced. (See, for instance Thornsberry, J., *Antimicrobial Chemotherapy* 21 Suppl C: 9-16 (1988), current versions of GENBANK and other nucleic acid databases, and references that relate to the genome of *S. aureus* such as those set out elsewhere herein.)

It is clear that the etiology of diseases mediated or exacerbated by *S. aureus* infection involves the programmed expression of *S. aureus* genes, and that characterizing the genes and their patterns of expression would add dramatically to our understanding of the organism and its host interactions. Knowledge of *S. aureus* genes and genomic organization would dramatically improve understanding of disease etiology and lead to improved and new ways of preventing, ameliorating, arresting and reversing diseases. Moreover, characterized genes and genomic fragments of *S. aureus* would provide reagents for, among other things, detecting, characterizing and controlling *S. aureus* infections. There is a need therefore to characterize the genome of *S. aureus* and for polynucleotides and sequences of this organism.

The present invention is based on the sequencing of fragments of the *Staphylococcus aureus* genome. The primary nucleotide sequences which were generated are provided in SEQ ID NOS: 1-5,191.

The present invention provides the nucleotide sequence of several thousand contigs of the *Staphylococcus aureus* genome, which are listed in tables below and set out in the Sequence Listing submitted herewith, and representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan. In one embodiment, the present invention is provided as contiguous strings of primary sequence information corresponding to the nucleotide sequences depicted in SEQ ID NOS:1-5,191.

The present invention further provides nucleotide sequences which are at least 95%, preferably 99% and most preferably 99.9%, identical to the nucleotide sequences of SEQ ID NOS:1-5,191.

The nucleotide sequence of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence which is at least 95%, preferably 99% and most preferably 99.9%, identical to the nucleotide sequence of SEQ ID NOS:1-5,191 may be provided in a variety of mediums to facilitate its use. In one application of this embodiment, the sequences of the present invention are recorded on computer readable media. Such media includes, but is not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

The present invention further provides systems, particularly computer-based systems which contain the sequence

information herein described stored in a data storage means. Such systems are designed to identify commercially important fragments of the *Staphylococcus aureus* genome.

Another embodiment of the present invention is directed to fragments, preferably isolated fragments, of the *Staphylococcus aureus* genome having particular structural or functional attributes. Such fragments of the *Staphylococcus aureus* genome of the present invention include, but are not limited to, fragments which encode peptides, hereinafter referred to as open reading frames or ORFs," fragments which modulate the expression of an operably linked ORF, hereinafter referred to as expression modulating fragments or EMFs," and fragments which can be used to diagnose the presence of *Staphylococcus aureus* in a sample, hereinafter referred to as diagnostic fragments or "DFs."

Each of the ORFs in fragments of the *Staphylococcus aureus* genome disclosed in Tables 1-3, and the EMFs found 5' to the ORFs, can be used in numerous ways as polynucleotide reagents. For instance, the sequences can be used as diagnostic probes or amplification primers for detecting or determining the presence of a specific microbe in a sample, to selectively control gene expression in a host and in the production of polypeptides, such as polypeptides encoded by ORFs of the present invention, particular those polypeptides that have a pharmacological activity.

The present invention further includes recombinant constructs comprising one or more fragments of the *Staphylococcus aureus* genome of the present invention. The recombinant constructs of the present invention comprise vectors, such as a plasmid or viral vector, into which a fragment of the *Staphylococcus aureus* has been inserted.

The present invention further provides host cells containing any of the isolated fragments of the *Staphylococcus aureus* genome of the present invention. The host cells can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic cell, such as a yeast cell, or a procaryotic cell such as a bacterial cell.

The present invention is further directed to polypeptides and proteins, preferably isolated polypeptides and proteins, encoded by ORFs of the present invention. A variety of methods, well known to those of skill in the art, routinely may be utilized to obtain any of the polypeptides and proteins of the present invention. For instance, polypeptides and proteins of the present invention having relatively short, simple amino acid sequences readily can be synthesized using commercially available automated peptide synthesizers. Polypeptides and proteins of the present invention also may be purified from bacterial cells which naturally produce the protein. Yet another alternative is to purify polypeptide and proteins of the present invention can from cells which have been altered to express them.

The invention further provides polypeptides, preferably isolated polypeptides, comprising *Staphylococcus aureus* epitopes and vaccine compositions comprising such polypeptides. Also provided are methods for vaccinating an individual against *Staphylococcus aureus* infection.

The invention further provides methods of obtaining homologs of the fragments of the *Staphylococcus aureus* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. Specifically, by using the nucleotide and amino acid sequences disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

The invention further provides antibodies which selectively bind polypeptides and proteins of the present invention. Such antibodies include both monoclonal and polyclonal antibodies.

The invention further provides hybridomas which produce the above-described antibodies. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

The present invention further provides methods of identifying test samples derived from cells which express one of the ORFs of the present invention, or a homolog thereof. Such methods comprise incubating a test sample with one or more of the antibodies of the present invention, or one or more of the DFs or antigens of the present invention, under conditions which allow a skilled artisan to determine if the sample contains the ORF or product produced therefrom.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the above-described assays.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the antibodies, antigens, or one of the DFs of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of bound antibodies, antigens or hybridized DFs.

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents capable of binding to a polypeptide or protein encoded by one of the ORFs of the present invention. Specifically, such agents include, as further described below, antibodies, peptides, carbohydrates, pharmaceutical agents and the like. Such methods comprise steps of: (a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention; and (b) determining whether the agent binds to said protein.

The present genomic sequences of *Staphylococcus aureus* will be of great value to all laboratories working with this organism and for a variety of commercial purposes. Many fragments of the *Staphylococcus aureus* genome will be immediately identified by similarity searches against GenBank or protein databases and will be of immediate value to *Staphylococcus aureus* researchers and for immediate commercial value for the production of proteins or to control gene expression.

The methodology and technology for elucidating extensive genomic sequences of bacterial and other genomes

has and will greatly enhance the ability to analyze and understand chromosomal organization. In particular, sequenced contigs and genomes will provide the models for developing tools for the analysis of chromosome structure and function, including the ability to identify genes within large segments of genomic DNA, the structure, position, and spacing of regulatory elements, the identification of genes with potential industrial applications, and the ability to do comparative genomic and molecular phylogeny.

FIGURE 1 is a block diagram of a computer system (102) that can be used to implement computer-based systems of present invention.

FIGURE 2 is a schematic diagram depicting the data flow and computer programs used to collect, assemble, edit and annotate the contigs of the *Staphylococcus aureus* genome of the present invention. Both Macintosh and Unix platforms are used to handle the AB 373 and 377 sequence data files, largely as described in Kerlavage *et al.*, *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences*, 585, IEEE Computer Society Press, Washington D.C. (1993). Factura (AB) is a Macintosh program designed for automatic vector sequence removal and end-trimming of sequence files. The program Loadis runs on a Macintosh platform and parses the feature data extracted from the sequence files by Factura to the Unix based *Staphylococcus aureus* relational database. Assembly of contigs (and whole genome sequences) is accomplished by retrieving a specific set of sequence files and their associated features using extrseq, a Unix utility for retrieving sequences from an SQL database. The resulting sequence file is processed by seq_filter to trim portions of the sequences with more than 2% ambiguous nucleotides. The sequence files were assembled using TIGR Assembler, an assembly engine designed at The Institute for Genomic Research (TIGR) for rapid and accurate assembly of thousands of sequence fragments. The collection of contigs generated by the assembly step is loaded into the database with the lassie program. Identification of open reading frames (ORFs) is accomplished by processing contigs with zorf. The ORFs are searched against *S. aureus* sequences from Genbank and against all protein sequences using the BLASTN and BLASTP programs, described in Altschul *et al.*, *J. Mol. Biol.* 215: 403-410 (1990)). Results of the ORF determination and similarity searching steps were loaded into the database. As described below, some results of the determination and the searches are set out in Tables 1-3.

The present invention is based on the sequencing of fragments of the *Staphylococcus aureus* genome and analysis of the sequences. The primary nucleotide sequences generated by sequencing the fragments are provided in SEQ ID NOS:1-5,191. (As used herein, the "primary sequence" refers to the nucleotide sequence represented by the IUPAC nomenclature system.)

In addition to the aforementioned *Staphylococcus aureus* polynucleotide and polynucleotide sequences, the present invention provides the nucleotide sequences of SEQ ID NOS:1-5,191, or representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan.

As used herein, a "representative fragment of the nucleotide sequence depicted in SEQ ID NOS:1-5,191" refers to any portion of the SEQ ID NOS:1-5,191 which is not presently represented within a publicly available database. Preferred representative fragments of the present invention are *Staphylococcus aureus* open reading frames (ORFs), expression modulating fragment (EMFs) and fragments which can be used to diagnose the presence of *Staphylococcus aureus* in sample (DFs). A non-limiting identification of preferred representative fragments is provided in Tables 1-3.

As discussed in detail below, the information provided in SEQ ID NOS:1-5,191 and in Tables 1-3 together with routine cloning, synthesis, sequencing and assay methods will enable those skilled in the art to clone and sequence all "representative fragments" of interest, including open reading frames encoding a large variety of *Staphylococcus aureus* proteins.

While the presently disclosed sequences of SEQ ID NOS:1-5,191 are highly accurate, sequencing techniques are not perfect and, in relatively rare instances, further investigation of a fragment or sequence of the invention may reveal a nucleotide sequence error present in a nucleotide sequence disclosed in SEQ ID NOS:1-5,191. However, once the present invention is made available (*i.e.*, once the information in SEQ ID NOS:1-5,191 and Tables 1-3 has been made available), resolving a rare sequencing error in SEQ ID NOS:1-5,191 will be well within the skill of the art. The present disclosure makes available sufficient sequence information to allow any of the described contigs or portions thereof to be obtained readily by straightforward application of routine techniques. Further sequencing of such polynucleotide may proceed in like manner using manual and automated sequencing methods which are employed ubiquitous in the art. Nucleotide sequence editing software is publicly available. For example, Applied Biosystem's (AB) AutoAssembler can be used as an aid during visual inspection of nucleotide sequences. By employing such routine techniques potential errors readily may be identified and the correct sequence then may be ascertained by targeting further sequencing effort, also of a routine nature, to the region containing the potential error.

Even if all of the very rare sequencing errors in SEQ ID NOS:1-5,191 were corrected, the resulting nucleotide sequences would still be at least 95% identical, nearly all would be at least 99% identical, and the great majority would be at least 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-5,191.

As discussed elsewhere hererin, polynucleotides of the present invention readily may be obtained by routine application of well known and standard procedures for cloning and sequencing DNA. Detailed methods for obtaining

libraries and for sequencing are provided below, for instance. A wide variety of *Staphylococcus aureus* strains that can be used to prepare *S aureus* genomic DNA for cloning and for obtaining polynucleotides of the present invention are available to the public from recognized depository institutions, such as the American Type Culture Collection (ATCC®).

The nucleotide sequences of the genomes from different strains of *Staphylococcus aureus* differ somewhat. However, the nucleotide sequences of the genomes of all *Staphylococcus aureus* strains will be at least 95% identical, in corresponding part, to the nucleotide sequences provided in SEQ ID NOS:1-5,191. Nearly all will be at least 99% identical and the great majority will be 99.9% identical.

Thus, the present invention further provides nucleotide sequences which are at least 95%, preferably 99% and most preferably 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-5,191, in a form which can be readily used, analyzed and interpreted by the skilled artisan.

Methods for determining whether a nucleotide sequence is at least 95%, at least 99% or at least 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-5,191 are routine and readily available to the skilled artisan. For example, the well known fasta algorithm described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* **85**: 2444 (1988) can be used to generate the percent identity of nucleotide sequences. The BLASTN program also can be used to generate an identity score of polynucleotides compared to one another.

COMPUTER RELATED EMBODIMENTS

The nucleotide sequences provided in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide sequence of SEQ ID NOS:1-5,191 may be "provided" in a variety of mediums to facilitate use thereof. As used herein, "provided" refers to a manufacture, other than an isolated nucleic acid molecule, which contains a nucleotide sequence of the present invention; *i.e.*, a nucleotide sequence provided in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide of SEQ ID NOS:1-5,191. Such a manufacture provides a large portion of the *Staphylococcus aureus* genome and parts thereof (*e.g.*, a *Staphylococcus aureus* open reading frame (ORF)) in a form which allows a skilled artisan to examine the manufacture using means not directly applicable to examining the *Staphylococcus aureus* genome or a subset thereof as it exists in nature or in purified form.

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories, such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. Likewise, it will be clear to those of skill how additional computer readable media that may be developed also can be used to create analogous manufactures having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data-processor structuring formats (*e.g.*, text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. Thus, by providing in computer readable form the nucleotide sequences of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a sequence of SEQ ID NOS:1-5,191 the present invention enables the skilled artisan routinely to access the provided sequence information for a wide variety of purposes.

The examples which follow demonstrate how software which implements the BLAST (Altschul *et al.*, *J. Mol. Biol.* **215**:403410 (1990)) and BLAZE (Brutlag *et al.*, *Comp. Chem.* **17**:203-207 (1993)) search algorithms on a Sybase system was used to identify open reading frames (ORFs) within the *Staphylococcus aureus* genome which contain homology to ORFs or proteins from both *Staphylococcus aureus* and from other organisms. Among the ORFs discussed

herein are protein encoding fragments of the *Staphylococcus aureus* genome useful in producing commercially important proteins, such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify, among other things, commercially important fragments of the *Staphylococcus aureus* genome.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means.

As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the present genomic sequences which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *Staphylococcus aureus* genomic sequences possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the *Staphylococcus aureus* genome. In the present examples, implementing software which implement the BLAST and BLAZE algorithms, described in Altschul *et al.*, *J. Mol. Biol.* **215**: 403-410 (1990), was used to identify open reading frames within the *Staphylococcus aureus* genome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention. Of course, suitable proprietary systems that may be known to those of skill also may be employed in this regard.

Figure 1 provides a block diagram of a computer system illustrative of embodiments of this aspect of present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard drive 112 and a removable medium storage device 114. The removable medium storage device 114 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, *etc.* A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic tape, *etc.*) containing control logic and/or data recorded therein may be inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the data from the removable medium storage device 114, once it is inserted into the removable medium storage device 114.

A nucleotide sequence of the present invention may be stored in a well known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. During execution, software for

accessing and processing the genomic sequence (such as search tools, comparing tools, etc.) reside in main memory 108, in accordance with the requirements and operating parameters of the operating system, the hardware system and the software program or programs.

BIOCHEMICAL EMBODIMENTS

Other embodiments of the present invention are directed to fragments of the *Staphylococcus aureus* genome, preferably to isolated fragments. The fragments of the *Staphylococcus aureus* genome of the present invention include, but are not limited to fragments which encode peptides, hereinafter open reading frames (ORFs), fragments which modulate the expression of an operably linked ORF, hereinafter expression modulating fragments (EMFs) and fragments which can be used to diagnose the presence of *Staphylococcus aureus* in a sample, hereinafter diagnostic fragments (DFs).

As used herein, an "isolated nucleic acid molecule" or an "isolated fragment of the *Staphylococcus aureus* genome" refers to a nucleic acid molecule possessing a specific nucleotide sequence which has been subjected to purification means to reduce, from the composition, the number of compounds which are normally associated with the composition. Particularly, the term refers to the nucleic acid molecules having the sequences set out in SEQ ID NOS:1-5,191, to representative fragments thereof as described above, to polynucleotides at least 95%, preferably at least 99% and especially preferably at least 99.9% identical in sequence thereto, also as set out above.

A variety of purification means can be used to generated the isolated fragments of the present invention. These include, but are not limited to methods which separate constituents of a solution based on charge, solubility, or size.

In one embodiment, *Staphylococcus aureus* DNA can be mechanically sheared to produce fragments of 15-20 kb in length. These fragments can then be used to generate an *Staphylococcus aureus* library by inserting them into lambda clones as described in the Examples below. Primers flanking, for example, an ORF, such as those enumerated in Tables 1-3 can then be generated using nucleotide sequence information provided in SEQ ID NOS: 1-5,191. Well known and routine techniques of PCR cloning then can be used to isolate the ORF from the lambda DNA library of *Staphylococcus aureus* genomic DNA. Thus, given the availability of SEQ ID NOS:1-5,191, the information in Tables 1, 2 and 3, and the information that may be obtained readily by analysis of the sequences of SEQ ID NOS:1-5,191 using methods set out above, those of skill will be enabled by the present disclosure to isolate any ORF-containing or other nucleic acid fragment of the present invention.

The isolated nucleic acid molecules of the present invention include, but are not limited to single stranded and double stranded DNA, and single stranded RNA.

As used herein, an "open reading frame," ORF, means a series of triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

Tables 1, 2 and 3 list ORFs in the *Staphylococcus aureus* genomic contigs of the present invention that were identified as putative coding regions by the GeneMark software using organism-specific second-order Markov probability transition matrices. It will be appreciated that other criteria can be used, in accordance with well known analytical methods, such as those discussed herein, to generate more inclusive, more restrictive or more selective lists.

Table 1 sets out ORFs in the *Staphylococcus aureus* contigs of the present invention that are at least 80 amino acids long and over a continuous region of at least 50 bases which are 95% or more identical (by BLAST analysis) to an *S. aureus* nucleotide sequence available through Genbank in November 1996.

Table 2 sets out ORFs in the *Staphylococcus aureus* contigs of the present invention that are not in Table 1 and match, with a BLASTP probability score of 0.01 or less, a polypeptide sequence available through Genbank by September 1996.

Table 3 sets out ORFs in the *Staphylococcus aureus* contigs of the present invention that do not match significantly, by BLASTP analysis, a polypeptide sequence available through Genbank by September 1996.

In each table, the first and second columns identify the ORF by, respectively, contig number and ORF number within the contig; the third column indicates the reading frame, taking the first 5' nucleotide of the contig as the start of the +1 frame; the fourth column indicates the first nucleotide of the ORF, counting from the 5' end of the contig strand; and the fifth column indicates the length of each ORF in nucleotides.

In Tables 1 and 2, column six, lists the "Reference" for the closest matching sequence available through Genbank. These reference numbers are the databases entry numbers commonly used by those of skill in the art, who will be familiar with their denominators. Descriptions of the nomenclature are available from the National Center for Biotechnology Information. Column seven in Tables 1 and 2 provides the "gene name" of the matching sequence; column eight provides the BLAST identity score from the comparison of the ORF and the homologous gene; and column nine indicates the length in nucleotides of the highest scoring segment pair identified by the BLAST identity analysis.

In Table 3, the last column, column six, indicates the length of each ORF in amino acid residues.

The concepts of percent identity and percent similarity of two polypeptide sequences is well understood in the art. For example, two polypeptides 10 amino acids in length which differ at three amino acid positions (e.g., at positions

1, 3 and 5) are said to have a percent identity of 70%. However, the same two polypeptides would be deemed to have a percent similarity of 80% if, for example at position 5, the amino acids moieties, although not identical, were "similar" (*i.e.*, possessed similar biochemical characteristics). Many programs for analysis of nucleotide or amino acid sequence similarity, such as fasta and BLAST specifically list per cent identity of a matching region as an output parameter. Thus, for instance, Tables 1 and 2 herein enumerate the per cent identity of the highest scoring segment pair in each ORF and its listed relative. Further details concerning the algorithms and criteria used for homology searches are provided below and are described in the pertinent literature highlighted by the citations provided below.

It will be appreciated that other criteria can be used to generate more inclusive and more exclusive listings of the types set out in the tables. As those of skill will appreciate, narrow and broad searches both are useful. Thus, a skilled artisan can readily identify ORFs in contigs of the *Staphylococcus aureus* genome other than those listed in Tables 1-3, such as ORFs which are overlapping or encoded by the opposite strand of an identified ORF in addition to those ascertainable using the computer-based systems of the present invention.

As used herein, an "expression modulating fragment," EMF, means a series of nucleotide molecules which modulates the expression of an operably linked ORF or EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

EMF sequences can be identified within the contigs of the *Staphylococcus aureus* genome by their proximity to the ORFs provided in Tables 1-3. An intergenic segment, or a fragment of the intergenic segment, from about 10 to 200 nucleotides in length, taken from any one of the ORFs of Tables 1-3 will modulate the expression of an operably linked ORF in a fashion similar to that found with the naturally linked ORF sequence. As used herein, an "intergenic segment" refers to fragments of the *Staphylococcus aureus* genome which are between two ORF(s) herein described. EMFs also can be identified using known EMFs as a target sequence or target motif in the computer-based systems of the present invention. Further, the two methods can be combined and used together.

The presence and activity of an EMF can be confirmed using an EMF trap vector. An EMF trap vector contains a cloning site linked to a marker sequence. A marker sequence encodes an identifiable phenotype, such as antibiotic resistance or a complementing nutrition auxotrophic factor, which can be identified or assayed when the EMF trap vector is placed within an appropriate host under appropriate conditions. As described above, a EMF will modulate the expression of an operably linked marker sequence. A more detailed discussion of various marker sequences is provided below.

A sequence which is suspected as being an EMF is cloned in all three reading frames in one or more restriction sites upstream from the marker sequence in the EMF trap vector. The vector is then transformed into an appropriate host using known procedures and the phenotype of the transformed host is examined under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence.

As used herein, a "diagnostic fragment," DF, means a series of nucleotide molecules which selectively hybridize to *Staphylococcus aureus* sequences. DFs can be readily identified by identifying unique sequences within contigs of the *Staphylococcus aureus* genome, such as by using well-known computer analysis software, and by generating and testing probes or amplification primers consisting of the DF sequence in an appropriate diagnostic format which determines amplification or hybridization selectivity.

The sequences falling within the scope of the present invention are not limited to the specific sequences herein described, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequences provided in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably 99% and most preferably 99.9% identical to SEQ ID NOS:1-5,191, with a sequence from another isolate of the same species.

Furthermore, to accomodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the nucleic acid sequences mentioned above. In other words, in the coding region of an ORF, substitution of one codon for another which encodes the same amino acid is expressly contemplated.

Any specific sequence disclosed herein can be readily screened for errors by resequencing a particular fragment, such as an ORF, in both directions (*i.e.*, sequence both strands). Alternatively, error screening can be performed by sequencing corresponding polynucleotides of *Staphylococcus aureus* origin isolated by using part or all of the fragments in question as a probe or primer.

Each of the ORFs of the *Staphylococcus aureus* genome disclosed in Tables 1, 2 and 3, and the EMFs found 5' to the ORFs, can be used as polynucleotide reagents in numerous ways. For example, the sequences can be used as diagnostic probes or diagnostic amplification primers to detect the presence of a specific microbe in a sample, particular *Staphylococcus aureus*. Especially preferred in this regard are ORF such as those of Table 3, which do not match previously characterized sequences from other organisms and thus are most likely to be highly selective for *Staphylococcus aureus*. Also particularly preferred are ORFs that can be used to distinguish between strains of *Sta-*

phylococcus aureus, particularly those that distinguish medically important strain, such as drug-resistant strains.

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Information from the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides. Polynucleotides suitable for use in these methods are usually 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription, for triple-helix formation, or to the mRNA itself, for antisense inhibition. Both techniques have been demonstrated to be effective in model systems, and the requisite techniques are well known and involve routine procedures. Triple helix techniques are discussed in, for example, Lee *et al.*, *Nucl. Acids Res.* **6**: 3073 (1979); Cooney *et al.*, *Science* **241**: 456 (1988); and Dervan *et al.*, *Science* **251**: 1360 (1991). Antisense techniques in general are discussed in, for instance, Okano, *J. Neurochem.* **56**: 560 (1991) and OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION, CRC Press, Boca Raton, FL (1988)).

The present invention further provides recombinant constructs comprising one or more fragments of the *Staphylococcus aureus* genomic fragments and contigs of the present invention. Certain preferred recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a fragment of the *Staphylococcus aureus* genome has been inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. For vectors comprising the EMFs of the present invention, the vector may further comprise a marker sequence or heterologous ORF operably linked to the EMF.

Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Useful bacterial vectors include phagescript, PsiX174, pBluescript SK and KS (+ and -), pNH8a, pNH16a, pNH18a, pNH46a (available from Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (available from Pharmacia). Useful eukaryotic vectors include pWLneo, pSV2cat, pOG44, pXT1, pSG (available from Stratagene), pSVK3, pBPV, pMSG, pSVL (available from Pharmacia).

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

The present invention further provides host cells containing any one of the isolated fragments of the *Staphylococcus aureus* genomic fragments and contigs of the present invention, wherein the fragment has been introduced into the host cell using known methods. The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or a procaryotic cell, such as a bacterial cell.

A polynucleotide of the present invention, such as a recombinant construct comprising an ORF of the present invention, may be introduced into the host by a variety of well established techniques that are standard in the art, such as calcium phosphate transfection, DEAE, dextran mediated transfection and electroporation, which are described in, for instance, Davis, L. *et al.*, BASIC METHODS IN MOLECULAR BIOLOGY (1986).

A host cell containing one of the fragments of the *Staphylococcus aureus* genomic fragments and contigs of the present invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the Genetic Code, encode an identical polypeptide sequence.

Preferred nucleic acid fragments of the present invention are the ORFs depicted in Tables 2 and 3 which encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. This is particularly useful in producing small peptides and fragments of larger polypeptides. Such short fragments as may be obtained most readily by synthesis are useful, for example, in generating antibodies against the native polypeptide, as discussed further below.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily employ well-known methods for isolating polypeptides and proteins to isolate and purify polypeptides or proteins of the present invention produced naturally by a bacterial strain, or by other methods. Methods for isolation and purification that can be employed in this regard include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immu-

no-affinity chromatography.

The polypeptides and proteins of the present invention also can be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. Those skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, CV-1 cell, COS cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or, which expresses the polypeptide or protein at low natural level.

"Recombinant," as used herein, means that a polypeptide or protein is derived from recombinant (e.g., microbial or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern different from that expressed in mammalian cells.

"Nucleotide sequence" refers to a heteropolymer of deoxyribonucleotides. Generally, DNA segments encoding the polypeptides and proteins provided by this invention are assembled from fragments of the *Staphylococcus aureus* genome and short oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic gene which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon.

"Recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. The expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic regulatory elements necessary for gene expression in the host, including elements required to initiate and maintain transcription at a level sufficient for suitable expression of the desired polypeptide, including, for example, promoters and, where necessary, an enhancers and a polyadenylation signal; (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate signals to initiate translation at the beginning of the desired coding region and terminate translation at its end. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an N-terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

"Recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extra chromosomally. The cells can be prokaryotic or eukaryotic. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed.

Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described in Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL, 2nd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference in its entirety.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), alpha-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and, when desirable, provide amplification within the host.

Suitable prokaryotic hosts for transformation include strains of *Staphylococcus aureus*, *E. coli*, *B. subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*. Others

may, also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (available from Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (available from Promega Biotec, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter, where it is inducible, is derepressed or induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period to provide for expression of the induced gene product. Thereafter cells are typically harvested, generally by centrifugation, disrupted to release expressed protein, generally by physical or chemical means, and the resulting crude extract is retained for further purification.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described in Gluzman, *Cell* 23: 175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines.

Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Recombinant polypeptides and proteins produced in bacterial culture is usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

An additional aspect of the invention includes *Staphylococcus aureus* polypeptides which are useful as immuno-diagnostic antigens and/or immunoprotective vaccines, collectively "immunologically useful polypeptides". Such immunologically useful polypeptides may be selected from the ORFs disclosed herein based on techniques well known in the art and described elsewhere herein. The inventors have used the following criteria to select several immunologically useful polypeptides:

As is known in the art, an amino terminal type I signal sequence directs a nascent protein across the plasma and outer membranes to the exterior of the bacterial cell. Such outer membrane polypeptides are expected to be immunologically useful. According to Izard, J. W. et al., *Mol. Microbiol.* 13, 765-773; (1994), polypeptides containing type I signal sequences contain the following physical attributes: The length of the type I signal sequence is approximately 15 to 25 primarily hydrophobic amino acid residues with a net positive charge in the extreme amino terminus; the central region of the signal sequence must adopt an alpha-helical conformation in a hydrophobic environment; and the region surrounding the actual site of cleavage is ideally six residues long, with small side-chain amino acids in the -1 and -3 positions.

Also known in the art is the type IV signal sequence which is an example of the several types of functional signal sequences which exist in addition to the type I signal sequence detailed above. Although functionally related, the type IV signal sequence possesses a unique set of biochemical and physical attributes (Strom, M. S. and Lory, S., *J. Bacteriol.* 174, 7345-7351; 1992). These are typically six to eight amino acids with a net basic charge followed by an additional sixteen to thirty primarily hydrophobic residues. The cleavage site of a type IV signal sequence is typically after the initial six to eight amino acids at the extreme amino terminus. In addition, all type IV signal sequences contain a phenylalanine residue at the +1 site relative to the cleavage site.

Studies of the cleavage sites of twenty-six bacterial lipoprotein precursors has allowed the definition of a consensus amino acid sequence for lipoprotein cleavage. Nearly three-fourths of the bacterial lipoprotein precursors examined contained the sequence L-(A,S)-(G,A)-C at positions -3 to +1, relative to the point of cleavage (Hayashi, S. and Wu, H. C. *Lipoproteins in bacteria*. *J. Bioenerg. Biomembr.* 22, 451-471; 1990).

It well known that most anchored proteins found on the surface of gram-positive bacteria possess a highly conserved carboxy terminal sequence. More than fifty such proteins from organisms such as *S. pyogenes*, *S. mutans*, *E. faecalis*, *S. pneumoniae*, and others, have been identified based on their extracellular location and carboxy terminal amino acid sequence (Fischetti, V. A. *Gram-positive commensal bacteria deliver antigens to elicit mucosal and systemic immunity*. *ASM News* 62, 405410; 1996). The conserved region is comprised of six charged amino acids at the extreme carboxy terminus coupled to 15-20 hydrophobic amino acids presumed to function as a transmembrane domain. Immediately adjacent to the transmembrane domain is a six amino acid sequence conserved in nearly all proteins ex-

aminated. The amino acid sequence of this region is L-P-X-T-G-X, where X is any amino acid.

Amino acid sequence similarities to proteins of known function by BLAST enables the assignment of putative functions to novel amino acid sequences and allows for the selection of proteins thought to function outside the cell wall. Such proteins are well known in the art and include "lipoprotein", "periplasmic", or "antigen".

An algorithm for selecting antigenic and immunogenic *Staphylococcus aureus* polypeptides including the foregoing criteria was developed by the present inventors. Use of the algorithm by the inventors to select immunologically useful *Staphylococcus aureus* polypeptides resulted in the selection of several ORFs which are predicted to be outer-membrane-associated proteins. These proteins are identified in Table 4, below, and shown in the Sequence Listing as SEQ ID NOS:5,192 to 5,255. Thus the amino acid sequence of each of several antigenic *Staphylococcus aureus* polypeptides listed in Table 4 can be determined, for example, by locating the amino acid sequence of the ORF in the Sequence Listing. Likewise the polynucleotide sequence encoding each ORF can be found by locating the corresponding polynucleotide SEQ ID in Tables 1, 2, or 3, and finding the corresponding nucleotide sequence in the sequence listing.

As will be appreciated by those of ordinary skill in the art, although a polypeptide representing an entire ORF may be the closest approximation to a protein found *in vivo*, it is not always technically practical to express a complete ORF *in vitro*. It may be very challenging to express and purify a highly hydrophobic protein by common laboratory methods. As a result, the immunologically useful polypeptides described herein as SEQ ID NOS:5,192-5,255 may have been modified slightly to simplify the production of recombinant protein, and are the preferred embodiments. In general, nucleotide sequences which encode highly hydrophobic domains, such as those found at the amino terminal signal sequence, are excluded for enhanced *in vitro* expression of the polypeptides. Furthermore, any highly hydrophobic amino acid sequences occurring at the carboxy terminus are also excluded. Such truncated polypeptides include for example the mature forms of the polypeptides expected to exist in nature.

Those of ordinary skill in the art can identify soluble portions the polypeptide identified in Table 4, and in the case of truncated polypeptides sequences shown as SEQ ID NOS:5,192-5,255, may obtain the complete predicted amino acid sequence of each polypeptide by translating the corresponding polynucleotides sequences of the corresponding ORF listed in Tables 1, 2 and 3 and found in the sequence listing.

Accordingly, polypeptides comprising the complete amino acid of an immunologically useful polypeptide selected from the group of polypeptides encoded by the ORFs identified in Table 4, or an amino acid sequence at least 95% identical thereto, preferably at least 97% identical thereto, and most preferably at least 99% identical thereto form an embodiment of the invention; in addition polypeptides comprising an amino acid sequence selected from the group of amino acid sequences shown in the sequence listing as SEQ ID NOS:5,191-5,255, or an amino acid sequence at least 95% identical thereto, preferably at least 97% identical thereto and most preferably at least 99% identical thereto, form an embodiment of the invention. Polynucleotides encoding the foregoing polypeptides also form part of the present invention.

In another aspect, the invention provides a peptide or polypeptide comprising an epitope-bearing portion of a polypeptide of the invention, particularly those epitope-bearing portions (antigenic regions) identified in Table 4. The epitope-bearing portion is an immunogenic or antigenic epitope of a polypeptide of the invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein is the immunogen. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998-4002 (1983).

As to the selection of peptides or polypeptides bearing an antigenic epitope (i.e., that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, for instance, Sutcliffe, J. G., Shinnick, T. M., Green, N. and Leamer, R. A. (1983) "Antibodies that react with predetermined sites on proteins", Science, 219:660-666. Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (i.e., immunogenic epitopes) nor to the amino or carboxyl terminals. Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide of the invention. See, for instance, Wilson et al., Cell 37:767-778 (1984) at 777.

Antigenic epitope-bearing peptides and polypeptides of the invention preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 15 to about 30 amino acids contained within the amino acid sequence of a polypeptide of the invention. Non-limiting examples of antigenic polypeptides or peptides that can be used to generate *S. aureus* specific antibodies include: a polypeptide comprising peptides shown in Table 4 below. These polypeptide fragments have been determined to bear antigenic epitopes of indicated *S. aureus* proteins by the analysis of the Jameson-Wolf antigenic index, a representative sample of which is shown in Figure 3.

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means. See, e.g., Houghten, R. A. (1985) General method for the rapid solid-phase synthesis of large numbers of peptides:

specificity of antigen-antibody interaction at the level of individual amino acids. Proc. Natl. Acad. Sci. USA 82: 5131-5135; this "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No. 4,631,211 to Houghten et al. (1986). Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies according to methods well known in the art. See, for instance, Sutcliffe et al., supra; Wilson et al., supra;

Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et al., J. Gen. Virol. 66:2347-2354 (1985). Immunogenic epitope-bearing peptides of the invention, i.e., those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. See, for instance; Geysen et al., supra. Further still, U.S. Patent No. 5,194,392 to Geysen (1990) describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (i.e., a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092 to Geysen (1989) describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971 to Houghten, R. A. et al. (1996) on Per-alkylated Oligopeptide Mixtures discloses linear C1-C7-alkyl peralkylated oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and libraries for determining the sequence of a per-alkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods.

Table 4 lists immunologically useful polypeptides identified by an algorithm which locates novel *Staphylococcus aureus* outer membrane proteins, as is described above. Also listed are epitopes or "antigenic regions" of each of the identified polypeptides. The antigenic regions, or epitopes, are delineated by two numbers x-y, where x is the number of the first amino acid in the open reading frame included within the epitope and y is the number of the last amino acid in the open reading frame included within the epitope. For example, the first epitope in ORF 168-6 is comprised of amino acids 36 to 45 of SEQ ID NO:5,192, as is described in Table 4. The inventors have identified several epitopes for each of the antigenic polypeptides identified in Table 4. Accordingly, forming part of the present invention are polypeptides comprising an amino acid sequence of one or more antigenic regions identified in Table 4. The invention further provides polynucleotides encoding such polypeptides.

The present invention further includes isolated polypeptides, proteins and nucleic acid molecules which are substantially equivalent to those herein described. As used herein, substantially equivalent can refer both to nucleic acid and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between reference and subject sequences. For purposes of the present invention, sequences having equivalent biological activity, and equivalent expression characteristics are considered substantially equivalent. For purposes of determining equivalence, truncation of the mature sequence should be disregarded.

The invention further provides methods of obtaining homologs from other strains of *Staphylococcus aureus*, of the fragments of the *Staphylococcus aureus* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. As used herein, a sequence or protein of *Staphylococcus aureus* is defined as a homolog of a fragment of the *Staphylococcus aureus* fragments or contigs or a protein encoded by one of the ORFs of the present invention, if it shares significant homology to one of the fragments of the *Staphylococcus aureus* genome of the present invention or a protein encoded by one of the ORFs of the present invention. Specifically, by using the sequence disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

As used herein, two nucleic acid molecules or proteins are said to "share significant homology" if the two contain regions which possess greater than 85% sequence (amino acid or nucleic acid) homology. Preferred homologs in this regard are those with more than 90% homology. Especially preferred are those with 93% or more homology. Among especially preferred homologs those with 95% or more homology are particularly preferred. Very particularly preferred among these are those with 97% and even more particularly preferred among these are homologs with 99% or more homology. The most preferred homologs among these are those with 99.9% homology or more. It will be understood that, among measures of homology, identity is particularly preferred in this regard.

Region specific primers or probes derived from the nucleotide sequence provided in SEQ ID NOS:1-5,191 or from a nucleotide sequence at least 95%, particularly at least 99%, especially at least 99.5% identical to a sequence of SEQ ID NOS:1-5,191 can be used to prime DNA synthesis and PCR amplification, as well as to identify colonies containing cloned DNA encoding a homolog. Methods suitable to this aspect of the present invention are well known and have been described in great detail in many publications such as, for example, Innis et al., PCR PROTOCOLS, Academic Press, San Diego, CA (1990)).

When using primers derived from SEQ ID NOS:1-5,191 or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS:1-5,191, one skilled in the art will recognize that by employing high stringency conditions (e.g., annealing at 50-60°C in 6X SSPE and 50% formamide, and washing at 50-65°C in 0.5X SSPE) only sequences which are greater than 75% homologous to the primer will be amplified. By employing lower stringency

conditions (e.g., hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences which are greater than 40-50% homologous to the primer will also be amplified.

When using DNA probes derived from SEQ ID NOS:1-5,191, or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS:1-5,191, for colony/plaque hybridization, one skilled in the art will recognize that by employing high stringency conditions (e.g., hybridizing at 50-65°C in 5X SSPC and 50% formamide, and washing at 50-65°C in 0.5X SSPC), sequences having regions which are greater than 90% homologous to the probe can be obtained, and that by employing lower stringency conditions (e.g., hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences having regions which are greater than 35-45% homologous to the probe will be obtained.

Any organism can be used as the source for homologs of the present invention so long as the organism naturally expresses such a protein or contains genes encoding the same. The most preferred organism for isolating homologs are bacteria which are closely related to *Staphylococcus aureus*.

ILLUSTRATIVE USES OF COMPOSITIONS OF THE INVENTION

Each ORF provided in Tables 1 and 2 is identified with a function by homology to a known gene or polypeptide. As a result, one skilled in the art can use the polypeptides of the present invention for commercial, therapeutic and industrial purposes consistent with the type of putative identification of the polypeptide. Such identifications permit one skilled in the art to use the *Staphylococcus aureus* ORFs in a manner similar to the known type of sequences for which the identification is made; for example, to ferment a particular sugar source or to produce a particular metabolite. A variety of reviews illustrative of this aspect of the invention are available, including the following reviews on the industrial use of enzymes, for example, BIOCHEMICAL ENGINEERING AND BIOTECHNOLOGY HANDBOOK, 2nd Ed., Macmillan Publications, Ltd. NY (1991) and BIOCATALYSTS IN ORGANIC SYNTHESIS, Tramper *et al.*, Eds., Elsevier Science Publishers, Amsterdam, The Netherlands (1985). A variety of exemplary uses that illustrate this and similar aspects of the present invention are discussed below.

1. Biosynthetic Enzymes

Open reading frames encoding proteins involved in mediating the catalytic reactions involved in intermediary and macromolecular metabolism, the biosynthesis of small molecules, cellular processes and other functions includes enzymes involved in the degradation of the intermediary products of metabolism, enzymes involved in central intermediary metabolism, enzymes involved in respiration, both aerobic and anaerobic, enzymes involved in fermentation, enzymes involved in ATP proton motor force conversion, enzymes involved in broad regulatory function, enzymes involved in amino acid synthesis, enzymes involved in nucleotide synthesis, enzymes involved in cofactor and vitamin synthesis, can be used for industrial biosynthesis.

The various metabolic pathways present in *Staphylococcus aureus* can be identified based on absolute nutritional requirements as well as by examining the various enzymes identified in Table 1-3 and SEQ ID NOS:1-5,191.

Of particular interest are polypeptides involved in the degradation of intermediary metabolites as well as non-macromolecular metabolism. Such enzymes include amylases, glucose oxidases, and catalase.

Proteolytic enzymes are another class of commercially important enzymes. Proteolytic enzymes find use in a number of industrial processes including the processing of flax and other vegetable fibers, in the extraction, clarification and depectinization of fruit juices, in the extraction of vegetables' oil and in the maceration of fruits and vegetables to give unicellular fruits. A detailed review of the proteolytic enzymes used in the food industry is provided in Rombouts *et al.*, *Symbiosis* 21: 79 (1986) and Voragen *et al.* in BIOCATALYSTS IN AGRICULTURAL BIOTECHNOLOGY, Whitaker *et al.*, Eds., American Chemical Society Symposium Series 389: 93 (1989).

The metabolism of sugars is an important aspect of the primary metabolism of *Staphylococcus aureus*. Enzymes involved in the degradation of sugars, such as, particularly, glucose, galactose, fructose and xylose, can be used in industrial fermentation. Some of the important sugar transforming enzymes, from a commercial viewpoint, include sugar isomerases such as glucose isomerase. Other metabolic enzymes have found commercial use such as glucose oxidases which produces ketogulonic acid (KGA). KGA is an intermediate in the commercial production of ascorbic acid using the Reichstein's procedure, as described in Krueger *et al.*, *Biotechnology* 6(A), Rhine *et al.*, Eds., Verlag Press, Weinheim, Germany (1984).

Glucose oxidase (GOD) is commercially available and has been used in purified form as well as in an immobilized form for the deoxygenation of beer. See, for instance, Hartmeir *et al.*, *Biotechnology Letters* 1: 21 (1979). The most important application of GOD is the industrial scale fermentation of gluconic acid. Market for gluconic acids which are used in the detergent, textile, leather, photographic, pharmaceutical, food, feed and concrete industry, as described, for example, in Bigelis *et al.*, beginning on page 357 in GENE MANIPULATIONS AND FUNGI; Benett *et al.*, Eds., Academic Press, New York (1985). In addition to industrial applications, GOD has found applications in medicine for

quantitative determination of glucose in body fluids recently in biotechnology for analyzing syrups from starch and cellulose hydrosylates. This application is described in Owusu *et al.*, *Biochem. et Biophysica. Acta.* 872: 83 (1986), for instance.

The main sweetener used in the world today is sugar which comes from sugar beets and sugar cane. In the field of industrial enzymes, the glucose isomerase process shows the largest expansion in the market today. Initially, soluble enzymes were used and later immobilized enzymes were developed (Krueger *et al.*, *Biotechnology, The Textbook of Industrial Microbiology*, Sinauer Associated Incorporated, Sunderland, Massachusetts (1990)). Today, the use of glucose- produced high fructose syrups is by far the largest industrial business using immobilized enzymes. A review of the industrial use of these enzymes is provided by Jorgensen, *Starch* 40:307 (1988).

Proteinases, such as alkaline serine proteinases, are used as detergent additives and thus represent one of the largest volumes of microbial enzymes used in the industrial sector. Because of their industrial importance, there is a large body of published and unpublished information regarding the use of these enzymes in industrial processes. (See Faultman *et al.*, *Acid Proteases Structure Function and Biology*, Tang, J., ed., Plenum Press, New York (1977) and Godfrey *et al.*, *Industrial Enzymes*, MacMillan Publishers, Surrey, UK (1983) and Hepner *et al.*, *Report Industrial Enzymes by 1990*, Hel Hepner & Associates, London (1986)).

Another class of commercially usable proteins of the present invention are the microbial lipases, described by, for instance, Macrae *et al.*, *Philosophical Transactions of the Chiral Society of London* 310:227 (1985) and Poserke, *Journal of the American Oil Chemist Society* 61:1758 (1984). A major use of lipases is in the fat and oil industry for the production of neutral glycerides using lipase catalyzed inter-esterification of readily available triglycerides. Application of lipases include the use as a detergent additive to facilitate the removal of fats from fabrics in the course of the washing procedures.

The use of enzymes, and in particular microbial enzymes, as catalyst for key steps in the synthesis of complex organic molecules is gaining popularity at a great rate. One area of great interest is the preparation of chiral intermediates. Preparation of chiral intermediates is of interest to a wide range of synthetic chemists particularly those scientists involved with the preparation of new pharmaceuticals, agrochemicals, fragrances and flavors. (See Davies *et al.*, *Recent Advances in the Generation of Chiral Intermediates Using Enzymes*, CRC Press, Boca Raton, Florida (1990)). The following reactions catalyzed by enzymes are of interest to organic chemists: hydrolysis of carboxylic acid esters, phosphate esters, amides and nitriles, esterification reactions, trans-esterification reactions, synthesis of amides, reduction of alkanones and oxoalkanates, oxidation of alcohols to carbonyl compounds, oxidation of sulfides to sulfoxides, and carbon bond forming reactions such as the aldol reaction.

When considering the use of an enzyme encoded by one of the ORFs of the present invention for biotransformation and organic synthesis it is sometimes necessary to consider the respective advantages and disadvantages of using a microorganism as opposed to an isolated enzyme. Pros and cons of using a whole cell system on the one hand or an isolated partially purified enzyme on the other hand, has been described in detail by Bud *et al.*, *Chemistry in Britain* (1987), p. 127.

Amino transferases, enzymes involved in the biosynthesis and metabolism of amino acids, are useful in the catalytic production of amino acids. The advantages of using microbial based enzyme systems is that the amino transferase enzymes catalyze the stereo- selective synthesis of only L-amino acids and generally possess uniformly high catalytic rates. A description of the use of amino transferases for amino acid production is provided by Roselle-David, *Methods of Enzymology* 136:479 (1987).

Another category of useful proteins encoded by the ORFs of the present invention include enzymes involved in nucleic acid synthesis, repair, and recombination. A variety of commercially important enzymes have previously been isolated from members of *Staphylococcus aureus*. These include Sau3A and Sau96I.

2. Generation of Antibodies

As described here, the proteins of the present invention, as well as homologs thereof, can be used in a variety of procedures and methods known in the art which are currently applied to other proteins. The proteins of the present invention can further be used to generate an antibody which selectively binds the protein. Such antibodies can be either monoclonal or polyclonal antibodies, as well fragments of these antibodies, and humanized forms.

The invention further provides antibodies which selectively bind to one of the proteins of the present invention and hybridomas which produce these antibodies. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A. M., *MONOCLONAL ANTIBODY TECHNOLOGY: LABORATORY TECHNIQUES IN BIOCHEMISTRY AND MOLECULAR BIOLOGY*, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth *et al.*, *J. Immunol. Methods* 35: 1-21 (1980), Kohler and Milstein, *Nature* 256: 495-497 (1975)), the trioma technique, the human B- cell hybridoma technique (Kozbor *et al.*, *Immunology Today*

4: 72 (1983), pgs. 77-96 of Cole *et al.*, in MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc. (1985)).

Any animal (mouse, rabbit, *etc.*) which is known to produce antibodies can be immunized with the pseudogene polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or interperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of the protein encoded by the ORF of the present invention used for immunization will vary based on the animal which is immunized, the antigenicity of the peptide and the site of injection.

The protein which is used as an immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to coupling the antigen with a heterologous protein (such as globulin or galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/O-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells.

Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, *Exp. Cell Res.* 175: 109-124 (1988)).

Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using procedures known in the art (Campbell, A. M., *Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1984)).

Techniques described for the production of single chain antibodies (U. S. Patent 4,946,778) can be adapted to produce single chain antibodies to proteins of the present invention.

For polyclonal antibodies, antibody containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures.

The present invention further provides the above-described antibodies in detectably labelled form. Antibodies can be detectably labelled through the use of radioisotopes, affinity labels (such as biotin, avidin, *etc.*), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase, *etc.*) fluorescent labels (such as FITC or rhodamine, *etc.*), paramagnetic atoms, *etc.* Procedures for accomplishing such labelling are well-known in the art, for example see Sternberger *et al.*, *J. Histochem. Cytochem.* 18:315 (1970); Bayer, E. A. *et al.*, *Meth. Enzym.* 62:308 (1979); Engval, E. *et al.*, *Immunol.* 109:129 (1972); Goding, J. W. J. *Immunol. Meth.* 13:215 (1976)).

The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and in situ assays to identify cells or tissues in which a fragment of the *Staphylococcus aureus* genome is expressed.

The present invention further provides the above-described antibodies immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir, D. M. *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby, W. D. *et al.*, *Meth. Enzym.* 34 Academic Press, N. Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and in situ assays as well as for immunoaffinity purification of the proteins of the present invention.

3. Diagnostic Assays and Kits

The present invention further provides methods to identify the expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using one of the DFs, antigens or antibodies of the present invention.

In detail, such methods comprise incubating a test sample with one or more of the antibodies, or one or more of the DFs, or one or more antigens of the present invention and assaying for binding of the DFs, antigens or antibodies to components within the test sample.

Conditions for incubating a DF, antigen or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the DF or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the DFs, antigens or antibodies of the present invention. Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G. R. *et al.*, *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry*, PCT publication WO95/32291, and *Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985), all of which are hereby incorporated herein by reference.

The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based

on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the Dfs, antigens or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound DF, antigen or antibody.

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody, antigen or DF.

Types of detection reagents include labelled nucleic acid probes, labelled secondary antibodies, or in the alternative, if the primary antibody is labelled, the enzymatic, or antibody binding reagents which are capable of reacting with the labelled antibody. One skilled in the art will readily recognize that the disclosed Dfs, antigens and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4. Screening Assay for Binding Agents

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents which bind to a protein encoded by one of the ORFs of the present invention or to one of the fragments and the *Staphylococcus aureus* fragment and contigs herein described.

In general, such methods comprise steps of:

- (a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention, or an isolated fragment of the *Staphylococcus aureus* genome; and
- (b) determining whether the agent binds to said protein or said fragment.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention.

Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides, for example see Hurby *et al.*, Application of Synthetic Peptides: Antisense Peptides, "In Synthetic Peptides, A User's Guide, W. H. Freeman, NY (1992), pp. 289-307, and Kaspiczak *et al.*, Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control.

One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods usually contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, Nucl. Acids Res. 6:3073 (1979); Cooney *et al.*, Science 241:456 (1988); and Dervan *et al.*, Science 251: 1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated

to be effective in model systems. Information contained in the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides, and other DNA binding agents.

5. Pharmaceutical Compositions and Vaccine

The present invention further provides pharmaceutical agents which can be used to modulate the growth or pathogenicity of *Staphylococcus aureus*, or another related organism, *in vivo* or *in vitro*. As used herein, a "pharmaceutical agent" is defined as a composition of matter which can be formulated using known techniques to provide a pharmaceutical compositions. As used herein, the "pharmaceutical agents of the present invention" refers the pharmaceutical agents which are derived from the proteins encoded by the ORFs of the present invention or are agents which are identified using the herein described assays.

As used herein, a pharmaceutical agent is said to "modulate the growth or pathogenicity of *Staphylococcus aureus* or a related organism, *in vivo* or *in vitro*," when the agent reduces the rate of growth, rate of division, or viability of the organism in question. The pharmaceutical agents of the present invention can modulate the growth or pathogenicity of an organism in many fashions, although an understanding of the underlying mechanism of action is not needed to practice the use of the pharmaceutical agents of the present invention. Some agents will modulate the growth or pathogenicity by binding to an important protein thus blocking the biological activity of the protein, while other agents may bind to a component of the outer surface of the organism blocking attachment or rendering the organism more prone to act the bodies nature immune system. Alternatively, the agent may comprise a protein encoded by one of the ORFs of the present invention and serve as a vaccine. The development and use of vaccines derived from membrane associated polypeptides are well known in the art. The inventors have identified particularly preferred immunogenic *Staphylococcus aureus* polypeptides for use as vaccines. Such immunogenic polypeptides are described above and summarized in Table 4, below.

As used herein, a "related organism" is a broad term which refers to any organism whose growth or pathogenicity can be modulated by one of the pharmaceutical agents of the present invention. In general, such an organism will contain a homolog of the protein which is the target of the pharmaceutical agent or the protein used as a vaccine. As such, related organisms do not need to be bacterial but may be fungal or viral pathogens.

The pharmaceutical agents and compositions of the present invention may be administered in a convenient manner, such as by the oral, topical, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes. The pharmaceutical compositions are administered in an amount which is effective for treating and/or prophylaxis of the specific indication. In general, they are administered in an amount of at least about 1 mg/kg body weight and in most cases they will be administered in an amount not in excess of about 1 g/kg body weight per day. In most cases, the dosage is from about 0.1 mg/kg to about 10 g/kg body weight daily, taking into account the routes of administration, symptoms, etc.

The agents of the present invention can be used in native form or can be modified to form a chemical derivative. As used herein, a molecule is said to be a "chemical derivative" of another molecule when it contains additional chemical moieties not normally a part of the molecule. Such moieties may improve the molecule's solubility, absorption, biological half life, etc. The moieties may alternatively decrease the toxicity of the molecule, eliminate or attenuate any undesirable side effect of the molecule, etc. Moieties capable of mediating such effects are disclosed in, among other sources, REMINGTON'S PHARMACEUTICAL SCIENCES (1980) cited elsewhere herein.

For example, such moieties may change an immunological character of the functional derivative, such as affinity for a given antibody. Such changes in immunomodulation activity are measured by the appropriate assay, such as a competitive type immunoassay. Modifications of such protein properties as redox or thermal stability, biological half-life, hydrophobicity, susceptibility to proteolytic degradation or the tendency to aggregate with carriers or into multimers also may be effected in this way and can be assayed by methods well known to the skilled artisan.

The therapeutic effects of the agents of the present invention may be obtained by providing the agent to a patient by any suitable means (e.g., inhalation, intravenously, intramuscularly, subcutaneously, enterally, or parenterally). It is preferred to administer the agent of the present invention so as to achieve an effective concentration within the blood or tissue in which the growth of the organism is to be controlled. To achieve an effective blood concentration, the preferred method is to administer the agent by injection. The administration may be by continuous infusion, or by single or multiple injections.

In providing a patient with one of the agents of the present invention, the dosage of the administered agent will vary depending upon such factors as the patient's age, weight, height, sex, general medical condition, previous medical history, etc. In general, it is desirable to provide the recipient with a dosage of agent which is in the range of from about 1 pg/kg to 10 mg/kg (body weight of patient), although a lower or higher dosage may be administered. The therapeutically effective dose can be lowered by using combinations of the agents of the present invention or another agent.

As used herein, two or more compounds or agents are said to be administered "in combination" with each other when either (1) the physiological effects of each compound, or (2) the serum concentrations of each compound can

be measured at the same time. The composition of the present invention can be administered concurrently with, prior to, or following the administration of the other agent.

The agents of the present invention are intended to be provided to recipient subjects in an amount sufficient to decrease the rate of growth (as defined above) of the target organism.

The administration of the agent(s) of the invention may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the agent(s) are provided in advance of any symptoms indicative of the organisms growth. The prophylactic administration of the agent(s) serves to prevent, attenuate, or decrease the rate of onset of any subsequent infection. When provided therapeutically, the agent(s) are provided at (or shortly after) the onset of an indication of infection. The therapeutic administration of the compound(s) serves to attenuate the pathological symptoms of the infection and to increase the rate of recovery.

The agents of the present invention are administered to a subject, such as a mammal, or a patient, in a pharmaceutically acceptable form and in a therapeutically effective concentration. A composition is said to be "pharmacologically acceptable" if its administration can be tolerated by a recipient patient. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

The agents of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby these materials, or their functional derivatives, are combined in admixture with a pharmaceutically acceptable carrier vehicle. Suitable vehicles and their formulation, inclusive of other human proteins, e. g., human serum albumin, are described, for example, in REMINGTON'S PHARMACEUTICAL SCIENCES, 16th Ed., Osol, A., Ed., Mack Publishing, Easton PA (1980). In order to form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of one or more of the agents of the present invention, together with a suitable amount of carrier vehicle.

Additional pharmaceutical methods may be employed to control the duration of action. Control release preparations may be achieved through the use of polymers to complex or absorb one or more of the agents of the present invention. The controlled delivery may be effectuated by a variety of well known techniques, including formulation with macromolecules such as, for example, polyesters, polyamino acids, polyvinyl, pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, or protamine, sulfate, adjusting the concentration of the macromolecules and the agent in the formulation, and by appropriate use of methods of incorporation, which can be manipulated to effectuate a desired time course of release. Another possible method to control the duration of action by controlled release preparations is to incorporate agents of the present invention into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization with, for example, hydroxymethylcellulose or gelatine-microcapsules and poly(methylmethacrylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions. Such techniques are disclosed in REMINGTON'S PHARMACEUTICAL SCIENCES (1980).

The invention further provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

In addition, the agents of the present invention may be employed in conjunction with other therapeutic compounds.

6. Shot-Gun Approach to Megabase DNA Sequencing

The present invention further demonstrates that a large sequence can be sequenced using a random shotgun approach. This procedure, described in detail in the examples that follow, has eliminated the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols.

Certain aspects of the present invention are described in greater detail in the examples that follow. The examples are provided by way of illustration. Other aspects and embodiments of the present invention are contemplated by the inventors, as will be clear to those of skill in the art from reading the present disclosure.

ILLUSTRATIVE EXAMPLES

LIBRARIES AND SEQUENCING

1. Shotgun Sequencing Probability Analysis

The overall strategy for a shotgun approach to whole genome sequencing follows from the Lander and Waterman (Landerman and Waterman, *Genomics* 2: 231 (1988)) application of the equation for the Poisson distribution. According to this treatment, the probability, P_0 , that any given base in a sequence of size L , in nucleotides, is not sequenced after a certain amount, n , in nucleotides, of random sequence has been determined can be calculated by the equation $P_0 = e^{-m}$, where m is L/n , the fold coverage." For instance, for a genome of 2.8 Mb, $m=1$ when 2.8 Mb of sequence has been randomly generated (1X coverage). At that point, $P_0 = e^{-1} = 0.37$. The probability that any given base has not been sequenced is the same as the probability that any region of the whole sequence L has not been determined and, therefore, is equivalent to the fraction of the whole sequence that has yet to be determined. Thus, at one-fold coverage, approximately 37% of a polynucleotide of size L , in nucleotides has not been sequenced. When 14 Mb of sequence has been generated, coverage is 5X for a 2.8 Mb and the unsequenced fraction drops to .0067 or 0.67%. 5X coverage of a 2.8 Mb sequence can be attained by sequencing approximately 17,000 random clones from both insert ends with an average sequence read length of 410 bp.

Similarly, the total gap length, G , is determined by the equation $G = Le^{-m}$, and the average gap size, g , follows the equation, $g = L/n$. Thus, 5X coverage leaves about 240 gaps averaging about 82 bp in size in a sequence of a polynucleotide 2.8 Mb long.

The treatment above is essentially that of Lander and Waterman, *Genomics* 2: 231 (1988).

2. Random Library Construction

In order to approximate the random model described above during actual sequencing, a nearly ideal library of cloned genomic fragments is required. The following library construction procedure was developed to achieve this end.

Staphylococcus aureus DNA was prepared by phenol extraction. A mixture containing 600 ug DNA in 3.3 ml of 300 mM sodium acetate, 10 mM Tris-HCl, 1 mM Na-EDTA, 30% glycerol was sonicated for 1 min. at 0°C in a Branson Model 450 Sonicator at the lowest energy setting using a 3 mm probe. The sonicated DNA was ethanol precipitated and redissolved in 500 ul TE buffer.

To create blunt-ends, a 100 ul aliquot of the resuspended DNA was digested with 5 units of BAL31 nuclease (New England BioLabs) for 10 min at 30°C in 200 ul BAL31 buffer. The digested DNA was phenol-extracted, ethanol-precipitated, redissolved in 100 ul TE buffer, and then size-fractionated by electrophoresis through a 1.0% low melting temperature agarose gel. The section containing DNA fragments 1.6-2.0 kb in size was excised from the gel, and the LGT agarose was melted and the resulting solution was extracted with phenol to separate the agarose from the DNA. DNA was ethanol precipitated and redissolved in 20 ul of TE buffer for ligation to vector.

A two-step ligation procedure was used to produce a plasmid library with 97% inserts, of which >99% were single inserts. The first ligation mixture (50 ul) contained 2 ug of DNA fragments, 2 ug pUC18 DNA (Pharmacia) cut with SmaI and dephosphorylated with bacterial alkaline phosphatase, and 10 units of T4 ligase (GIBCO/BRL) and was incubated at 14°C for 4 hr. The ligation mixture then was phenol extracted and ethanol precipitated, and the precipitated DNA was dissolved in 20 ul TE buffer and electrophoresed on a 1.0% low melting agarose gel. Discrete bands in a ladder were visualized by ethidium bromide-staining and UV illumination and identified by size as insert (i), vector (v), v+i, v+2i, v+3i, etc. The portion of the gel containing v+i DNA was excised and the v+i DNA was recovered and resuspended into 20 ul TE. The v+i DNA then was blunt-ended by T4 polymerase treatment for 5 min. at 37°C in a reaction mixture (50 ul) containing the v+i linears, 500 uM each of the 4 dNTPs, and 9 units of T4 polymerase (New England BioLabs), under recommended buffer conditions. After phenol extraction and ethanol precipitation the repaired v+i linears were dissolved in 20 ul TE. The final ligation to produce circles was carried out in a 50 ul reaction containing 5 ul of v+i linears and 5 units of T4 ligase at 14°C overnight. After 10 min. at 70°C the following day, the reaction mixture was stored at -20°C.

This two-stage procedure resulted in a molecularly random collection of single-insert plasmid recombinants with minimal contamination from double-insert chimeras (<1%) or free vector (<3%).

Since deviation from randomness can arise from propagation the DNA in the host, *E. coli* host cells deficient in all recombination and restriction functions (A. Greener, *Strategies* 3 (1):5 (1990)) were used to prevent rearrangements, deletions, and loss of clones by restriction. Furthermore, transformed cells were plated directly on antibiotic diffusion plates to avoid the usual broth recovery phase which allows multiplication and selection of the most rapidly growing cells.

Plating was carried out as follows. A 100 ul aliquot of Epicurian Coli SURE II Supercompetent Cells (Stratagene 200152) was thawed on ice and transferred to a chilled Falcon 2059 tube on ice. A 1.7 ul aliquot of 1.42 M beta-

mercaptoethanol was added to the aliquot of cells to a final concentration of 25 mM. Cells were incubated on ice for 10 min. A 1 ul aliquot of the final ligation was added to the cells and incubated on ice for 30 min. The cells were heat pulsed for 30 sec. at 42° C and placed back on ice for 2 min. The outgrowth period in liquid culture was eliminated from this protocol in order to minimize the preferential growth of any given transformed cell. Instead the transformation mixture was plated directly on a nutrient rich SOB plate containing a 5 ml bottom layer of SOB agar (5% SOB agar: 20 g tryptone, 5 g yeast extract, 0.5 g NaCl, 1.5% Difco Agar per liter of media). The 5 ml bottom layer is supplemented with 0.4 ml of 50 mg/ml ampicillin per 100 ml SOB agar. The 15 ml top layer of SOB agar is supplemented with 1 ml X-Gal (2%), 1 ml MgCl₂ (1 M), and 1 ml MgSO₄/100 ml SOB agar. The 15 ml top layer was poured just prior to plating. Our titer was approximately 100 colonies/10 ul aliquot of transformation.

All colonies were picked for template preparation regardless of size. Thus, only clones lost due to "poison" DNA or deleterious gene products would be deleted from the library, resulting in a slight increase in gap number over that expected.

3. Random DNA Sequencing

High quality double stranded DNA plasmid templates were prepared using an alkaline lysis method developed in collaboration with 5Prime → 3Prime Inc. (Boulder, CO). Plasmid preparation was performed in a 96-well format for all stages of DNA preparation from bacterial growth through final DNA purification. Average template concentration was determined by running 25% of the samples on an agarose gel. DNA concentrations were not adjusted.

Templates were also prepared from a *Staphylococcus aureus* lambda genomic library. An unamplified library was constructed in Lambda DASH II vector (Stratagene). *Staphylococcus aureus* DNA (> 100 kb) was partially digested in a reaction mixture (200 ul) containing 50 ug DNA, 1X Sau3AI buffer, 20 units Sau3AI for 6 min. at 23 C. The digested DNA was phenol-extracted and centrifuges over a 10- 40% sucrose gradient. Fractions containing genomic DNA of 15-25 kb were recovered by precipitation. One ul of fragments was used with 1 ul of DASHII vector (Stratagene) in the recommended ligation reaction. One ul of the ligation mixture was used per packaging reaction following the recommended protocol with the Gigapack II XL Packaging Extract Phage were plated directly without amplification from the packaging mixture (after dilution with 500 ul of recommended SM buffer and chloroform treatment). Yield was about 2.5x10⁹ pfu/ul.

An amplified library was prepared from the primary packaging mixture according to the manufacturer's protocol. The amplified library is stored frozen in 7% dimethylsulfoxide. The phage titer is approximately 1x10⁹ pfu/ml.

Mini-liquid lysates (0.1ul) are prepared from randomly selected plaques and template is prepared by long range PCR. Samples are PCR amplified using modified T3 and T7 primers, and Elongase Supermix (LTI).

Sequencing reactions are carried out on plasmid templates using a combination of two workstations (BIOMEK 1000 and Hamilton Microlab 2200) and the Perkin-Elmer 9600 thermocycler with Applied Biosystems PRISM Ready Reaction Dye Primer Cycle Sequencing Kits for the M13 forward (M13-21) and the M13 reverse (M13RP1) primers. Dye terminator sequencing reactions are carried out on the lambda templates on a Perkin-Elmer 9600 Thermocycler using the Applied Biosystems Ready Reaction Dye Terminator Cycle Sequencing kits. Modified T7 and T3 primers are used to sequence the ends of the inserts from the Lambda DASH II library. Sequencing reactions are on a combination of AB 373 DNA Sequencers and ABI 377 DNA sequencers. All of the dye terminator sequencing reactions are analyzed using the 2X 9 hour module on the AB 377. Dye primer reactions are analyzed on a combination of ABI 373 and ABI 377 DNA sequencers. The overall sequencing success rate very approximately is about 85% for M13-21 and M13RP1 sequences and 65% for dye-terminator reactions. The average usable read length is 485 bp for M13-21 sequences, 445bp for M13RP1 sequences, and 375 bp for dye-terminator reactions.

4. Protocol for Automated Cycle Sequencing

The sequencing was carried out using Hamilton Microstation 2200, Perkin Elmer 9600 thermocyclers, ABI 373 and ABI 377 Automated DNA Sequencers. The Hamilton combines pre-aliquoted templates and reaction mixes consisting of deoxy- and dideoxynucleotides, the thermostable Taq DNA polymerase, fluorescently-labelled sequencing primers, and reaction buffer. Reaction mixes and templates were combined in the wells of a 96-well thermocycling plate and transferred to the Perkin Elmer 9600 thermocycler. Thirty consecutive cycles of linear amplification (i.e., one primer synthesis) steps were performed including denaturation, annealing of primer and template, and extension; i.e., DNA synthesis. A heated lid with rubber gaskets on the thermocycling plate prevents evaporation without the need for an oil overlay.

Two sequencing protocols were used: one for dye-labelled primers and a second for dye-labelled dideoxy chain terminators. The shotgun sequencing involves use of four dye-labelled sequencing primers, one for each of the four terminator nucleotide. Each dye-primer was labelled with a different fluorescent dye, permitting the four individual reactions to be combined into one lane of the 373 or 377 DNA Sequencer for electrophoresis, detection, and base-

calling. ABI currently supplies premixed reaction mixes in bulk packages containing all the necessary non-template reagents for sequencing. Sequencing can be done with both plasmid and PCR-generated templates with both dye-primers and dye-terminators with approximately equal fidelity, although plasmid templates generally give longer usable sequences.

Thirty-two reactions were loaded per ABI 373 Sequencer each day and 96 samples can be loaded on an ABI 377 per day. Electrophoresis was run overnight (ABI 373) or for 2 1/2 hours (ABI 377) following the manufacturer's protocols. Following electrophoresis and fluorescence detection, the ABI 373 or ABI 377 performs automatic lane tracking and base-calling. The lane-tracking was confirmed visually. Each sequence electropherogram (or fluorescence lane trace) was inspected visually and assessed for quality. Trailing sequences of low quality were removed and the sequence itself was loaded via software to a Sybase database (archived daily to 8mm tape). Leading vector polylinker sequence was removed automatically by a software program. Average edited lengths of sequences from the standard ABI 373 or ABI 377 were around 400 bp and depend mostly on the quality of the template used for the sequencing reaction.

INFORMATICS

1. Data Management

A number of information management systems for a large-scale sequencing lab have been developed. (For review see, for instance, Kerlavage *et al.*, *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences*, IEEE Computer Society Press, Washington D. C., 585 (1993)) The system used to collect and assemble the sequence data was developed using the Sybase relational database management system and was designed to automate data flow wherever possible and to reduce user error. The database stores and correlates all information collected during the entire operation from template preparation to final analysis of the genome. Because the raw output of the ABI 373 Sequencers was based on a Macintosh platform and the data management system chosen was based on a Unix platform, it was necessary to design and implement a variety of multi-user, client-server applications which allow the raw data as well as analysis results to flow seamlessly into the database with a minimum of user effort.

2. Assembly

An assembly engine (TIGR Assembler) developed for the rapid and accurate assembly of thousands of sequence fragments was employed to generate contigs. The TIGR assembler simultaneously clusters and assembles fragments of the genome. In order to obtain the speed necessary to assemble more than 10^4 fragments, the algorithm builds a hash table of 12 bp oligonucleotide subsequences to generate a list of potential sequence fragment overlaps. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Beginning with a single seed sequence fragment, TIGR Assembler extends the current contig by attempting to add the best matching fragment based on oligonucleotide content. The contig and candidate fragment are aligned using a modified version of the Smith-Waterman algorithm which provides for optimal gapped alignments (Waterman, M. S., *Methods in Enzymology* 164: 765 (1988)). The contig is extended by the fragment only if strict criteria for the quality of the match are met. The match criteria include the minimum length of overlap, the maximum length of an unmatched end, and the minimum percentage match. These criteria are automatically lowered by the algorithm in regions of minimal coverage and raised in regions with a possible repetitive element. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Fragments representing the boundaries of repetitive elements and potentially chimeric fragments are often rejected based on partial mismatches at the ends of alignments and excluded from the current contig. TIGR Assembler is designed to take advantage of clone size information coupled with sequencing from both ends of each template. It enforces the constraint that sequence fragments from two ends of the same template point toward one another in the contig and are located within a certain ranged of base pairs (definable for each clone based on the known clone size range for a given library).

3. Identifying Genes

The predicted coding regions of the *Staphylococcus aureus* genome were initially defined with the program zorf, which finds ORFs of a minimum length. The predicted coding region sequences were used in searches against a database of all *Staphylococcus aureus* nucleotide sequences from GenBank (release 92.0), using the BLASTN search method to identify overlaps of 50 or more nucleotides with at least a 95% identity. Those ORFs with nucleotide sequence matches are shown in Table 1. The ORFs without such matches were translated to protein sequences and compared to a non-redundant database of known proteins generated by combining the Swiss-prot, PIR and GenPept databases. ORFs of at least 80 amino acids that matched a database protein with BLASTP probability less than or equal to 0.01 are shown in Table 2. The table also lists assigned functions based on the closest match in the databases.

ORFs of at least 120 amino acids that did not match protein or nucleotide sequences in the databases at these levels are shown in Table 3.

ILLUSTRATIVE APPLICATIONS

1. Production of an Antibody to a *Staphylococcus aureus* Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells using any one of the methods known in the art. The protein can also be produced in a recombinant prokaryotic expression system, such as *E. coli*, or can be chemically synthesized. Concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows.

2. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature* 256:495 (1975) or modifications of the methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., *Meth. Enzymol.* 70:419 (1980), and modified methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. *et al.* *Basic Methods in Molecular Biology* Elsevier, New York. Section 21-2 (1989).

3. Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogeneous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than others and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. *et al.*, *J. Clin. Endocrinol. Metab.* 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. *et al.*, Chap. 19 in: *Handbook of Experimental Immunology*, Wier, D., ed, Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, second edition, Rose and Friedman, eds., Amer. Soc. For Microbiology, Washington, D. C. (1980).

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. In addition, they are useful in various animal models of *Staphylococcal* disease known to those of skill in the art as a means of evaluating the protein used to make the antibody as a potential vaccine target or as a means of evaluating the antibody as a potential immunotherapeutic reagent.

3. Preparation of PCR Primers and Amplification of DNA

Various fragments of the *Staphylococcus aureus* genome, such as those of Tables 1-3 and SEQ ID NOS:1-5,191 can be used, in accordance with the present invention, to prepare PCR primers for a variety of uses. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approxi-

mately the same. The PCR primers and amplified DNA of this Example find use in the Examples that follow.

4. Gene expression from DNA Sequences Corresponding to ORFs

A fragment of the *Staphylococcus aureus* genome provided in Tables 1-3 is introduced into an expression vector using conventional technology. Techniques to transfer cloned sequences into expression vectors that direct protein translation in mammalian, yeast, insect or bacterial expression systems are well known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism, as explained by Hatfield *et al.*, U. S. Patent No. 5,082,767, incorporated herein by this reference.

The following is provided as one exemplary method to generate polypeptide(s) from cloned ORFs of the *Staphylococcus aureus* genome fragment. Bacterial ORFs generally lack a poly A addition signal. The addition signal sequence can be added to the construct by, for example, splicing out the poly A addition sequence from pSG5 (Stratagene) using BglI and SalI restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene) for use in eukaryotic expression systems. pXT1 contains the LTRs and a portion of the gag gene of Moloney Murine Leukemia Virus. The positions of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The *Staphylococcus aureus* DNA is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the *Staphylococcus aureus* DNA and containing restriction endonuclease sequences for PstI incorporated into the 5' primer and BglII at the 5' end of the corresponding *Staphylococcus aureus* DNA 3' primer, taking care to ensure that the *Staphylococcus aureus* DNA is positioned such that its followed with the poly A addition sequence. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with BglII, purified and ligated to pXT1, now containing a poly A addition sequence and digested BglII.

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 ug/ml G418 (Sigma, St. Louis, Missouri). The protein is preferably released into the supernatant. However if the protein has membrane binding domains, the protein may additionally be retained within the cell or expression may be restricted to the cell surface. Since it may be necessary to purify and locate the transfected product, synthetic 15-mer peptides synthesized from the predicted *Staphylococcus aureus* DNA sequence are injected into mice to generate antibody to the polypeptide encoded by the *Staphylococcus aureus* DNA.

Alternatively and if antibody production is not possible, the *Staphylococcus aureus* DNA sequence is additionally incorporated into eukaryotic expression vectors and expressed as, for example, a globin fusion. Antibody to the globin moiety then is used to purify the chimeric protein. Corresponding protease cleavage sites are engineered between the globin moiety and the polypeptide encoded by the *Staphylococcus aureus* DNA so that the latter may be freed from the formed by simple protease digestion. One useful expression vector for generating globin chimerics is pSG5 (Stratagene). This vector encodes a rabbit globin. Intron II of the rabbit globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques are well known to those skilled in the art of molecular biology. Standard methods are published in methods texts such as Davis *et al.*, cited elsewhere herein, and many of the methods are available from the technical assistance representatives from Stratagene, Life Technologies, Inc., or Promega. Polypeptides of the invention also may be produced using *in vitro* translation systems such as *in vitro* ExpressTM Translation Kit (Stratagene).

While the present invention has been described in some detail for purposes of clarity and understanding, one skilled in the art will appreciate that various changes in form and detail can be made without departing from the true scope of the invention.

All patents, patent applications and publications referred to above are hereby incorporated by reference.

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
1	1	1419	757	[emb]M17301 SAILD	S. aureus DNA for hld gene and for part of agr gene	100	663	663
1	2	3273	2452	[emb]M52543 SAG	S. aureus agrA, agrB and hld genes	99	809	822
1	5	6418	5651	[dbj]D14711 STAM	Staphylococcus aureus HSP10 and HSP60 genes	98	223	768
5	1	807	439	[emb]X72700 SAPV	S. aureus genes for S and P components of Pantone-Valentine leucocidins	81	216	369
5	4	5031	3571	[emb]X72700 SAPV	S. aureus genes for S and P components of Pantone-Valentine leucocidins	95	424	1461
10	1	86	904	[gb]U25288	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	98	715	819
16	5	5302	6246	[gb]U35773	Staphylococcus aureus prolipoprotein diacylglycerol transferase (lgt) gene, complete cds	94	251	945
16	6	6249	7091	[gb]U35773	Staphylococcus aureus prolipoprotein diacylglycerol transferase (lgt) gene, complete cds	99	843	843
16	7	7084	7584	[gb]U35773	Staphylococcus aureus prolipoprotein diacylglycerol transferase (lgt) gene, complete cds	99	342	501
20	1	995	549	[gb]U19300	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	100	443	447
20	2	1011	841	[gb]U19300	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	91	137	171
20	3	2010	1798	[gb]U19300	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	100	110	213
20	4	5300	3825	[gb]U16714	Staphylococcus aureus peptidoglycan hydrolase gene, complete cds	100	946	1476
20	5	4788	4282	[gb]U16714	Staphylococcus aureus peptidoglycan hydrolase gene, complete cds	100	309	507
26	1	2	145	[gb]U41072	Staphylococcus aureus isoleucyl-tRNA synthetase (lles) gene, partial cds	100	126	144
26	2	84	557	[gb]U41072	Staphylococcus aureus isoleucyl-tRNA synthetase (lles) gene, partial cds	99	430	474
26	3	763	3531	[emb]X74219 SAIL	S. aureus gene for isoleucyl-tRNA synthetase	99	2769	2769
29	3	1261	4392	[gb]U66665	Staphylococcus aureus DNA fragment with class II promoter activity	100	117	3132
31	14	14977	13463	[emb]X73889 SAP1	S. aureus genes p1 and p2	99	1351	1515
31	15	14241	13855	[emb]X73889 SAP1	S. aureus genes p1 and p2	98	256	387
38	17	14284	13112	[gb]U12715	S. aureus geh gene encoding lipase (glycerol ester hydrolase)	100	372	1173
38	19	13434	15518	[gb]U12715	S. aureus geh gene encoding lipase (glycerol ester hydrolase)	100	2085	2085

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
46	2	519	1727	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	98	1209	1209
46	3	1720	2295	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	98	576	576
46	4	2259	3182	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	97	924	924
46	5	3173	4498	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	98	1283	1326
46	6	4536	5720	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	98	1185	1185
46	7	6455	6120	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	99	278	336
48	1	2	955	gb U25893	Staphylococcus aureus recA gene, complete cds	99	954	954
50	3	4465	2924	emb X85029 SAAH	S. aureus htpC gene	100	88	1542
50	4	4108	3515	emb X85029 SAAH	S. aureus htpC gene	98	540	594
54	3	5074	3392	emb X62992 SAFN	S. aureus fnbB gene for fibronectin binding protein B	100	1668	1683
54	4	4865	4122	emb X62992 SAFN	S. aureus fnbB gene for fibronectin binding protein B	99	720	744
54	5	5056	4562	emb X62992 SAFN	S. aureus fnbB gene for fibronectin binding protein B	100	463	495
54	6	11386	8300	gb J04151	S. aureus fibronectin-binding protein (fnbA) mRNA, complete cds	100	3087	3087
58	3	1743	2819	emb X87104 SADN	S. aureus mdr, pbp4 and tagD genes (SG511-55 isolate)	89	68	1077
58	4	2858	3280	emb X91786 SAPB	S. aureus abcA, pbp4, and tagD genes	99	423	423
58	5	6005	4701	emb X91786 SAPB	S. aureus abcA, pbp4, and tagD genes	99	1305	1305
58	6	5677	5378	gb U29478	Staphylococcus aureus ABC transporter-like protein AbcA (abcA) gene, partial cds	100	300	300
58	7	5086	6840	emb X91786 SAPB	S. aureus abcA, pbp4, and tagD genes	99	1755	1755
72	1	888	445	gb U21854	S. aureus agr gene encoding an accessory gene regulator protein, complete cds	100	444	444
72	2	2457	1453	emb X52543 SAAG	S. aureus agrA, agrB and hld genes	99	673	1005

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
82	1	337	3917	emb X64172 SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORP202, DNA-directed RNA polymerase beta & beta' chains	99	2396	3361
82	2	4027	7677	emb X89233 SARP	S.aureus DNA for rpoC gene	99	3171	3651
82	3	7745	8068	gb U20869	Staphylococcus aureus ribosomal protein S12 (rpsL) gene, complete cds, ribosomal protein S7 (rpsG) and ORF 1 genes, partial cds	100	320	324
82	4	8103	8579	gb U20869	Staphylococcus aureus ribosomal protein S12 (rpsL) gene, complete cds, ribosomal protein S7 (rpsG) and ORF 1 genes, partial cds	100	477	477
82	5	8618	8821	gb U20869	Staphylococcus aureus ribosomal protein S12 (rpsL) gene, complete cds, ribosomal protein S7 (rpsG) and ORF 1 genes, partial cds	100	154	204
84	1	18	191	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	98	166	174
84	2	189	893	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	94	705	705
84	3	887	1660	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	99	774	774
84	4	1584	3503	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	98	1920	1920
84	5	3394	4521	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	97	1128	1128
84	6	4519	5643	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	97	1125	1125
96	2	1245	3896	emb 218852 SACF	S.aureus gene for clumping factor	83	660	2652
97	2	625	882	gb U41072	Staphylococcus aureus isoleucyl-tRNA synthetase (ileS) gene, partial cds	97	88	258
111	1	3	452	gb U41499	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	100	450	450
111	2	526	1041	gb U41499	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	99	516	516
117	2	1278	1958	gb W83994	Staphylococcus aureus prolipoprotein signal peptidase (lap) gene, complete cds	100	61	681

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
118	4	3787	4254	[dbj U0690 STAN]	Staphylococcus aureus genes for ONF37; HSP20; HSP70; HSP10; ORF35, complete cds	99	467	468
130	4	2597	3640	[emb X13290 SATN]	Staphylococcus aureus multi-resistance plasmid pSKI DNA containing transposon Tn4003	78	956	1044
130	5	3813	4265	[emb Z16422 SADI]	S. aureus dfrB gene for dihydrofolate reductase	98	416	453
130	6	4309	5172	[emb Z16422 SADI]	S. aureus dfrB gene for dihydrofolate reductase	98	607	864
136	4	5296	6207	[emb X71437 SAGY]	S. aureus genes gyrB, gyrA and recF (partial)	97	838	912
136	5	11680	8987	[dbj U0489 STAG]	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	100	2694	2694
136	6	112886	10940	[dbj U0489 STAG]	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	99	1947	1947
136	7	12592	11765	[gb S77055]	recF cluster: dnaA-rep100 assembly protein...gyrB-DNA gyrase beta subunit [Staphylococcus aureus, Y8886, Genomic, 5 genes, 3573 nt]	99	822	828
143	3	4171	2867	[gb U36379]	Staphylococcus aureus S-adenosylmethionine synthetase gene, complete cds	99	1105	1305
143	4	3100	4281	[gb U42943]	Staphylococcus aureus (clone KIN50) phosphoenolpyruvate carboxykinase (pckA) gene, complete cds	100	1170	1182
143	5	4254	4718	[gb U51133]	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pckA) gene, complete cds	100	449	465
143	9	6977	7261	[gb U51132]	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (menc), and o-succinylbenzoic acid synthetase (menc) genes, complete cds	100	75	285
143	10	9464	8361	[gb U51132]	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (menc), and o-succinylbenzoic acid synthetase (menc) genes, complete cds	100	1104	1104
143	11	11232	9748	[gb U51132]	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (menc), and o-succinylbenzoic acid synthetase (menc) genes, complete cds	100	1485	1485
143	12	10739	10320	[gb U51132]	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (menc), and o-succinylbenzoic acid synthetase (menc) genes, complete cds	100	332	420
152	5	2454	3437	[emb X58434 SAPD]	S. aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydroliipoamide acetyltransferase and dihydroliipoamide dehydrogenase	99	305	984
152	6	3513	4820	[emb X58434 SAPD]	S. aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydroliipoamide acetyltransferase and dihydroliipoamide dehydrogenase	98	1308	1308
152	7	4818	6230	[emb X58434 SAPD]	S. aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydroliipoamide acetyltransferase and dihydroliipoamide dehydrogenase	99	1413	1413
153	1	387	1526	[gb S77055]	recF cluster: dnaA-rep100 assembly protein...gyrB-DNA gyrase beta subunit [Staphylococcus aureus, Y8886, Genomic, 5 genes, 3573 nt]	99	1140	1140
153	2	1877	2152	[gb S77055]	recF cluster: dnaA-rep100 assembly protein...gyrB-DNA gyrase beta subunit [Staphylococcus aureus, Y8886, Genomic, 5 genes, 3573 nt]	100	276	276

TABLE I

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	percent ident	HSP nt length	ORF nt length
153	3	2143	2289	gb J77055	recF cluster: dnaA replisome assembly protein...gyrB-DNA gyrase beta subunit (Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt)	99	113	147
154	10	10792	9314	gb U06451	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	91	154	1479
154	11	9935	9615	gb U06451	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	99	229	321
154	12	9943	10167	gb U06451	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	94	123	225
154	13	10089	11501	gb U06451	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	99	1326	1413
159	2	2195	1212	dbj D28479 STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	100	71	984
161	3	2596	2270	gb H83994	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	92	203	327
162	1	1406	705	gb U21221	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	100	702	702
163	4	1263	1772	gb U19770	Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds	96	127	510
164	7	4774	9117	dbj D86727 D867	Staphylococcus aureus DNA for DNA polymerase III, complete cds	99	3470	4344
168	7	7448	6447	gb U21636	Staphylococcus aureus cmp-binding-factor 1 (cbf1) and ORF X genes, complete cds	100	1002	1002
168	8	9538	7961	gb U21636	Staphylococcus aureus cmp-binding-factor 1 (cbf1) and ORF X genes, complete cds	99	1158	1578
173	6	9240	7801	gb J03479	S. aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	100	1440	1440
173	7	11252	9522	gb J03479	S. aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	99	1731	1731
173	8	8285	8706	gb J03479	S. aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	100	420	420
173	9	10168	9839	gb J03479	S. aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	100	330	330
173	10	11815	10829	emb X14827 SALA	Staphylococcus aureus lacC and lacD genes	100	987	987
173	11	12721	11774	emb X14827 SALA	Staphylococcus aureus lacC and lacD genes	100	948	948
173	12	12838	12305	gb H64724	S. aureus tagatose 6-phosphate isomerase gene, complete cds	100	534	534
173	13	13243	12773	gb H32103	Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds	100	471	471
173	14	14633	113866	gb H32103	Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds	100	768	768

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
178	1	2	655	gb U52961	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	115	654
178	2	2201	1482	gb U52961	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	720	720
178	3	2361	1909	gb U52961	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	453	453
178	4	1551	1853	gb U52961	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	303	303
178	5	3541	2777	gb U42945	Staphylococcus aureus lytS and lytR genes, complete cds	99	765	765
178	6	3294	3025	gb U42945	Staphylococcus aureus lytS and lytR genes, complete cds	99	270	270
181	1	1114	590	gb H61177	S. aureus sigma factor (plac) gene, complete cds	99	499	525
182	1	3	341	emb X61307 SASP	Staphylococcus aureus spa gene for protein A	98	277	339
182	2	690	2312	gb U01786	S. aureus spa gene coding for protein A, complete cds	97	1332	1623
182	3	5861	4251	emb X61307 SASP	Staphylococcus aureus spa gene for protein A	99	119	1611
185	1	3	824	gb U31979	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydrogenase synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	90	132	822
191	3	841	2760	emb X17679 SACO	Staphylococcus aureus coa gene for coagulase	99	1920	1920
191	4	2567	3143	emb X16457 SAST	Staphylococcus aureus gene for staphylocoagulase	99	177	177
191	5	5768	4566	emb X16457 SAST	Staphylococcus aureus gene for staphylocoagulase	99	250	1203
196	1	1741	872	gb U36472	Staphylococcus aureus lysyl-tRNA synthetase gene, complete cds, transfer RNA (tRNA) genes, 5S ribosomal RNA (5S rRNA) gene, 16S ribosomal RNA (16S rRNA) gene, 23S ribosomal RNA (23S rRNA) gene	99	870	870
198	3	1688	2011	emb X93205 SAPT	S. aureus pteH and pteI genes	99	324	324
198	4	2005	2310	emb X93205 SAPT	S. aureus pteH and pteI genes	97	304	306
202	1	163	1305	emb X97985 SA12	S. aureus orfs 1,2,3 & 4	99	1143	1143
202	2	1303	2175	emb X73889 SA91	S. aureus genes P1 and P2	94	444	873
210	1	3114	1538	dbj D17366 STAA	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	99	1552	1557
210	2	2919	2232	gb U41499	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	99	684	708
214	11	7429	7770	dbj D86240 D862	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	96	157	342

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
216	3	398	1318	emb X72700 SAPV	S. aureus genes for S and F components of Pantone-Valentine leucocidins	88	265	921
219	2	1810	1073	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	100	60	738
219	3	2979	2035	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	99	945	945
219	4	4359	3196	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	99	1164	1164
219	5	7044	5176	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	98	1869	1869
219	6	6557	5883	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	99	675	675
219	7	6801	6134	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	98	468	468
221	8	10816	10034	gb U19298	Staphylococcus aureus phosphatidylinositol-specific phospholipase C (plc) gene, complete cds	91	67	783
223	1	2855	1506	gb U19298	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	99	102	1350
234	1	2	1357	emb X97985 SA12	S. aureus orfs 1,2,3 & 4	100	176	1356
234	2	1694	2485	emb X97985 SA12	S. aureus orfs 1,2,3 & 4	100	792	792
234	3	2648	3148	emb X97985 SA12	S. aureus orfs 1,2,3 & 4	99	501	501
234	4	3120	4604	emb X97985 SA12	S. aureus orfs 1,2,3 & 4	99	1305	1485
236	5	3826	5322	gb U48826	Staphylococcus aureus elastin binding protein (ebpS) gene, complete cds	96	648	1497
248	1	2	403	emb X62288 SAPV	S. aureus DNA for penicillin-binding protein 2	100	303	402
248	2	388	852	gb U35426	Staphylococcus aureus penicillin-binding protein 2 (pbp2) gene, complete cds	99	465	465
253	2	1519	1093	gb U46541	Staphylococcus aureus sara gene, complete cds	96	447	447
254	2	150	1835	gb U57060	Staphylococcus aureus sda gene, complete cds	94	142	1686
254	3	1973	2728	gb U57060	Staphylococcus aureus sda gene, complete cds	99	756	756
260	1	2	1900	gb H90693	Staphylococcus aureus glycerol ester hydrolase (lip) gene, complete cds	99	1213	1899
265	1	1	942	dbj D21131 STAS	Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds	99	941	942

TABLE I

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	patch gene name	percent ident	ORF nt length	ORF nt length
265	2	688	476	[dbj D21131 STAS	Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds	99	213	213
265	3	2418	1765	[dbj D21131 STAS	Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds	98	63	654
266	1	2	1018	[dbj D14711 STAH	Staphylococcus aureus HSP10 and HSP60 genes	98	743	1017
282	1	1	525	[gb J72488	hemB-porphobilinogen synthase (Staphylococcus aureus, SA1959, Genomic, 1087 nt)	100	110	525
282	2	516	1502	[gb J72488	hemB-porphobilinogen synthase (Staphylococcus aureus, SA1959, Genomic, 1087 nt)	100	952	987
284	1	3	170	[gb J63176	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	98	84	168
284	2	282	1034	[gb J63176	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	100	712	753
284	3	1028	2026	[gb J63176	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	99	979	999
284	4	1990	2202	[gb J63176	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	98	187	213
289	3	1536	1991	[gb J432470	S. aureus Sau3AI-restriction-enzyme and Sau3AI-modification-enzyme genes, complete cds	99	338	456
303	1	2	868	[gb J401055	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hlgC) genes, complete cds	99	867	867
303	2	1409	2383	[gb J401055	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hlgC) genes, complete cds	100	975	975
303	3	2167	3161	[gb J401055	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hlgC) genes, complete cds	99	793	795
305	1	2707	1355	[dbj D17366 STAA	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	99	1343	1353
311	1	2628	1315	[gb J42945	Staphylococcus aureus lysS and lysR genes, complete cds	98	1314	1314
312	6	7019	7870	[gb J44017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	74	351	852
323	1	1998	1003	[gb J31175	Staphylococcus aureus D-specific D-2-hydroxyacid dehydrogenase (ddh) gene, complete cds	98	996	996
326	1	1	237	[emb Y00356 SASP	Staphylococcus aureus V8 serine protease gene	100	108	237
338	1	687	388	[emb X64389 SALE	S. aureus leuF-P83 gene for F component of leucocidin R	98	259	300
338	2	1828	1088	[emb X64389 SALE	S. aureus leuF-P83 gene for F component of leucocidin R	97	137	741

TABLE I

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
342	2	579	1754	gb U06462	Staphylococcus aureus SA Pts2 (fts2) gene, complete cds	100	1176	1176
344	2	517	1248	emb V01281 SAAU	S. aureus mRNA for nuclease	98	732	732
349	1	457	210	gb H20393	S. aureus bacteriophage phi-11 attachment site (attB)	96	172	228
353	1	1016	516	gb H9394	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	100	187	501
353	2	1582	1046	gb H8394	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	99	537	537
356	1	3	674	gb U20503	Staphylococcus aureus MIC class II analog gene, complete cds	75	671	672
361	1	1	903	gb U19298	Staphylococcus aureus phosphatidylinositol-specific phospholipase C (plc) gene, complete cds	98	747	903
361	2	1103	1507	gb U19298	Staphylococcus aureus phosphatidylinositol-specific phospholipase C (plc) gene, complete cds	97	68	405
373	1	3	1148	emb X62268 SAFE	S. aureus DNA for penicillin-binding protein 2	99	1146	1146
389	3	1904	1248	emb X62262 SATS	S. aureus target site DNA for IS431 insertion	97	349	657
400	1	1	540	emb X61716 SMHL	S. aureus hlb gene encoding sphingomyelinase	99	389	540
400	2	1693	1187	emb X13404 SAHL	Staphylococcus aureus hlb gene for beta-hemolysin	99	178	507
408	1	1810	1049	gb S76213	asp23-alkaline shock protein 23 (methicillin resistant) (Staphylococcus aureus, 912, Genomic, 1360 nt)	99	163	762
418	1	2	217	gb A1489	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	100	216	216
418	2	854	639	dbj D17366 STAA	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	100	188	216
421	2	1262	2509	gb U43098	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	99	1248	1248
422	1	2	325	gb K02985	S. aureus (strain RN450) transposon Tn554 insertion site	96	200	374
427	1	865	434	dbj D28879 STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	100	432	432
427	2	1829	1122	dbj D28879 STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	100	151	708
435	1	2	808	dbj D6240 D862	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	100	556	807
435	2	832	999	dbj D6240 D862	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	100	134	168
436	1	1341	685	emb X17688 SAFE	S. aureus factor essential for expression of methicillin resistance (fema) gene, complete cds, and trpA gene, 3' and	97	657	657

TABLE I

3. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
436	2	2403	1657	[emb]N17648 SNPE	S.aureus factor essential for expression of methicillin resistance (femaA) gene, complete cds, and trpA gene, 3' and	100	294	747
442	1	347	1300	[emb]X72700 SAPV	S.aureus genes for S and F components of Pantone-Valentine leucocidins	84	204	954
445	2	1906	2178	[gb]U01055	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hlgC) genes, complete cds	98	187	273
447	1	167	1078	[gb]U19770	Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds	100	51*	912
447	2	1176	1784	[gb]U19770	Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds	96	597	609
454	3	7309	4319	[emb]Z18852 SNCF	S.aureus gene for clumping factor	75	653	2991
472	4	7896	5479	[gb]U25288	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grIA and grIB) genes, complete cds	99	2418	2418
472	5	8120	6792	[gb]U25288	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grIA and grIB) genes, complete cds	99	1328	1329
475	2	566	889	[emb]X52543 SNAG	S.aureus agrA, agrB and hld genes	100	76	324
481	4	1922	1560	[emb]X64172 SNRP	S.aureus rplL, rplM, rplN, rplP and rplQ genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	250	363
481	5	1244	1534	[emb]X64172 SNRP	S.aureus rplL, rplM, rplN, rplP and rplQ genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	224	291
487	2	1388	1188	[gb]M83994	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	98	72	201
489	1	2737	1370	[gb]U21221	Staphylococcus aureus hyaluronate lyase (hyla) gene, complete cds	99	1368	1368
501	2	1135	653	[gb]M83994	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	100	108	483
511	3	1613	2242	[gb]U14017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	84	323	630
511	4	3122	2700	[gb]S76213	esp23-alkaline shock protein 23 (methicillin resistant) [Staphylococcus aureus, 912, Genomic, 1360 nt]	96	423	423
520	2	758	1297	[emb]X72014 SAFI	S.aureus fib gene for fibrinogen-binding protein	99	540	540
520	3	1436	1801	[emb]X72013 SAFI	S.aureus fib gene for fibrinogen-binding protein	99	221	366
526	1	2150	1092	[dbj]D17366 STAA	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	99	641	1059

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	percent ident	ORF nt length
528	2	58	963	gb U19100	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homolog, 5' flank	99	260
528	3	1098	2870	gb U19100	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homolog, 5' flank	99	866
530	1	3	434	gb U1979	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroquinase synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	99	432
530	2	1211	2395	gb U1979	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroquinase synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	91	1185
530	3	2409	2801	gb U1979	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroquinase synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	88	181
530	4	2690	3484	gb U05004	Staphylococcus aureus dehydroquinase synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	100	75
530	5	3482	4792	gb U05004	Staphylococcus aureus dehydroquinase synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	99	905
530	6	4790	5380	gb U05004	Staphylococcus aureus dehydroquinase synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	100	196
539	1	3	338	emb X76490 SAGL	S. aureus (bb270) glnA and glnR genes	99	336
539	2	336	527	emb X76490 SAGL	S. aureus (bb270) glnA and glnR genes	100	189
554	1	727	365	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	100	54
554	2	2175	1252	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	99	918
554	3	1574	1374	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	96	122
584	2	1019	705	gb U21221	Staphylococcus aureus hyaluronate lyase (hyla) gene, complete cds	99	306
587	3	1475	4288	emb Z18852 SACF	S. aureus gene for clumping factor	98	2588
59A	1	3881	1953	dbj D28879 STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	99	1873
							1929

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
605	1	2	745	[gb D66240 D662]	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	98	338	744
609	1	1628	816	[emb X76490 SAGL]	S. aureus (bb270) gltA and gltK genes	100	495	813
614	1	1280	642	[gb M32103]	Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds	99	639	639
626	1	2508	1255	[gb M63176]	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	100	225	1253
626	2	3315	2284	[gb M63176]	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	99	838	1032
629	1	1999	1001	[emb X17608 SAFE]	S. aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	99	990	999
629	2	1407	1195	[emb X17608 SAFE]	S. aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	98	194	213
631	2	5126	3228	[emb 218852 SACF]	S. aureus gene for clumping factor	82	489	1899
632	1	3	551	[emb 230568 SAST]	S. aureus (RM4220) genes for potential ABC transporter and potential membrane spanning protein	99	549	549
632	2	529	1323	[emb 210568 SAST]	S. aureus (RM4220) genes for potential ABC transporter and potential membrane spanning protein	99	795	795
651	1	1909	1070	[gb L19300]	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	99	478	840
657	2	1800	1105	[gb L14017]	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	84	456	696
662	1	908	456	[emb X13404 SAHL]	Staphylococcus aureus hlb gene for beta-hemolysin	100	369	453
662	2	230	475	[emb X13404 SAHL]	Staphylococcus aureus hlb gene for beta-hemolysin	100	246	246
662	3	746	1399	[emb X13404 SAHL]	Staphylococcus aureus hlb gene for beta-hemolysin	99	653	654
682	1	956	480	[gb M63177]	S. aureus sigma factor (plac) gene, complete cds	100	136	477
685	1	1182	592	[gb U65000]	Staphylococcus aureus type-I signal peptidase SpsA (spsA) gene, and type-I signal peptidase SpsB (spsB) gene, complete cds	98	534	591
685	2	1716	1153	[gb U65000]	Staphylococcus aureus type-I signal peptidase SpsA (spsA) gene, and type-I signal peptidase SpsB (spsB) gene, complete cds	96	564	564
697	1	3	527	[gb M63177]	S. aureus sigma factor (plac) gene, complete cds	100	195	525
697	2	485	784	[gb M63177]	S. aureus sigma factor (plac) gene, complete cds	97	280	300

TABLE I

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	Percent Ident	RSP nt length	ORF nt length
710	1	15	503	dbj DRC240 DR62	Staphylococcus aureus gene for unknown function and dit operon dltA, dltB, dltC and dltD genes, complete cds	99	217	489
733	1	26	205	gb M80252	Staphylococcus aureus norA199 gene (which mediates active efflux of fluoroquinolones), complete cds	97	140	180
741	1	1736	1197	dbj D83953 STAL	Staphylococcus aureus DNA for LukM component, LukP-PV like component, complete cds	81	522	540
752	1	1	636	emb Y00356 SASP	Staphylococcus aureus V8 serine protease gene	99	618	636
752	2	588	956	emb Y00356 SASP	Staphylococcus aureus V8 serine protease gene	99	340	369
756	1	1308	709	emb X01645 SATO	Staphylococcus aureus (Wood 46) gene for alpha-toxin	98	567	600
777	1	1582	950	emb Z49245 SAK2	S. aureus partial sod gene for superoxide dismutase	99	429	633
780	1	1111	557	gb U20503	Staphylococcus aureus HMC class-II analog gene, complete cds	86	550	555
784	1	73	687	gb U63529	Staphylococcus aureus novel antigen gene, complete cds	99	568	615
797	1	182	544	dbj D14711 STAH	Staphylococcus aureus HSP10 and HSP60 genes	98	363	363
798	1	532	302	emb X58434 SNPD	S. aureus pdaB, pdaC and pdaD genes for pyruvate decarboxylase, dihydrodipicolinate acetyltransferase and dihydrodipicolinate dehydrogenase	95	196	231
823	1	3	467	gb S77055	recF cluster: dnaA, replisome assembly protein, gyrB-DNA gyrase beta subunit [Staphylococcus aureus, Y8886, Genomic, 5 genes, 3573 nt]	99	156	465
848	1	348	175	gb L25288	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	99	174	174
848	2	476	318	gb L25288	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	100	131	159
866	1	792	397	emb X64172 SNRP	S. aureus rplL, rplM, rplN, rplO, rplP, rplQ, rplR, rplS, rplT, rplU, rplV, rplW, rplX, rplY, rplZ, rpl30, rpl31, rpl32, rpl33, rpl34, rpl35, rpl36, rpl37, rpl38, rpl39, rpl40, rpl41, rpl42, rpl43, rpl44, rpl45, rpl46, rpl47, rpl48, rpl49, rpl50, rpl51, rpl52, rpl53, rpl54, rpl55, rpl56, rpl57, rpl58, rpl59, rpl60, rpl61, rpl62, rpl63, rpl64, rpl65, rpl66, rpl67, rpl68, rpl69, rpl70, rpl71, rpl72, rpl73, rpl74, rpl75, rpl76, rpl77, rpl78, rpl79, rpl80, rpl81, rpl82, rpl83, rpl84, rpl85, rpl86, rpl87, rpl88, rpl89, rpl90, rpl91, rpl92, rpl93, rpl94, rpl95, rpl96, rpl97, rpl98, rpl99, rpl100, rpl101, rpl102, rpl103, rpl104, rpl105, rpl106, rpl107, rpl108, rpl109, rpl110, rpl111, rpl112, rpl113, rpl114, rpl115, rpl116, rpl117, rpl118, rpl119, rpl120, rpl121, rpl122, rpl123, rpl124, rpl125, rpl126, rpl127, rpl128, rpl129, rpl130, rpl131, rpl132, rpl133, rpl134, rpl135, rpl136, rpl137, rpl138, rpl139, rpl140, rpl141, rpl142, rpl143, rpl144, rpl145, rpl146, rpl147, rpl148, rpl149, rpl150, rpl151, rpl152, rpl153, rpl154, rpl155, rpl156, rpl157, rpl158, rpl159, rpl160, rpl161, rpl162, rpl163, rpl164, rpl165, rpl166, rpl167, rpl168, rpl169, rpl170, rpl171, rpl172, rpl173, rpl174, rpl175, rpl176, rpl177, rpl178, rpl179, rpl180, rpl181, rpl182, rpl183, rpl184, rpl185, rpl186, rpl187, rpl188, rpl189, rpl190, rpl191, rpl192, rpl193, rpl194, rpl195, rpl196, rpl197, rpl198, rpl199, rpl200, rpl201, rpl202, rpl203, rpl204, rpl205, rpl206, rpl207, rpl208, rpl209, rpl210, rpl211, rpl212, rpl213, rpl214, rpl215, rpl216, rpl217, rpl218, rpl219, rpl220, rpl221, rpl222, rpl223, rpl224, rpl225, rpl226, rpl227, rpl228, rpl229, rpl230, rpl231, rpl232, rpl233, rpl234, rpl235, rpl236, rpl237, rpl238, rpl239, rpl240, rpl241, rpl242, rpl243, rpl244, rpl245, rpl246, rpl247, rpl248, rpl249, rpl250, rpl251, rpl252, rpl253, rpl254, rpl255, rpl256, rpl257, rpl258, rpl259, rpl260, rpl261, rpl262, rpl263, rpl264, rpl265, rpl266, rpl267, rpl268, rpl269, rpl270, rpl271, rpl272, rpl273, rpl274, rpl275, rpl276, rpl277, rpl278, rpl279, rpl280, rpl281, rpl282, rpl283, rpl284, rpl285, rpl286, rpl287, rpl288, rpl289, rpl290, rpl291, rpl292, rpl293, rpl294, rpl295, rpl296, rpl297, rpl298, rpl299, rpl300, rpl301, rpl302, rpl303, rpl304, rpl305, rpl306, rpl307, rpl308, rpl309, rpl310, rpl311, rpl312, rpl313, rpl314, rpl315, rpl316, rpl317, rpl318, rpl319, rpl320, rpl321, rpl322, rpl323, rpl324, rpl325, rpl326, rpl327, rpl328, rpl329, rpl330, rpl331, rpl332, rpl333, rpl334, rpl335, rpl336, rpl337, rpl338, rpl339, rpl340, rpl341, rpl342, rpl343, rpl344, rpl345, rpl346, rpl347, rpl348, rpl349, rpl350, rpl351, rpl352, rpl353, rpl354, rpl355, rpl356, rpl357, rpl358, rpl359, rpl360, rpl361, rpl362, rpl363, rpl364, rpl365, rpl366, rpl367, rpl368, rpl369, rpl370, rpl371, rpl372, rpl373, rpl374, rpl375, rpl376, rpl377, rpl378, rpl379, rpl380, rpl381, rpl382, rpl383, rpl384, rpl385, rpl386, rpl387, rpl388, rpl389, rpl390, rpl391, rpl392, rpl393, rpl394, rpl395, rpl396, 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rpl522, rpl523, rpl524, rpl525, rpl526, rpl527, rpl528, rpl529, rpl530, rpl531, rpl532, rpl533, rpl534, rpl535, rpl536, rpl537, rpl538, rpl539, rpl540, rpl541, rpl542, rpl543, rpl544, rpl545, rpl546, rpl547, rpl548, rpl549, rpl550, rpl551, rpl552, rpl553, rpl554, rpl555, rpl556, rpl557, rpl558, rpl559, rpl560, rpl561, rpl562, rpl563, rpl564, rpl565, rpl566, rpl567, rpl568, rpl569, rpl570, rpl571, rpl572, rpl573, rpl574, rpl575, rpl576, rpl577, rpl578, rpl579, rpl580, rpl581, rpl582, rpl583, rpl584, rpl585, rpl586, rpl587, rpl588, rpl589, rpl590, rpl591, rpl592, rpl593, rpl594, rpl595, rpl596, rpl597, rpl598, rpl599, rpl600, rpl601, rpl602, rpl603, rpl604, rpl605, rpl606, rpl607, rpl608, rpl609, rpl610, rpl611, rpl612, rpl613, rpl614, rpl615, rpl616, rpl617, rpl618, rpl619, rpl620, rpl621, rpl622, rpl623, rpl624, rpl625, rpl626, rpl627, rpl628, rpl629, rpl630, rpl631, rpl632, rpl633, rpl634, rpl635, rpl636, rpl637, rpl638, rpl639, rpl640, rpl641, rpl642, rpl643, rpl644, rpl645, rpl646, rpl647, rpl648, rpl649, rpl650, rpl651, rpl652, rpl653, rpl654, rpl655, rpl656, rpl657, rpl658, rpl659, rpl660, rpl661, rpl662, rpl663, rpl664, rpl665, rpl666, rpl667, rpl668, rpl669, rpl670, rpl671, rpl672, rpl673, rpl674, rpl675, rpl676, rpl677, rpl678, rpl679, rpl680, rpl681, rpl682, rpl683, rpl684, rpl685, rpl686, rpl687, rpl688, rpl689, rpl690, rpl691, rpl692, rpl693, rpl694, rpl695, rpl696, rpl697, rpl698, rpl699, rpl700, rpl701, rpl702, rpl703, rpl704, rpl705, rpl706, rpl707, rpl708, rpl709, rpl710, rpl711, rpl712, rpl713, rpl714, rpl715, rpl716, rpl717, rpl718, rpl719, rpl720, rpl721, rpl722, rpl723, rpl724, rpl725, rpl726, rpl727, rpl728, rpl729, rpl730, rpl731, rpl732, rpl733, rpl734, rpl735, rpl736, rpl737, rpl738, rpl739, rpl740, rpl741, rpl742, rpl743, rpl744, rpl745, rpl746, rpl747, rpl748, rpl749, rpl750, rpl751, rpl752, rpl753, rpl754, rpl755, rpl756, rpl757, rpl758, rpl759, rpl760, rpl761, rpl762, rpl763, rpl764, rpl765, rpl766, rpl767, rpl768, rpl769, rpl770, rpl771, 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S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	percent ident	ORF nt length
967	1	1	411	[dbj 090119 STAM	S. aureus nra gene	97	395
991	1	672	337	[emb X52543 SAG	S. aureus agrA, agrB and hid genes	99	336
1000	1	1117	845	[gb L14017	Staphylococcus aureus methicillin-resistance protein (mecA) gene and unknown ORF, complete cds	78	190
1001	1	498	265	[dbj D86240 D862	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	99	234
1010	1	1	285	[gb U21221	Staphylococcus aureus hyaluronate lyase (hyaA) gene, complete cds	99	224
1046	1	656	330	[emb X72700 SAPV	S. aureus genes for S and F components of Pantone-Valentine leucocidins	85	205
1060	1	480	286	[emb X58434 SAPD	S. aureus pdhA, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolypamide acetyltransferase and dihydrolypamide dehydrogenase	99	180
1073	1	1176	589	[gb K02985	S. aureus (strain RN450) transposon Tn554 insertion site	100	131
1079	1	3	230	[dbj D86240 D862	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	99	228
1079	2	218	484	[dbj D86240 D862	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	100	267
1079	3	460	645	[dbj D86240 D862	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	100	186
1092	1	289	146	[emb X58434 SAPD	S. aureus pdhA, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolypamide acetyltransferase and dihydrolypamide dehydrogenase	98	124
1143	1	1	243	[gb W0177	S. aureus sigma factor (plac) gene, complete cds	99	243
1157	1	2	136	[emb Z48003 SAND	S. aureus gene for DNA polymerase III	97	127
1189	1	720	361	[gb S74031	nraA-nraA (ISP794) [Staphylococcus aureus, NCTC 8325, Insertion, 1820 nt]	99	360
1190	1	2	283	[gb W21854	S. aureus agr gene encoding an accessory gene regulator protein, complete cds	100	282
1190	2	1127	888	[emb X52543 SAG	S. aureus agrA, agrB and hid genes	100	240
1225	1	2	163	[emb X17679 SACO	Staphylococcus aureus coa gene for coagulase	97	124
1243	1	2	529	[dbj D86240 D862	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	99	495
1244	1	1	210	[gb S74031	nraA-nraA (ISP794) [Staphylococcus aureus, NCTC 8325, Insertion, 1820 nt]	100	210
1301	1	41	472	[emb X76490 SAGL	S. aureus (bb270) glbA and glbB genes	99	299

TABLE I

5. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
1315	1	18	326	emb X64172 SARP	[S.aureus rplL, orf202, rpoB(rif)] and rpoC genes for ribosomal protein L7/L12; hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	98	277	309
1519	1	2	175	dbj D28879 STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	98	139	174
1663	1	1346	675	dbj D66240 D862	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	98	672	672
1797	1	644	324	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	99	321	321
1857	1	1	192	gb H90536	Staphylococcus aureus alpha-hemolysin gene, 3' and	98	192	192
1921	1	2	181	emb X17688 SAFE	[S.aureus factor essential for expression of methicillin resistance (fema) gene, complete cds, and trpA gene, 3' and	100	180	180
1957	1	2	346	gb U60589	Staphylococcus aureus novel antigen gene, complete cds	99	345	345
1988	1	1	402	dbj D66240 D862	Staphylococcus aureus gene for unknown function and dlt operon dltA, dltB, dltC and dltD genes, complete cds	100	402	402
2100	1	414	208	gb H63177	[S.aureus sigma factor (plac) gene, complete cds	99	207	207
2199	1	1	402	gb U66664	Staphylococcus aureus DNA fragment with class II promoter activity	99	131	402
2537	1	308	156	emb X17688 SAFE	[S.aureus factor essential for expression of methicillin resistance (fema) gene, complete cds, and trpA gene, 3' end	99	153	153
2891	1	2	400	gb J25426	Staphylococcus aureus penicillin-binding protein 2 (pbp2) gene, complete cds	99	399	399
2950	1	718	398	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP70; HSP40; ORF35, complete cds	100	358	381
2971	1	3	398	gb U51132	Staphylococcus aureus o-nucinylbenzoic acid CoA ligase (nuc), and o-succinylbenzoic acid synthetase (nuc) genes, complete cds	97	272	396
2978	1	618	328	gb U31979	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroquinase synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	98	250	291
2985	1	832	464	emb X17679 SACO	Staphylococcus aureus coa gene for coagulase	98	347	369
3006	1	2170	1784	gb U11779	Staphylococcus aureus methicillin-resistant ATCC 33952 clone RNNV30 16S-23S rRNA spacer region	87	82	387
3008	1	474	238	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP70; HSP40; ORF35, complete cds	88	178	237
3008	2	451	281	dbj U30690 STAN	Staphylococcus aureus genes for ORF37; HSP70; HSP40; ORF35, complete cds	97	120	171

TABLE I

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP length	ORF nt length
3011	1	793	398	emb X62992 SAFN	S. aureus fnbB gene for fibronectin binding protein B	93	72	396
3019	1	2	235	gb J03479	S. aureus enzyme III-lac (lacP), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	97	234	234
3023	1	81	233	gb U06451	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	87	100	153
3029	1	90	287	gb U51133	Staphylococcus aureus phosphoenolpyruvate carboxylase (pckA) gene, complete cds	100	135	198
3039	1	18	164	gb U51133	Staphylococcus aureus phosphoenolpyruvate carboxylase (pckA) gene, complete cds	97	135	147
3039	2	70	327	gb U51133	Staphylococcus aureus phosphoenolpyruvate carboxylase (pckA) gene, complete cds	77	183	258
3056	1	3	215	emb X64172 SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	213	213
3059	1	1	261	dbj D30690 STAN	Staphylococcus aureus genes for ORF37; HSP70; HSP70; ORF35, complete cds	98	234	261
3073	1	27	284	gb U06451	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	99	229	258
3074	1	2	397	emb X64172 SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	96	250	396
3088	1	3	239	dbj D86727 D867	Staphylococcus aureus DNA for DNA polymerase III, complete cds	95	215	237
3097	1	444	244	emb Z18003 SARR	S. aureus gene for DNA polymerase III	97	160	201
3102	1	307	155	gb J03479	S. aureus enzyme III-lac (lacP), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	97	142	153
3121	1	568	398	emb X58434 SAPD	S. aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydroliipoamide acetyltransferase and dihydroliipoamide dehydrogenase	100	88	171
3125	1	463	233	emb X89233 SAMP	S. aureus DNA for rpoC gene	98	192	231
3133	1	2	175	emb Z18852 SACF	S. aureus gene for clumping factor	96	154	174
3160	1	420	211	dbj U10489 STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	89	197	210
3176	1	1	378	emb X58434 SAPD	S. aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydroliipoamide acetyltransferase and dihydroliipoamide dehydrogenase	96	91	378
3192	1	420	211	gb J03479	S. aureus enzyme III-lac (lacP), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	98	72	210
3210	1	3	143	gb U76714	Staphylococcus aureus peptidoglycan hydrolase gene, complete cds	96	141	141

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	Percent ident	ISI nt length	ORF nt length
3232	3	2106	1282	gb L14017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	71	257	825
333A	1	2	374	emb X49233 SARP	S. aureus DNA for rpoC gene	99	356	393
3343	1	192	634	gb L11530	Staphylococcus aureus transfer RNA sequence with two rRNAs	99	102	243
3555	1	637	320	emb Z18852 SACF	S. aureus gene for clumping factor	99	307	318
3559	1	3	182	emb X17679 SACO	Staphylococcus aureus coa gene for coagulase	100	141	180
3559	2	95	313	emb X17679 SACO	Staphylococcus aureus coa gene for coagulase	98	174	219
3563	1	278	141	gb U35733	Staphylococcus aureus prolipoprotein diacylglycerol transferase (lgt) gene, complete cds	100	79	138
3563	2	527	363	gb L35733	Staphylococcus aureus prolipoprotein diacylglycerol transferase (lgt) gene, complete cds	98	162	165
3566	1	3	422	emb X16457 SAST	Staphylococcus aureus gene for staphylocoagulase	98	175	420
3588	1	2	262	gb L43098	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	99	253	261
3593	1	3	350	gb J03479	S. aureus enzyme III-lac (lacF), enzyme III-lac (lacF), and phospho-beta-galactosidase (lacZ) genes, complete cds	99	345	348
3600	1	758	381	emb Z18852 SACF	S. aureus gene for clumping factor	72	346	378
3602	1	786	396	emb Z18852 SACF	S. aureus gene for clumping factor	98	319	393
3656	1	1013	528	emb Z18852 SACF	S. aureus gene for clumping factor	84	403	486
3682	1	3	236	emb X64172 SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	231	234
3682	2	224	415	emb X64172 SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	112	152
3693	1	758	423	emb X62992 SAFH	S. aureus fnbB gene for fibronectin binding protein B	100	229	336
3702	1	593	154	gb L11530	Staphylococcus aureus transfer RNA sequence with two rRNAs	94	81	240
3725	1	924	463	emb Z18852 SACF	S. aureus gene for clumping factor	71	367	462
3761	1	809	450	gb L14017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	85	333	360
3767	1	1	402	emb X64172 SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	98	387	402

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	percent ident	HSP nt length	ORF nt length
3775	1	2	286	emb X64172 SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	227	285
3786	1	456	229	dbj D10489 STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	100	204	228
3786	2	542	366	dbj D10489 STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	95	123	177
3798	1	3	251	emb X17679 SACO	Staphylococcus aureus coa gene for coagulase	99	249	249
3813	1	793	398	gb J04151	S. aureus fibronectin-binding protein (fnbA) mRNA, complete cds	98	356	396
3819	1	184	402	emb X68425 SA23	S. aureus gene for 23S rRNA	99	161	219
3844	1	932	468	gb U48826	Staphylococcus aureus elastin binding protein (ebpS) gene, complete cds	87	204	465
3845	1	1	381	emb X58434 SAPD	S. aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	94	356	381
3856	1	798	400	gb U14017	Staphylococcus aureus methicillin-resistance protein (mecA) gene and unknown ORF, complete cds	76	192	399
3859	1	1049	573	emb Z18852 SACP	S. aureus gene for clumping factor	85	347	477
3871	1	650	327	gb U76714	Staphylococcus aureus peptidoglycan hydrolase gene, complete cds	100	299	324
3876	1	2	253	dbj D10489 STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	100	217	252
3877	1	572	288	gb U03479	S. aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	97	209	285
3878	1	1	237	emb X58434 SAPD	S. aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	96	155	237
3888	1	3	173	emb X16457 SAST	Staphylococcus aureus gene for staphylocoagulase	98	171	171
3893	1	1	183	emb X89233 SARP	S. aureus DNA for rpoC gene	100	170	183
3893	2	181	357	emb X89233 SARP	S. aureus DNA for rpoC gene	98	79	177
3894	1	3	485	emb X64172 SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	450	483
3895	1	816	420	gb J04151	S. aureus fibronectin-binding protein (fnbA) mRNA, complete cds	99	411	417
3905	1	48	239	gb U05004	Staphylococcus aureus dehydroquinase synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	100	159	192
3905	2	188	400	gb U05004	Staphylococcus aureus dehydroquinase synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	97	88	213

TABLE I

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
3910	1	3	359	emb X58434 SAPP	S. aureus pds, pdhC and pdsD genes for pyruvate decarboxylase, dihydrolypoamide acetyltransferase and dihydrolypoamide dehydrogenase	99	278	357
3915	1	1	330	gb U14017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	75	175	330
3964	1	691	347	emb Z48003 SADN	S. aureus gene for DNA polymerase III	100	295	345
4007	1	199	390	emb X16457 SNST	Staphylococcus aureus gene for staphylocoagulase	98	163	192
4036	1	3	371	dbj D10489 STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	99	339	369
4046	1	692	348	emb Z18852 SACF	S. aureus gene for clumping factor	87	221	345
4060	1	1	375	emb Z18852 SACF	S. aureus gene for clumping factor	96	271	375
4061	1	860	432	emb Z48003 SADN	S. aureus gene for DNA polymerase III	99	429	429
4062	1	606	304	gb U14017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	75	198	303
4085	1	58	402	gb U11786	Staphylococcus aureus methicillin-resistant ATCC 33952 clone RN42165-235 rRNA spacer region	98	127	345
4088	1	2	301	gb U43098	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	99	227	300
4093	1	2	277	emb X58434 SAPP	S. aureus pds, pdhC and pdsD genes for pyruvate decarboxylase, dihydrolypoamide acetyltransferase and dihydrolypoamide dehydrogenase	99	276	276
4097	1	1	402	emb Z18852 SACF	S. aureus gene for clumping factor	74	307	402
4116	1	22	402	gb U05004	Staphylococcus aureus dehydroquinase synthase (aroH) gene, 3' end cds; 3-phosphoshikimate-3-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	98	157	381
4125	1	240	401	gb U73374	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	100	86	162
4149	1	35	247	gb U04151	S. aureus fibronectin-binding protein (fnbA) mRNA, complete cds	99	200	213
4151	1	629	366	gb U14017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	87	150	264
4154	1	754	398	emb X64172 SAPP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	297	357
4179	1	1	294	emb X64172 SAPP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	98	240	294

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	Percent Ident	HSP nt length	ORF nt length
4203	1	1	255	emb X89233 SARP	S. aureus DNA for rpoC gene	99	239	255
4206	1	1	303	emb Z18852 SACF	S. aureus gene for clumping factor	100	236	303
4206	2	195	344	emb Z18852 SACF	S. aureus gene for clumping factor	95	65	150
4208	1	108	314	emb X58434 SAPD	S. aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydroliipoamide acetyltransferase and dihydroliipoamide dehydrogenase	89	76	207
4216	1	656	330	emb X58434 SAPD	S. aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydroliipoamide acetyltransferase and dihydroliipoamide dehydrogenase	98	126	327
4226	1	594	298	gb L11530	Staphylococcus aureus transfer RNA sequence with two rRNAs	97	132	297
4260	1	216	383	gb U11784	Staphylococcus aureus methicillin-resistant ATCC 33952 clone RNNV40 16S-23S rRNA spacer region	83	141	168
4272	1	355	179	emb Z48003 SADN	S. aureus gene for DNA polymerase III	100	164	177
4276	1	4	177	emb X16457 SAST	Staphylococcus aureus gene for staphylocoagulase	99	150	174
4277	1	1	270	emb X64172 SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	265	270
4282	1	691	377	emb X64172 SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	98	282	315
4291	1	379	191	emb X64172 SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	183	189
4295	1	3	329	emb X16457 SAST	Staphylococcus aureus gene for staphylocoagulase	94	144	327
4313	1	435	260	gb L11530	Staphylococcus aureus transfer RNA sequence with two rRNAs	100	94	156
4315	1	3	185	gb J03479	S. aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	100	158	183
4315	2	101	310	gb J03479	S. aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	98	75	210
4327	1	1	294	gb J41098	Trinsepson Tn5104 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	98	294	294
4360	1	603	319	gb J02910	Staphylococcus aureus ATCC 25923 16S rRNA gene, partial sequence	100	116	285
4364	1	3	146	emb X64172 SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	95	140	144
4388	1	167	310	emb X62992 SAPN	S. aureus fnbB gene for fibronectin binding protein B	73	119	144

TABLE I

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	MSP nt length	ORF nt length
4401	1	2	313	emb X62992 SAFN	S. aureus fnbB gene for fibronectin binding protein B	97	243	312
4421	1	36	281	dbj D12572 STA2	Staphylococcus aureus rna gene for 23S ribosomal RNA	100	112	246
4426	1	3	293	emb Z18852 SACF	S. aureus gene for clumping factor	85	185	291
4428	1	493	248	emb X64172 SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	139	246
4462	1	2	271	emb X64172 SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	270	270
4466	1	1	240	emb Z18852 SACF	S. aureus gene for clumping factor	99	231	240
4469	1	1	312	gb J03479	S. aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	99	265	312
4485	1	3	263	gb U43098	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	98	259	261
4492	1	74	400	gb H68227	Staphylococcus aureus DNA gyrase B subunit (gyrB) RecP homologue (recP) and DNA gyrase A subunit (gyrA) gene, complete cds	85	104	327
4497	1	515	269	emb Z18852 SACF	S. aureus gene for clumping factor	99	213	267
4529	1	2	172	emb X64172 SARP	S. aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	151	171
4547	1	1	300	emb X62992 SAFN	S. aureus fnbB gene for fibronectin binding protein B	100	157	300
4554	1	318	160	emb Z18852 SACF	S. aureus gene for clumping factor	84	126	159
4565	1	9	227	emb Z18852 SACF	S. aureus gene for clumping factor	84	213	219
4569	1	79	222	emb Z18852 SACF	S. aureus gene for clumping factor	98	127	144
4608	1	22	216	emb X58434 SAPD	S. aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	92	168	195
4614	1	464	234	emb Z18852 SACF	S. aureus gene for clumping factor	86	169	231
4623	1	105	302	gb J04151	S. aureus fibronectin-binding protein (fnbA) mRNA, complete cds	99	152	198
4632	1	18	206	gb J03479	S. aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	98	183	189
4646	1	1	222	emb Z18852 SACF	S. aureus gene for clumping factor	84	100	222
4687	1	2	166	gb J04151	S. aureus fibronectin-binding protein (fnbA) mRNA, complete cds	98	156	165

TABLE I

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
4695	1	313	158	gb U14017	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	75	155	156
4703	1	1	153	emb X58434 SAPD	S. aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	98	103	153

TABLE I

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
20	6	5089	4679	gi 5118139	ORF1 [Staphylococcus bacteriophage phi 11]	100	100	411
149	3	2032	1577	phr B49703 B497	int gene activator RlnA - bacteriophage phi 11	100	100	456
149	5	2109	1912	gi 166161	Bacteriophage phi-11 int gene activator [Staphylococcus acteriophage phi 11]	100	100	198
349	2	558	409	gi 166159	integrase (int) [Staphylococcus bacteriophage phi 11]	100	100	150
398	1	1372	707	gi 166159	integrase (int) [Staphylococcus bacteriophage phi 11]	100	99	666
398	2	783	1001	gi 455128	excisionase (xis) [Staphylococcus bacteriophage phi 11]	100	100	219
502	4	1914	1744	gi 1204912	H. influenzae predicted coding region H10660 [Haemophilus influenzae]	100	71	171
849	1	2	262	gi 1373002	polyprotein [Bee common mosaic virus]	100	46	261
1349	1	277	140	gi 143359	protein synthesis initiation factor 2 (infB) [Bacillus subtilis] gi 49319	100	82	138
2880	1	21	308	gi 862933	protein kinase C inhibitor-1 (Homo sapiens)	100	98	288
3085	1	428	216	gi 1354211	PER112-like protein [Bacillus subtilis]	100	100	213
4168	2	571	398	gi 1354211	PER112-like protein [Bacillus subtilis]	100	100	174
331	1	2	247	gi 426473	nusG gene product [Staphylococcus carnosus]	98	95	246
207	2	1272	1463	gi 460259	enolase [Bacillus subtilis]	97	90	192
331	2	395	850	gi 581638	h11 protein [Staphylococcus carnosus]	97	93	456
366	1	39	215	gi 66161	Bacteriophage phi-11 int gene activator [Staphylococcus acteriophage phi 11]	97	95	177
680	3	718	936	gi 426473	nusG gene product [Staphylococcus carnosus]	97	97	219
3578	1	284	144	gi 1339950	large subunit of NAMH-dependent glutamate synthase [Plectonura boryanum]	97	79	141
157	1	321	518	gi 1022726	unknown [Staphylococcus haemolyticus]	96	88	198
205	33	16470	16147	gi 1165302	S10 [Bacillus subtilis]	96	91	324
3919	1	48	401	gi 871784	Clp-like ATP-dependent protease binding subunit [Bos taurus]	96	81	354
4133	1	830	417	gi 1022726	unknown [Staphylococcus haemolyticus]	96	84	414
4168	1	708	355	gi 1354211	PER112-like protein [Bacillus subtilis]	96	95	354
4207	1	312	157	gi 602031	similar to triaethylamine DH [Mycoplasma capricolum] pir 849550 849550 probable triaethylamine dehydrogenase (EC 5.99.7) - Mycoplasma capricolum (SQC) (fragment)	96	86	156

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	Length (nt)
4227	2	152	331	gi 871784	Cip-like ATP-dependent protease binding subunit (Bos taurus)	96	81	180
4416	1	570	286	gi 1022726	unknown (Staphylococcus haemolyticus)	96	84	285
22	1	858	430	gi 511070	UreC (Staphylococcus xylosus)	95	88	429
22	7	4362	4036	gi 581787	urease gamma subunit (Staphylococcus xylosus)	95	79	327
82	6	8794	9114	pir JC00008 JC00	ribosomal protein S7 - Bacillus stearothermophilus	95	83	321
154	9	9280	7838	gi 1354211	PET112-like protein (Bacillus subtilis)	95	92	1443
186	3	2798	2055	gi 1514656	serine O-acetyltransferase (Staphylococcus xylosus)	95	87	744
205	5	4406	4014	gi 142462	ribosomal protein S11 (Bacillus subtilis)	95	85	393
205	7	5017	4793	gi 142459	initiation factor 1 (Bacillus subtilis)	95	84	225
205	21	11365	10991	gi 1044974	ribosomal protein L14 (Bacillus subtilis)	95	93	375
259	5	7288	6644	sp P47995 VSEA	HYPOTHETICAL PROTEIN IN SECA 5' REGION (ORF1) (FRAGMENT)	95	85	645
302	3	795	1097	gi 40186	homologous to E.coli ribosomal protein L27 (Bacillus subtilis) I143592 L27 ribosomal protein (Bacillus subtilis) r C21895 C21895 ribosomal protein L27 - Bacillus subtilis p P05657 RL27_BACSU 50S RIBOSOMAL PROTEIN L27 (BL10) (RL24) I40175 L24 gene prod	95	89	303
310	1	579	1523	gi 1177684	chorismate mutase (Staphylococcus xylosus)	95	92	945
414	1	2	163	pir C48396 C483	ribosomal protein L14 - Bacillus stearothermophilus	95	90	162
4185	2	125	277	gi 1276841	glutamate synthase (GOGAT) (Porphyra purpurea)	95	86	153
22	2	1028	723	gi 511069	UreC (Staphylococcus xylosus)	94	91	306
22	5	5046	3310	gi 410516	urease alpha subunit (Staphylococcus xylosus)	94	85	1737
40	4	815	1372	gi 666116	glucose kinase (Staphylococcus xylosus)	94	87	558
205	18	10012	9536	gi 1044978	ribosomal protein S8 (Bacillus subtilis)	94	78	477
326	4	3378	2542	gi 557492	dihydroxynaphthoic acid (DHNA) synthetase (Bacillus subtilis) gi 143186 dihydroxynaphthoic acid (DHNA) synthetase (Bacillus subtilis)	94	85	837
414	3	737	955	gi 467386	chlorophen and furan oxidation (Bacillus subtilis)	94	77	219
426	3	2260	1823	gi 1263908	putative (Staphylococcus epidermidis)	94	87	438
534	1	2	355	gi 633650	enzyme II (mannitol) (Staphylococcus carnosus)	94	84	354
1017	1	2	229	gi 1149435	putative (Lactococcus lactis)	94	73	228
3098	1	330	184	gi 143952	ipa-26d gene product (Bacillus subtilis)	94	50	147

TABLE 2

S. aureus - putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
3232	1	630	316	gi 1022725	unknown [Staphylococcus haemolyticus]	94	84	315
42	5	2089	2259	pir B48396 B483	ribosomal protein L3 - Bacillus stearothermophilus	93	81	171
101	2	1745	1983	gi 155345	arsenic efflux pump protein [Plasmid pS267]	93	82	363
205	24	12227	11865	sp P14577 KJ16_1	50S RIBOSOMAL PROTEIN L16	93	83	363
259	4	8291	5673	gi 499335	secA protein [Staphylococcus carnosus]	93	85	2619
275	1	2226	1114	gi 631650	enzyme II(mannitol) [Staphylococcus carnosus]	93	86	1113
444	6	6207	5773	gi 1022726	unknown [Staphylococcus haemolyticus]	93	81	435
491	1	152	622	gi 46912	ribosomal protein L13 [Staphylococcus carnosus]	93	88	471
607	6	1674	2033	gi 1022726	unknown [Staphylococcus haemolyticus]	93	83	360
653	1	973	488	gi 580890	translation initiation factor IF3 (AA 1-172) [Bacillus teichotheophilus]	93	77	486
1864	1	3	194	gi 106553	ribosomal protein small subunit (Homo sapiens)	93	93	192
2997	1	28	300	gi 143390	[carbamyl] phosphate synthetase [Bacillus subtilis]	93	82	273
3232	2	907	596	gi 1022725	unknown [Staphylococcus haemolyticus]	93	84	312
3761	2	794	621	gi 1022725	unknown [Staphylococcus haemolyticus]	93	88	174
16	1	3	374	gi 142781	putative cytoplasmic protein; putative [Bacillus subtilis] sp P27954 UVRB_BACSU EXCINUCLEASE ABC SUBUNIT B (DNA PROTEIN) FRAGMENT	92	83	372
31	7	5915	6124	gi 1136430	KIAA0185 protein (Homo sapiens)	92	46	210
56	19	26483	27391	gi 467401	unknown [Bacillus subtilis]	92	80	909
69	6	5882	6110	gi 530200	trophoblastin (Ovis aries)	92	53	249
145	3	2568	2038	gi 1022725	unknown [Staphylococcus haemolyticus]	92	80	531
171	3	2760	2362	gi 517475	D-amino acid transaminase [Staphylococcus haemolyticus]	92	86	399
205	12	7495	6962	gi 49189	secY gene product [Staphylococcus carnosus]	92	85	534
205	19	10812	10255	gi 1044976	ribosomal protein u5 [Bacillus subtilis]	92	82	558
219	1	210	357	gi 1303812	YgeV [Bacillus subtilis]	92	88	354
344	3	1575	1805	gi 1405474	CspC protein [Bacillus cereus]	92	85	231
699	1	20	361	gi 413999	lpa-75d gene product [Bacillus subtilis]	92	81	342
1343	1	2	160	pir A45434 A454	ribosomal protein L19 - Bacillus stearothermophilus	92	84	159

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1958	1	524	264	gi 407908	[E]lacr [Staphylococcus xylosus]	92	80	261
3578	2	718	386	gi 1339950	large subunit of NADH-dependent glutamate synthase [Plectonaea boryanum]	92	78	333
3585	1	644	324	gi 1339950	large subunit of NADH-dependent glutamate synthase [Plectonaea boryanum]	92	81	321
3640	1	4	402	gi 1022726	unknown [Staphylococcus haemolyticus]	92	81	399
4362	1	14	178	gi 450688	hscdm gene of Escherichia coli product [Escherichia coli] pif[S38437]S38437 hsdM protein - Escherichia coli pif[S09629]S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	92	76	165
4446	1	358	182	gi 1022725	unknown [Staphylococcus haemolyticus]	92	82	177
4549	1	462	232	gi 1022726	unknown [Staphylococcus haemolyticus]	92	80	231
4626	1	3	224	gi 1022725	unknown [Staphylococcus haemolyticus]	92	84	222
2	4	3880	4531	gi 535349	[Codr] [Bacillus subtilis]	91	74	552
28	1	2	1126	gi 1001376	hypothetical protein [Synechocystis sp.]	91	78	1125
60	5	1354	1701	gi 1226043	[orf2 downstream of glucose kinase [Staphylococcus xylosus]	91	80	348
101	1	1989	1036	gi 150728	[arsenic efflux pump protein [Plasmid p158]	91	80	954
187	2	412	1194	gi 142559	[ATP synthase alpha subunit [Bacillus megaterium]	91	79	783
205	22	11579	11298	gi 40149	[S17 protein (AA 1-87) [Bacillus subtilis]	91	83	282
206	7	8184	10262	gi 1072418	[glcA gene product [Staphylococcus carnosus]	91	83	2079
306	2	3885	2326	gi 143012	[GMP synthetase [Bacillus subtilis]	91	78	1560
306	3	5319	3826	gi 467399	[IMP dehydrogenase [Bacillus subtilis]	91	79	1494
310	3	2194	3207	gi 1177685	[cspA gene product [Staphylococcus xylosus]	91	81	1014
343	4	2974	3150	gi 949974	[sucrose repressor [Staphylococcus xylosus]	91	82	177
480	3	1606	1042	gi 433991	[ATP synthase subunit beta [Bacillus subtilis]	91	85	1437
536	3	2026	1280	gi 143366	[adenylosuccinate lyase (PUR-B) [Bacillus subtilis] pif[C29326]W25SDS adenylosuccinate lyase (EC 4.3.2.2) - Bacillus subtilis	91	79	747
552	1	1064	615	gi 297874	[fructose-bisphosphate aldolase [Staphylococcus carnosus] pif[A49943]A49943 fructose-bisphosphate aldolase (EC 4.1.2.13) - taphylococcus carnosus (strain TH100)	91	79	450
637	1	1	1536	gi 143597	[CTP synthetase [Bacillus subtilis]	91	79	1536
858	1	21	359	gi 385178	unknown [Bacillus subtilis]	91	66	339

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1327	1	339	530	gi 496558	orfX [Bacillus subtilis]	91	71	192
2515	1	466	275	gi 511070	UreG [Staphylococcus xyloosus]	91	85	192
2594	1	2	202	gi 146824	beta-cystathionase [Escherichia coli]	91	75	201
3764	1	847	425	gi 1022725	unknown [Staphylococcus haemolyticus]	91	78	423
4011	1	127	495	gi 1022726	unknown [Staphylococcus haemolyticus]	91	79	369
4227	1	1	177	gi 296464	ATPase [Lactococcus lactis]	91	66	177
42	3	815	1033	gi 520401	catalse [Haemophilus influenzae]	90	86	219
51	8	3717	4607	gi 580899	OppF gene product [Bacillus subtilis]	90	74	891
129	3	5317	4001	gi 1146206	glutamate dehydrogenase [Bacillus subtilis]	90	76	1317
164	17	16628	16933	sp P05766 RS15_	30S RIBOSOMAL PROTEIN S15 (BS18)	90	74	306
171	5	2983	2819	gi 517475	D-amino acid transaminase [Staphylococcus haemolyticus]	90	78	165
205	4	4497	3550	gi 142463	RNA polymerase alpha-core-subunit [Bacillus subtilis]	90	76	948
205	6	4748	4410	gi 1044989	ribosomal protein S13 [Bacillus subtilis]	90	73	339
205	10	7165	6404	gi 49189	secY gene product [Staphylococcus carnosus]	90	81	762
205	11	6645	6472	gi 49189	secY gene product [Staphylococcus carnosus]	90	78	174
205	27	13692	13345	gi 786157	ribosomal protein S19 [Bacillus subtilis]	90	79	348
205	31	15858	15496	gi 1165303	L3 [Bacillus subtilis]	90	79	363
240	5	7023	5773	gi 1161380	IceA [Staphylococcus epidermidis]	90	78	1251
299	6	3378	3947	gi 467440	phosphoribosylpyrophosphate synthetase [Bacillus subtilis] gi 40218 PRPP synthetase (AA 1-317) [Bacillus subtilis]	90	78	570
320	2	1025	1717	gi 312443	carbamoyl-phosphate synthase (glutamine-hydrolysing) [Bacillus aldolycicus]	90	75	693
330	4	1581	1769	gi 986963	beta-tubulin [Sporidiobolus pararoseus]	90	80	189
369	1	954	523	pir S34762 S347	L-serine dehydratase beta chain - Clostridium sp.	90	77	432
557	1	3	188	gi 1511589	M. jannaschii predicted coding region MJ1624 [Methanococcus jannaschii]	90	54	186
663	2	667	1200	gi 143786	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [Bacillus subtilis] pir J70481 WDS tryptophan-tRNA ligase (EC 6.1.1.2) - Bacillus ubtilis	90	73	534
717	1	1	261	gi 143065	hubat [Bacillus stearothermophilus]	90	79	261
745	4	1059	865	gi 1205433	H. influenzae predicted coding region H1190 [Haemophilus influenzae]	90	81	195

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
1007	1	386	585	gi 143366	adenylosuccinate lyase (Pur-B) [Bacillus subtilis] pir C29326 W2BS05 adenylosuccinate lyase (EC 4.3.2.2) - Bacillus subtilis	90	77	180
1054	1	579	331	gi 1033122	ORF_1729 [Escherichia coli]	90	50	249
1156	1	117	707	gi 1477776	ClpP [Bacillus subtilis]	90	80	591
1180	1	408	205	gi 1377831	unknown [Bacillus subtilis]	90	74	204
1253	1	1	462	gi 40046	phosphoglucose isomerase A (AA 1-449) [Bacillus stearothermophilus] ir S15936 NU85A glucose-6-phosphate isomerase (EC 5.3.1.9) A - cillus stearothermophilus	90	75	462
2951	1	3	269	gi 144816	(formyltetrahydrofolate synthetase (FTHFS) (tgg start codon) (EC 3.4.3) [Mooralla thermacetica]	90	76	267
3140	1	327	166	gi 1070014	protein-dependent [Bacillus subtilis]	90	52	162
4594	1	3	233	gi 871784	Clp-like ATP-dependent protease binding subunit [Bos taurus]	90	76	231
87	1	1028	1750	gi 467327	unknown [Bacillus subtilis]	89	75	723
112	1	2	505	gi 153741	ATP-binding protein [Streptococcus mutans]	89	77	504
118	1	120	398	gi 1303804	VqeQ [Bacillus subtilis]	89	75	279
128	4	3545	3757	gi 460257	triose phosphate isomerase [Bacillus subtilis]	89	84	213
164	12	11667	12755	gi 39954	IF2 (aa 1-741) [Bacillus stearothermophilus]	89	80	1089
205	11	7475	7405	ni 216338	ORF for 615 ribosomal protein [Bacillus subtilis]	89	76	471
205	32	16152	15823	gi 1165303	L3 [Bacillus subtilis]	89	80	330
270	3	2407	2207	pir C41902 C419	arsenate reductase (EC 1.-.-.-) - Staphylococcus xyloos plasmid pSX267	89	81	201
395	2	157	672	gi 520574	glutamate racemase [Staphylococcus haemolyticus]	89	80	516
494	1	3	839	gi 396259	protease [Staphylococcus epidermidis]	89	77	837
510	1	1	444	gi 40046	phosphoglucose isomerase A (AA 1-449) [Bacillus stearothermophilus] ir S15936 NU85A glucose-6-phosphate isomerase (EC 5.3.1.9) A - cillus stearothermophilus	89	74	444
615	1	2124	1210	gi 1303812	VqeV [Bacillus subtilis]	89	74	915
841	1	18	341	gi 1165303	L3 [Bacillus subtilis]	89	80	324
1111	1	352	813	gi 47146	thermonuclease [Staphylococcus intermedius]	89	70	462
1875	1	2	256	gi 1205108	ATP-dependent protease binding subunit [Haemophilus influenzae]	89	82	255
2963	1	11	367	gi 467458	cell division protein [Bacillus subtilis]	89	83	357

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3020	1	90	362	gi1123998	hypothetical protein [Bacillus subtilis]	89	66	273
3565	1	2	400	gi1125635	dihydroxy-acid dehydratase [Bacillus subtilis]	89	75	399
3586	1	105	314	gi1580832	ATP synthase subunit gamma [Bacillus subtilis]	89	82	210
3629	1	794	399	gi11009366	Respiratory nitrate reductase [Bacillus subtilis]	89	78	356
3688	1	2	400	gi1146206	glutamate dehydrogenase [Bacillus subtilis]	89	75	399
3699	1	794	399	gi1133950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	89	75	396
4016	1	428	216	gi11009366	Respiratory nitrate reductase [Bacillus subtilis]	89	71	213
4177	1	471	301	gi1149426	putative [Lactococcus lactis]	89	76	171
4636	1	601	302	gi11022725	unknown [Staphylococcus haemolyticus]	89	80	300
4635	1	320	162	gi11022725	unknown [Staphylococcus haemolyticus]	89	73	159
2	2	1330	2676	gi1520754	putative [Bacillus subtilis]	88	76	1347
42	2	468	848	sp142321[CATA_	CATALASE (EC 1.11.1.61)	88	76	381
53	5	6389	4722	gi1474177	alpha-D-1,4-glucosidase [Staphylococcus xylosus]	88	80	1668
56	16	18018	18617	gi1467411	recombination protein [Bacillus subtilis]	88	77	500
60	3	376	843	gi1666116	glucose kinase [Staphylococcus xylosus]	88	77	468
70	2	1583	1245	gi144095	replication initiator protein [Listeria monocytogenes]	88	74	339
82	8	11514	12719	gi1460663[A606	translation elongation factor Tu - Bacillus subtilis	88	79	1206
103	7	4179	4391	gi1167181	serine/threonine kinase receptor [Brassica napus]	88	77	213
114	8	7732	8232	gi11022726	unknown [Staphylococcus haemolyticus]	88	72	501
118	2	308	2011	gi11303804	YqeQ [Bacillus subtilis]	88	77	1704
141	3	657	1136	gi11405446	transketolase [Bacillus subtilis]	88	72	480
148	7	5871	6116	gi1118002	dihydroxyacetate synthase [Staphylococcus haemolyticus]	88	78	246
165	3	1428	2231	gi1460053	phenylalanyl-tRNA synthetase alpha subunit [Bacillus subtilis]	88	80	804
				trtS11730[YF85A phenylalanine--tRNA ligase (EC 6.1.1.20) alpha sub -				
				Bacillus subtilis				
205	28	15027	14185	gi11165306	L2 [Bacillus subtilis]	88	82	843
225	1	1569	898	gi11303840	YnfS [Bacillus subtilis]	88	78	672
235	1	2	1975	gi1452309	valyl-tRNA synthetase [Bacillus subtilis]	88	76	1974

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match	match gene name	% sim	% ident	length (nt)
339	3	2060	1566	gi 1118002		[dihydrodipicolinate synthase (Staphylococcus haemolyticus)]	88	73	495
443	4	4325	2928	gi 558559		[pyrimidine nucleoside phosphorylase (Bacillus subtilis)]	88	73	1398
532	1	3	419	gi 143797		[valyl-tRNA synthetase (Bacillus stearothermophilus) sp p1911 SVV_BACST VALYL-TRNA SYNTHETASE (EC 6.1.1.9) VALINE--TRNA LIGASE) (VALS)]	88	78	417
534	3	2504	2968	gi 153049		[mannitol-specific enzyme III (Staphylococcus carnosus) pir JQ0088 JQ0088 phosphotransferase system enzyme II (EC 7.1.1.69), mannitol-specific factor III - Staphylococcus carnosus sp P17876 PTMA_STACA PTS SYSTEM, MANNITOL-SPECIFIC IIA COMPONENT SIIA-HTU)]	88	82	465
705	2	584	399	gi 710018		[nitrite reductase (nirB) (Bacillus subtilis)]	88	70	186
1000	2	1824	1309	gi 1022726		[unknown (Staphylococcus haemolyticus)]	88	78	516
1299	1	587	324	gi 401786		[phosphomannosidase (Mycoplasma pirum)]	88	55	264
1341	2	170	400	gi 39963		[ribosomal protein L20 (AA 1-119) (Bacillus stearothermophilus) lr S05348 RS920 ribosomal protein L20 - Bacillus stearothermophilus]	88	82	231
1386	1	41	214	pir B47154 B471		[signal recognition particle 54K chain homolog 7th - Bacillus subtilis]	88	71	174
1386	2	183	533	pir B47154 B471		[signal recognition particle 54K chain homolog 7th - Bacillus subtilis]	88	73	351
2949	1	704	399	gi 535350		[CodX (Bacillus subtilis)]	88	73	306
2984	1	5	169	gi 218277		[O-acetylserine(thiol) lyase (Spinacia oleracea)]	88	70	165
3035	1	1	138	gi 493083		[dihydroxyacetone kinase (Citrobacter freundii)]	88	67	138
3089	1	3	152	gi 606055		[ORF_1746 (Escherichia coli)]	88	88	150
3917	1	817	410	gi 143378		[pyruvate decarboxylase (E-1) beta subunit (Bacillus subtilis) gi 1377836 pyruvate decarboxylase E-1 beta subunit (Bacillus subtilis)]	88	77	408
4199	1	680	342	gi 1405454		[aconitase (Bacillus subtilis)]	88	82	339
4201	1	734	369	gi 515938		[glutamate synthase (ferredoxin) (Synecocystis sp.) pir S46957 S46957 glutamate synthase (ferredoxin) (EC 1.4.7.1) - Synecocystis sp.]	88	84	366
4274	1	1	336	gi 515938		[glutamate synthase (ferredoxin) (Synecocystis sp.) pir S46957 S46957 glutamate synthase (ferredoxin) (EC 1.4.7.1) - Synecocystis sp.]	88	84	336
4308	1	794	399	gi 1146206		[glutamate dehydrogenase (Bacillus subtilis)]	88	71	396
2	5	4570	6000	gi 535350		[CodX (Bacillus subtilis)]	87	70	1431
52	8	6783	5482	gi 1064791		[function unknown (Bacillus subtilis)]	87	66	300

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
73	3	1584	2480	gi 142992	glycerol kinase (glpk) (EC 2.7.1.30) [Bacillus subtilis] pir B45868 B45868	87	72	897
					glycerol kinase (EC 2.7.1.30) - Bacillus subtilis ap P18157 GLPK_BACSU			
					GLYCEROL KINASE (EC 2.7.1.30) (ATP:GLYCEROL - PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK)			
98	12	8813	9100	gi 467433	unknown [Bacillus subtilis]	87	82	288
124	4	4265	2988	gi 556886	serine hydroxymethyltransferase [Bacillus subtilis] pir S49363 S49363	87	77	1278
					serine hydroxymethyltransferase - Bacillus ubtilla			
124	6	4457	4032	gi 556883	unknown [Bacillus subtilis]	87	66	426
148	5	3741	4559	gi 467460	unknown [Bacillus subtilis]	87	70	819
164	13	12710	13810	gi 39954	IF2 (aa 1-741) [Bacillus stearothermophilus]	87	72	1101
177	2	1104	2126	gi 467385	unknown [Bacillus subtilis]	87	78	1023
199	1	1982	1158	gi 140527	iron-sulfur protein [Bacillus subtilis]	87	77	825
199	2	4717	2933	pir A27763 A277	succinate dehydrogenase (EC 1.3.99.1) flavoprotein - Bacillus subtilis	87	80	1785
205	23	11782	11543	gi 1044972	ribosomal protein L29 [Bacillus subtilis]	87	78	240
205	25	13275	12607	gi 1165109	[S3 [Bacillus subtilis]	87	75	669
222	1	2033	1107	gi 1177249	rec23 gene product [Bacillus subtilis]	87	70	927
236	3	1635	1333	gi 1146198	ferredoxin [Bacillus subtilis]	87	80	303
246	5	2585	2392	gi 467373	ribosomal protein S18 [Bacillus subtilis]	87	77	294
260	2	4189	3422	gi 1161382	IceC [Staphylococcus epidermidis]	87	72	768
320	3	1696	2391	gi 312443	carbamoyl-phosphate synthase (glutamine-hydrolysing) [Bacillus aldyticus]	87	80	696
380	4	1165	1383	gi 142570	ATP synthase c subunit [Bacillus firmus]	87	80	219
414	4	900	1073	gi 467386	chlorophen and furan oxidation [Bacillus subtilis]	87	77	174
425	2	1003	794	gi 1046166	gillin repressor [Mycoplasma genitalium]	87	69	210
448	3	1255	722	gi 405134	acetate kinase [Bacillus subtilis]	87	75	534
480	1	1	711	gi 142559	ATP synthase alpha subunit [Bacillus megaterium]	87	79	711
481	1	2	352	sq Q06797 RL1_B	50S RIBOSOMAL PROTEIN L1 (BL1)	87	72	351
677	2	359	955	gi 460911	fructose-bisphosphate aldolase [Bacillus subtilis]	87	78	597
677	3	934	1284	gi 460911	fructose-bisphosphate aldolase [Bacillus subtilis]	87	78	351
876	1	3	452	gi 1146247	asparaginyl-tRNA synthetase [Bacillus subtilis]	87	79	450

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1376	1	426	214	gi11065555	F4H6.4 gene product [Caenorhabditis elegans]	87	75	213
2206	1	3	374	gi1215098	exclusionase [Bacteriophage 154a]	87	72	372
2938	1	3	290	gi1508979	GTP-binding protein [Bacillus subtilis]	87	69	288
3081	2	126	308	gi1467199	IMP dehydrogenase [Bacillus subtilis]	87	72	183
3515	1	3	401	gi11405454	aconitase [Bacillus subtilis]	87	80	399
4238	1	547	275	gi1603769	HutU protein, urocanase [Bacillus subtilis]	87	73	273
4	8	10427	8736	gi1603769	HutU protein, urocanase [Bacillus subtilis]	86	72	1692
22	6	4190	3738	gi1410515	urease beta subunit [Staphylococcus xylosum]	86	73	453
54	2	2480	1572	gi1289287	UDP-glucose pyrophosphorylase [Bacillus subtilis]	86	70	909
124	3	2336	1713	gi1556887	uracil phosphoribosyltransferase [Bacillus subtilis] pir[S49364][S49364] uracil phosphoribosyltransferase - Bacillus subtilis	86	74	624
148	3	1349	3448	gi1467458	cell division protein [Bacillus subtilis]	86	75	2100
148	4	3638	3859	gi1467460	unknown [Bacillus subtilis]	86	73	222
152	3	1340	2086	gi1337835	pyruvate decarboxylase E-1 alpha subunit [Bacillus subtilis]	86	75	747
164	18	17347	19467	gi1184680	polynucleotide phosphorylase [Bacillus subtilis]	86	72	2121
180	2	554	1159	gi1143467	ribosomal protein S4 [Bacillus subtilis]	86	80	606
205	3	2966	2592	gi1142464	ribosomal protein L17 [Bacillus subtilis]	86	77	375
205	26	13364	12990	gi140107	ribosomal protein L23 [Bacillus stearothermophilus] lr[S10612][S10612] ribosomal protein L22 - Bacillus stearothermophilus	86	75	375
246	7	3463	3140	gi1467375	ribosomal protein S6 [Bacillus subtilis]	86	70	324
299	3	1196	1540	gi139656	spoVG gene product [Bacillus megaterium]	86	70	345
299	7	3884	4345	gi1467440	phosphoribosylpyrophosphate synthetase [Bacillus subtilis] gi140218 PRPP synthetase (AA 1-317) [Bacillus subtilis]	86	78	462
304	5	2170	2523	gi1666983	putative ATP binding subunit [Bacillus subtilis]	86	65	354
310	2	1487	1678	gi1177684	chorismate mutase [Staphylococcus xylosum]	86	71	192
337	5	2086	3405	gi1487434	isocitrate dehydrogenase [Bacillus subtilis]	86	78	1320
339	2	1489	1109	gi1118003	dihydroonepterin aldolase [Staphylococcus haemolyticus]	86	77	381
358	2	2124	3440	gi1146219	38.2% of identity to the Escherichia coli GTP-binding protein Era; putative [Bacillus subtilis]	86	73	1317

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% idenc	length (nt)
404	2	1015	2058	gi 1303817	yqfa (Bacillus subtilis)	86	78	1044
581	2	661	452	gi 40056	phoP gene product (Bacillus subtilis)	86	71	210
642	2	338	1075	gi 1176399	spir (Staphylococcus epidermidis)	86	72	738
770	1	622	347	gi 141328	phoP protein (put.); putative (Bacillus subtilis)	86	69	276
865	1	1777	890	gi 1146247	asparaginyl-tRNA synthetase (Bacillus subtilis)	85	74	888
868	2	963	1133	gi 1002911	transmembrane protein (Saccharomyces cerevisiae)	85	59	171
904	1	1	162	gi 1303912	yqhw (Bacillus subtilis)	86	72	162
989	1	35	433	gi 1303993	yqxl (Bacillus subtilis)	86	76	399
1212	1	296	150	gi 414014	ipa-90d gene product (Bacillus subtilis)	86	70	147
1323	1	2	148	gi 40041	pyruvate dehydrogenase (lipoamide) (Bacillus stearothermophilus) - Bacillus stearothermophilus	86	75	147
1385	2	540	310	gi 1354211	PET112-like protein (Bacillus subtilis)	86	86	231
1847	1	1	228	gi 296464	ATPase (Lactococcus lactis)	86	63	228
4487	1	476	240	gi 1022726	unknown (Staphylococcus haemolyticus)	86	73	237
4583	1	372	187	gi 1022725	unknown (Staphylococcus haemolyticus)	86	79	186
25	5	4287	5039	gi 1502421	3-ketoacyl-acyl carrier protein reductase (Bacillus subtilis)	85	64	753
56	21	30627	29395	gi 1408507	pyrimidine nucleoside transport protein (Bacillus subtilis)	85	69	1213
68	2	332	1192	gi 467376	unknown (Bacillus subtilis)	85	74	861
73	2	880	1707	gi 142992	glycerol kinase (glpK) (EC 2.7.1.30) (Bacillus subtilis) pir B45968 B45969 glycerol kinase (EC 2.7.1.30) - Bacillus subtilis ep P18157 GLPK_BACSU GLYCEROL KINASE (EC 2.7.1.30) (ATP:GLYCEROL -PHOSPHOTRANSFERASE) (GLYCEROKINASE) (CK)	85	72	828
106	4	1505	3490	gi 143766	(thrSV) (EC 6.1.1.3) (Bacillus subtilis)	85	74	1986
128	2	1153	2202	gi 111924	glyceraldehyde-3-phosphate dehydrogenase (Clostridium pasteurianum) pir S14254 S14254 glyceraldehyde-3-phosphate dehydrogenase (EC 2.1.12) - Clostridium pasteurianum	85	75	1050
129	4	6466	5352	gi 1064807	ORTHONINE AMINOTRANSFERASE (Bacillus subtilis)	85	73	1215
138	6	3475	5673	gi 1072419	glcB gene product (Staphylococcus carnosus)	85	74	2199
189	1	2	169	gi 467385	unknown (Bacillus subtilis)	85	65	168

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
205	15	8624	8106	gi 1044981	ribosomal protein S5 [Bacillus subtilis]	85	75	519
205	20	10928	10596	pir A02819 RSBS	ribosomal protein L24 - Bacillus stearothermophilus	85	72	333
220	6	6490	6101	gi 48980	secA gene product [Bacillus subtilis]	85	66	390
231	4	4877	3159	gi 1002520	huts [Bacillus subtilis]	85	70	1719
243	9	8013	8783	gi 414011	lipA-87r gene product [Bacillus subtilis]	85	72	771
249	2	5894	3186	gi 1405454	aconitase [Bacillus subtilis]	85	73	2709
302	1	140	475	gi 40173	homolog of E. coli ribosomal protein L21 [Bacillus subtilis] ir S18439 S18439 Ribosomal protein L21 - Bacillus subtilis PIP26908 RL21_BACSU 50S RIBOSOMAL PROTEIN L21 (BL20)	85	72	336
333	1	5445	2968	gi 442360	ClpC adenosine triphosphatase [Bacillus subtilis]	85	69	2478
364	6	6082	8196	gi 871784	Clp-like ATP-dependent protease binding subunit [Bos taurus]	85	68	2115
448	2	1992	1339	gi 405134	acetate kinase [Bacillus subtilis]	85	68	654
747	1	1251	853	gi 1373157	orf-X1 hypothetical protein; Method: conceptual translation supplied by author [Bacillus subtilis]	85	73	399
886	2	159	467	gi 541768	hemin permease [Yersinia enterocolitica]	85	55	309
1089	1	1208	606	pir 847154 8471	signal recognition particle 54K chain homolog Fth - Bacillus subtilis	85	71	603
1163	1	816	409	gi 308155	diaminopimelate decarboxylase [Bacillus methanolicus] sp e41023 DCDA_BACMT DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20) DAP DECARBOXYLASE	85	62	408
1924	1	487	251	gi 215098	excisionase [Bacteriophage 154a]	85	73	237
2932	1	776	390	gi 1041099	Pyruvate Kinase [Bacillus licheniformis]	85	71	387
3030	1	3	275	gi 42370	pyruvate formate-lyase (AA 1-760) [Escherichia coli] ir S01788 S01788 formate C-acetyltransferase (EC 2.3.1.54) - Chierichia coli	85	74	273
3111	1	595	299	gi 63568	limb deformity protein [Gallus gallus]	85	85	297
3778	1	630	316	gi 391840	beta-subunit of HPT [Pseudomonas fragi]	85	67	315
3835	1	1	387	gi 1204472	type I restriction enzyme ECOR124/3 I M protein [Haemophilus influenzae]	85	56	387
4042	1	3	386	gi 18178	formate acetyltransferase [Chlamydomonas reinhardtii] ir S24997 S24997 formate C-acetyltransferase (EC 2.3.1.54) - Chlamydomonas reinhardtii	85	70	384
4053	1	35	340	gi 1204472	type I restriction enzyme ECOR124/3 I M protein [Haemophilus influenzae]	85	56	306
4108	1	2	181	gi 1072418	glcA gene product [Staphylococcus carnosus]	85	61	180
4300	1	575	330	gi 1151932	fructose enzyme II [Rhodospirillum rubrum]	85	59	246

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
4392	1	627	355	gi 1022725	unknown (Staphylococcus haemolyticus)	85	74	273
4408	1	2	235	gi 871744	[c]p-like ATP-dependent protease binding subunit (Bos taurus)	85	62	234
4430	1	578	291	gi 1009366	Respiratory nitrate reductase (Bacillus subtilis)	85	68	288
4555	1	2	253	gi 450688	hscM gene of Ecopri gene product (Escherichia coli) p1r S38437 S38437 hscM protein - Escherichia coli p1r S09629 S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	85	52	252
4611	1	481	242	gi 1256635	dihydroxy-acid dehydratase (Bacillus subtilis)	85	65	240
4	10	10061	10591	gi 46982	load gene product (Staphylococcus epidermidis)	84	68	531
13	2	1348	1172	gi 142450	leuC protein (Bacillus subtilis)	84	56	177
16	4	1803	4652	gi 1277198	DNA repair protein (Deinococcus radiodurans)	84	67	2850
22	3	1535	1128	gi 511069	uref (Staphylococcus xylosum)	84	73	408
23	7	5055	5306	gi 603320	Ver082p (Saccharomyces cerevisiae)	84	61	252
53	11	11597	11145	gi 1303948	YqjW (Bacillus subtilis)	84	68	453
53	12	14059	12770	gi 142613	branched chain alpha-keto acid dehydrogenase E2 (Bacillus subtilis)	84	71	1290
70	1	1332	982	gi 46847	ORF (rep2) (Staphylococcus aureus)	84	68	351
73	4	2512	4311	gi 142993	glycerol-3-phosphate dehydrogenase (gpdH) (EC 1.1.99.5) (Bacillus subtilis)	84	74	1800
98	7	4324	6096	gi 467427	methionyl-tRNA synthetase (Bacillus subtilis)	84	66	1713
100	9	9501	8680	gi 1340128	ORF (Staphylococcus aureus)	84	78	822
117	3	1934	3208	gi 1237019	Srb (Bacillus subtilis)	84	68	1275
148	6	4720	5670	gi 467462	cysteine synthetase A (Bacillus subtilis)	84	69	951
152	4	2064	2456	gi 143377	pyruvate decarboxylase (P-1) alpha subunit (Bacillus subtilis) p1r B36718 B36718 pyruvate decarboxylase (lipamide) (EC 1.2.4.1) lpha chain - Bacillus subtilis	84	70	393
169	7	1634	3861	gi 1001342	hypothetical protein (Synecocystis sp.)	84	66	228
171	4	2992	2657	gi 517475	D-amino acid transaminase (Staphylococcus haemolyticus)	84	71	336
186	6	6941	6216	gi 467475	unknown (Bacillus subtilis)	84	70	726
205	9	6261	5692	gi 216340	ORF for adenylate kinase (Bacillus subtilis)	84	71	570
224	2	915	1391	gi 288269	beta-fructofuranosidase (Staphylococcus xylosum)	84	70	477

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
251	1	92	388	gi 1303790	YqeI (Bacillus subtilis)	84	65	297
282	3	1526	2836	gi 143040	glutamate-1-semialdehyde 2,1-aminotransferase (Bacillus subtilis) pir D42728 D02728 glutamate-1-semialdehyde 2,1-aminomutase (EC 4.3.8) - Bacillus subtilis	84	75	1311
307	5	3136	2959	gi 1070014	protein-dependent (Bacillus subtilis)	84	62	180
320	4	2343	4229	gi 143390	(carbamyl) phosphate synthetase (Bacillus subtilis)	84	70	1887
372	1	3	286	gi 1022725	unknown (Staphylococcus haemolyticus)	84	70	294
413	2	2201	1341	gi 1256146	YbbQ (Bacillus subtilis)	84	65	861
439	1	3	392	gi 1046173	osmotically inducible protein (Mycoplasma genitalium)	84	53	390
461	3	1362	2270	gi 40211	threonine synthase (thrc) (AA 1-352) (Bacillus subtilis) tr A25364 A25364 threonine synthase (EC 4.2.99.2) - Bacillus subtilis	84	69	909
487	1	3	299	gi 1146531	integrin-like protein alpha Intlp (Candida albicans)	84	46	297
491	2	624	905	pir S08564 S08564	ribosomal protein S9 - Bacillus stearothermophilus	84	69	282
491	3	816	1033	pir S08564 S08564	ribosomal protein S9 - Bacillus stearothermophilus	84	77	198
548	1	3	341	gi 1411371	usacil peptidase (Bacillus caldolyticus)	84	74	339
728	2	2701	1748	gi 912445	DNA polymerase (Bacillus caldotenax)	84	68	954
769	1	3	257	gi 1510953	cobalamin biosynthesis protein N (Methanococcus jannaschii)	84	38	255
954	1	308	156	gi 1409454	aconitase (Bacillus subtilis)	84	57	151
957	1	3	395	gi 143402	recombination protein (tsg start codon) (Bacillus subtilis) gi 1303923 RecN (Bacillus subtilis)	84	68	393
975	1	3	452	gi 885934	ClpA (Synecococcus sp.)	84	70	450
1385	1	3	257	gi 510140	ligandopeptidase F (Lactococcus lactis)	84	56	255
2954	1	3	323	gi 603769	HutU protein, urocanase (Bacillus subtilis)	84	73	321
2996	1	650	348	gi 18178	formate acetyltransferase (Chlamydomonas reinhardtii) tr S24997 S24997 formate C-acetyltransferase (EC 2.3.1.54) - Chlamydomonas reinhardtii	84	65	303
3766	1	737	375	gi 517205	67 kDa myosin-crossreactive streptococcal antigen (Streptococcus yogenes)	84	72	363
4022	1	2	169	gi 1146206	glutamate dehydrogenase (Bacillus subtilis)	84	54	168
4058	1	620	312	gi 151932	fructose enzyme II (Rhodobacter capsulatus)	84	71	309
4108	2	106	351	gi 1072418	glcA gene product (Staphylococcus carnosus)	84	77	246

TABLE 2

B. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
4183	1	3	308	gi 603769	lutU protein, urocanase [Bacillus subtilis]	84	72	306
4726	1	55	234	gi 146208	glutamate synthase large subunit (EC 2.6.1.53) [Escherichia coli] p1r[A29617/A29617] glutamate synthase (NADPH) (EC 1.4.1.13) large hain - Escherichia coli	84	73	180
22	4	2043	1576	gi 393297	urease accessory protein [Bacillus sp.]	83	64	468
53	13	14722	13745	gi 142612	branched chain alpha-keto acid dehydrogenase E1-beta [Bacillus subtilis]	83	68	978
57	16	13357	12872	gi 143132	lactate dehydrogenase (AC 1.1.1.27) [Bacillus caldolyticus] p1r[B29704/B29704] L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus caldolyticus	83	66	486
66	3	3119	2274	gi 1303894	YqhM [Bacillus subtilis]	83	63	846
66	5	6118	4643	gi 1212730	YqhK [Bacillus subtilis]	83	68	1476
70	3	1864	1523	gi 64095	replication initiator protein [Listeria monocytogenes]	83	73	342
90	1	377	1429	gi 1555571	alcohol dehydrogenase 1 (adhA) (EC 1.1.1.1) [Zymomonas mobilis] p1r[A35260/A35260] alcohol dehydrogenase (EC 1.1.1.1) 1 - Zymomonas obilis	83	70	1053
95	2	708	2162	gi 506381	phospho-beta-glucosylase [Bacillus subtilis]	83	70	1455
137	1	68	694	gi 467391	initiation protein of replicaton [Bacillus subtilis]	83	77	627
140	4	3209	2742	gi 634107	kdpB [Escherichia coli]	83	65	468
142	3	3468	2989	gi 1212776	lumazine synthase (b-subunit) [Bacillus amyloliquefactions]	83	69	480
161	12	5749	6696	gi 903307	ORF75 [Bacillus subtilis]	83	64	948
164	9	9880	11070	gi 49316	ORF2 gene product [Bacillus subtilis]	83	66	1191
164	14	14148	14546	gi 580902	ORF6 gene product [Bacillus subtilis]	83	60	399
170	2	3144	2467	gi 530848	orf4 [Bacillus subtilis]	83	64	678
186	2	2029	1370	gi 289284	[cysteine]-tRNA synthetase [Bacillus subtilis]	83	72	660
205	14	7822	7607	gi 216337	ORF for L10 ribosomal protein [Bacillus subtilis]	83	74	216
237	6	3683	4540	gi 1510488	[imidazoleglycerol-phosphate synthase (cyclase) [Methanococcus jannaschii]	83	60	858
301	1	985	638	gi 467419	unknown [Bacillus subtilis]	83	65	348
302	4	1421	2743	gi 508979	GTP-binding protein [Bacillus subtilis]	83	68	1323
321	4	3933	3571	gi 39884	[fumarate (cicG) (aa 1-462) [Bacillus subtilis]	83	68	363
367	1	2	352	gi 1039479	[ORF1] [Lactococcus lactis]	83	54	351

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
387	1	3	662	gi 806281	DNA polymerase I (Bacillus stearothermophilus)	83	70	660
527	2	916	1566	gi 396259	protease (Staphylococcus epidermidis)	83	67	651
533	1	355	179	gi 142455	alanine dehydrogenase (EC 1.4.1.1) (Bacillus stearothermophilus) pir B34261 B34261 alanine dehydrogenase (EC 1.4.1.1) - Bacillus stearothermophilus	83	66	177
536	4	1617	1438	gi 143366	adenylosuccinate lyase (PDB-8) (Bacillus subtilis) pir C29326 W28SDS	83	67	180
652	1	2	859	gi 520753	adenylosuccinate lyase (EC 4.3.2.2) - Bacillus subtilis	83	72	858
774	2	200	361	gi 1522665	DNA topoisomerase I (Bacillus subtilis)	83	58	162
897	1	120	296	gi 1064807	M. jennaschii predicted coding region MJEC128 (Methanococcus jennaschii)	83	76	177
1213	1	3	491	gi 289288	ORTHONINE AMINOTRANSFERASE (Bacillus subtilis)	83	67	489
2529	1	296	350	gi 143786	lexA (Bacillus subtilis)	83	69	147
2973	1	649	326	gi 1109687	tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Bacillus subtilis) pir J70481 Y885 tryptophan-tRNA ligase (EC 6.1.1.2) - Bacillus subtilis	83	58	324
1009	1	728	366	gi 1425132	ProZ (Bacillus subtilis)	83	65	363
3035	2	45	305	gi 1950062	ORF_0294 (Escherichia coli)	83	59	261
3106	1	67	309	gi 1353197	hypothetical yeast protein 1 (Mycoplasma capricolum) pir S48578 S48578 hypothetical protein - Mycoplasma capricolum SOC3 (fragment)	83	61	243
445R	1	540	271	gi 397526	thioredoxin reductase (Escherichia coli)	83	78	270
4570	1	444	223	gi 1022726	clumping factor (Staphylococcus aureus)	83	74	222
4654	1	97	261	gi 1072419	unknown (Staphylococcus haemolyticus)	83	79	165
16	2	295	1191	gi 153854	glcB gene product (Staphylococcus carnosus)	82	67	897
16	3	1193	1798	gi 153854	lvs402 protein (Streptococcus pneumoniae)	82	70	606
38	12	9644	8724	gi 1204400	lvs402 protein (Streptococcus pneumoniae)	82	58	921
42	4	988	2019	gi 841192	N-acetylneuraminidase lyase (Haemophilus influenzae)	82	70	1032
51	6	2590	3489	gi 143607	catalase (Bacteroides fragilis)	82	69	900
56	11	12270	13925	gi 39431	sporulation protein (Bacillus subtilis)	82	60	1656
56	15	17673	18014	gi 467410	oligo-1,6-glucosidase (Bacillus cereus)	82	66	342
61	2	881	3313	gi 143148	unknown (Bacillus subtilis)	82	70	2433
					transfer RNA-Leu synthetase (Bacillus subtilis)			

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
82	7	9162	11318	gi 40240	elongation factor G (AA 1-691) [Thermus aquaticus thermophilus] r S15928 EFTW elongation factor G - Thermus aquaticus p P3351 EFG_THETH ELONGATION FACTOR G (EF-G).	82	64	2157
85	2	5470	3260	gi 143369	phosphoribosylformyl glycine synthetase II (pur-Q) [Bacillus subtilis]	82	66	2211
102	6	3662	5380	gi 1256635	dihydroxy-acid dehydratase [Bacillus subtilis]	82	65	1719
117	4	3242	3493	gi 147154 A471	orf1 5' of Pfh - Bacillus subtilis	82	55	252
128	6	4377	5933	gi 146058	phosphoglycerate mutase [Bacillus subtilis]	82	66	1557
129	2	1229	2182	gi 140377	glycerophosphoryl diester phosphodiesterase [Bacillus subtilis] p S3725 S3725 glycerophosphoryl diester phosphodiesterase - acillus subtilis	82	62	954
170	1	2	1441	gi 1377831	unknown [Bacillus subtilis]	82	67	1440
177	1	3	1094	gi 1467386	thiophen and furan oxidation [Bacillus subtilis]	82	65	1092
184	4	3572	4039	gi 153566	ORF (19K protein) [Enterococcus faecalis]	82	59	468
189	8	4455	4225	gi 1001878	CspL protein [Listeria monocytogenes]	82	73	231
206	19	32166	20707	gi 1473916	lipopeptide antibiotics (curin A [Bacillus subtilis] sp P39144 LP14_BACSU LIPOPEPTIDE ANTIBIOTICS ITURIN A AND SURFACTIN BIOSYNTHESIS PROTEIN.	82	50	660
221	2	805	1722	gi 1517205	67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus pyogenes]	82	63	918
223	4	3866	3651	gi 1439619	[Salmonella typhimurium IS200 insertion sequence from SAR417, att1A1.] gene product [Salmonella typhimurium]	82	69	216
260	3	5207	4296	gi 1161381	IcAB [Staphylococcus epidermidis]	82	61	912
315	3	4864	2855	gi 143397	quinol oxidase [Bacillus subtilis]	82	67	2010
321	10	8520	7945	gi 142981	ORF5: This ORF includes a region (aa23-103) containing a potential non-sulphur centre homologous to a region of Rhodospirillum rubrum nd Chromatium vinosum; putative [Bacillus stearothermophilus] p PQ0299 PQ0299 hypothetical protein 5 (gldA 3' region) -	82	62	576
331	3	1055	1342	gi 1436574	ribosomal protein L1 [Bacillus subtilis]	82	71	288
370	2	262	618	gi 1303793	Yqel [Bacillus subtilis]	82	59	357
404	4	3053	4024	gi 1303821	YqfE [Bacillus subtilis]	82	68	972
405	4	4440	3073	gi 1303913	YqkX [Bacillus subtilis]	82	67	1368
436	3	4096	2864	gi 149521	cryptophan synthase beta subunit [Lactococcus lactis] p S35129 S35129 cryptophan synthase (EC 4.2.1.20) beta chain - Lactococcus lactis subsp. lactis	82	67	1233

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
441	4	3394	2573	gi 142952	glyceraldehyde-3-phosphate dehydrogenase [Bacillus teurothermophilus]	82	67	822
444	12	10415	11227	gi 1204354	spore germination and vegetative growth protein [Haemophilus influenzae]	82	67	813
446	1	3	191	gi 143387	aspartate transcarbamylase [Bacillus subtilis]	82	66	189
462	3	1007	1210	gi 142521	deoxyribodipyrimidine photolyase [Bacillus subtilis] p1r[A37192/A37192_UVEB protein - Bacillus subtilis ap P14951 UVRC_BACSU_EXCINUCLEASE_ABC_SUBUNIT_C	82	64	204
537	1	1560	784	gi 853767	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis]	82	61	777
680	2	407	700	gi 1426472	secE gene product [Staphylococcus carnosus]	82	69	294
724	2	565	386	gi 143373	phosphoribosyl aminimidazole carboxy formyl ormyltransferase/inosine monophosphate cyclohydrolase [Pur-H(3)] [Bacillus subtilis]	82	68	180
763	1	422	213	gi 1467458	cell division protein [Bacillus subtilis]	82	35	210
818	1	564	283	gi 1064787	function unknown [Bacillus subtilis]	82	69	282
858	1	175	1176	gi 143043	uroporphyrinogen decarboxylase [Bacillus subtilis] p1r[B47045/B47045 uroporphyrinogen decarboxylase (EC 4.1.1.37) - acillus subtilis]	82	71	1002
895	1	3	599	gi 1027507	ATP binding protein [Borrelia burgdorferi]	82	72	597
939	1	10	399	gi 143795	transfer RNA-Tyr synthetase [Bacillus subtilis]	82	60	390
961	1	1	306	gi 157847	gamma-hemolysin [Staphylococcus aureus]	82	69	306
1192	1	307	155	gi 146974	NH3-dependent NAD synthetase [Escherichia coli]	82	71	153
1317	1	49	375	gi 1407908	EF1a [Staphylococcus xylosus]	82	72	327
1341	1	1	150	gi 139962	ribosomal protein L35 (AA 1-66) [Bacillus teurothermophilus]	82	68	150
2990	2	567	349	gi 1534855	ATPase subunit epsilon [Bacillus teurothermophilus] ap P42009 ATPE_BACST ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34)	82	47	219
3024	1	45	224	gi 1467402	unknown [Bacillus subtilis]	82	64	180
3045	1	276	139	gi 1467335	ribosomal protein L9 [Bacillus subtilis]	82	60	138
3045	2	558	400	gi 1467335	ribosomal protein L9 [Bacillus subtilis]	82	82	159
3091	1	474	238	gi 1499335	secA protein [Staphylococcus carnosus]	82	78	237
3107	1	416	210	gi 1546918	orfY 3' of conK [Bacillus subtilis, E26, Peptide Partial, 140 aa] p1r[343612/343612_hypothetical protein Y - Bacillus subtilis ap P40398 YHND_BACSU_HYPOTHETICAL PROTEIN IN CONK 3'-REGION (ORFY FRAGMENT)	82	64	207

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
4132	1	2	319	gi 42086	nitrate reductase alpha subunit [Escherichia coli] p109152[NARG_ECOLI] RESPIRATORY NITRATE REDUCTASE 1 ALPHA CHAIN (EC 7.99.4). (SUB 2-1247)	82	75	318
23	3	3275	2574	gi 1139573	spas [Shingomonas sp.]	81	64	702
42	1	638	321	gi 466778	lysine specific permease [Escherichia coli]	81	59	318
48	5	4051	4350	gi 1045937	H. genitalium predicted coding region M0246 [Mycoplasma genitalium]	81	62	300
51	4	1578	2579	gi 516649 S166	dclAC protein - Bacillus subtilis	81	55	1002
53	2	354	1494	gi 1303961	YggJ [Bacillus subtilis]	81	67	1131
53	8	9419	7971	gi 146930	6-phosphogluconate dehydrogenase [Escherichia coli]	81	66	1449
54	9	10757	10119	gi 143016	permease [Bacillus subtilis]	81	65	639
54	10	13360	11786	gi 143015	gluconate kinase [Bacillus subtilis]	81	64	1575
57	117	13983	13366	gi 1425805 A258	L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus subtilis	81	74	618
81	2	2708	2217	gi 1222302	Ni2O-related protein [Haemophilus influenzae]	81	54	492
86	1	745	374	gi 414017	/jpa-93d gene product [Bacillus subtilis]	81	70	372
103	6	6038	4861	gi 971342	nitrate reductase beta subunit [Bacillus subtilis] sp P42176 NARG_BACSU NITRATE REDUCTASE BETA CHAIN (EC 1.7.99.4).	81	64	1578
120	15	10845	12338	gi 1524392	GbsA [Bacillus subtilis]	81	67	1494
128	5	3676	4413	gi 143319	triose phosphate isomerase [Bacillus megaterium]	81	64	738
131	9	10308	9280	gi 299163	alanine dehydrogenase [Bacillus subtilis]	81	68	1029
143	6	6088	5471	gi 439619	[Salmonella typhimurium IS200 insertion sequence from SBA17, artial.], gene product [Salmonella typhimurium]	81	61	618
169	1	43	825	gi 697795	30S ribosomal protein (pediococcus acidilactici) sp P49566 RS2_PEDAC 30S RIBOSOMAL PROTEIN S2.	81	65	783
230	1	450	226	gi 1125826	short region of weak similarity to tyrosine-protein kinase receptors in a fibronectin type III-like domain [Caenorhabditis elegans]	81	54	225
233	5	2000	2677	gi 467404	unknown [Bacillus subtilis]	81	63	678
241	2	3081	2169	gi 16510	succinate-CoA ligase (GDP-forming) [Arabidopsis thaliana] tr S10579 S10579 succinate-CoA ligase (GDP-forming) [EC 6.2.1.4] pha chain - Arabidopsis thaliana (fragment)	81	69	933
256	1	1	981	gi S09411 S094	spoIIIE protein - Bacillus subtilis	81	65	981
259	3	3752	2691	sp P28367 RP2_B	PROBABLE PEPTIDE CHAIN RELEASE FACTOR 2 (RP-2) (FRAGMENT)	81	65	1062

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	Length (nt)
275	2	1728	3581	gi 726480	L-glutamine-O-fructose-6-phosphate amidotransferase [Bacillus subtilis]	81	68	1854
285	1	1466	735	gi 1204844	H. influenzae predicted coding region H0594 [Haemophilus influenzae]	81	63	732
296	1	99	1406	gi 467328	adenylosuccinate synthetase [Bacillus subtilis]	81	67	1308
302	9	5590	5889	gi 147485	queA [Escherichia coli]	81	64	300
317	2	1137	1376	gi 154961	resolvase [Transposon Tn917]	81	57	240
343	2	1034	1342	gi 405955	lyeB [Escherichia coli]	81	60	309
360	2	1404	2471	gi 1204570	sparty-tRNA synthetase [Haemophilus influenzae]	81	67	1066
364	5	6251	5706	gi 1204652	methylated-DNA-protein-cysteine methyltransferase [Haemophilus influenzae]	81	63	546
372	2	1707	1135	gi 467416	unknown [Bacillus subtilis]	81	65	573
392	1	43	603	pir S0941 S094	spoIIIE protein - Bacillus subtilis	81	65	561
404	9	5252	6154	gi 606745	Bex [Bacillus subtilis]	81	65	903
426	2	1727	1119	gi 39453	Manganese superoxide dismutase [Bacillus caldotenax] ir S22053 S22053 superoxide dismutase [EC 1.15.1.1] (Mn) - Bacillus lichenex	81	66	609
480	7	4653	5889	pi C370M3 C370	hypothetical protein II (ompII 3' region) - Salmonella typhimurium (fragment)	81	57	237
625	3	1105	2070	gi 1262360	protein kinase PknB [Mycobacterium leprae]	81	56	966
754	2	504	1064	gi 1303902	Vqpu [Bacillus subtilis]	81	71	561
842	1	86	430	gi 1405446	transketolase [Bacillus subtilis]	81	68	345
953	1	798	400	gi 1205429	dipeptide transport ATP-binding protein [Haemophilus influenzae]	81	57	399
961	2	252	401	gi 487686	synergohymenotropic toxin [Staphylococcus intermedius] pir S4494 S4494 synergohymenotropic toxin - Staphylococcus intermedius	81	72	150
1035	1	1	189	gi 1046138	H. genitalium predicted coding region MG423 [Mycoplasma genitalium]	81	43	189
1280	1	670	449	gi 559164	helicase [Autographa californica nuclear polyhedrosis virus] sp P24307 V143_NPAC HELICASE	81	43	222
3371	1	68	241	gi 1322245	isovalonate pyrophosphate decarboxylase [Rattus norvegicus]	81	62	174
3715	1	475	239	gi 537137	ORF_1388 [Escherichia coli]	81	58	217
3908	1	2	325	gi 439619	[Salmonella typhimurium IS200 insertion sequence from SARAI7, attal.1.] gene product [Salmonella typhimurium]	81	68	324
3940	1	3	401	nt 296464	ATPase [Lactococcus lactis]	81	69	399

TABLE 2

3. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match	match	match gene name	% sim	% ident	length (nt)
3954	1	1	318	gi 1224059	amidase [Moraxella catarrhalis]		81	68	318
4049	1	337	170	gi 603768	HutI protein, imidazole-5-propionate hydrolase (Bacillus subtilis) gi 603768 HutI protein, imidazole-5-propionate hydrolase (Bacillus subtilis)		81	68	168
4209	1	1	324	gi 403373	glycerophosphoryl diester phosphodiesterase (Bacillus subtilis) pir S37251 S37251 glycerophosphoryl diester phosphodiesterase - ecillus subtilis		81	56	324
4371	1	627	322	gi 216677	indolepyruvate decarboxylase (Enterobacter cloacae) pir S16013 S16013 indolepyruvate decarboxylase (EC 4.1.1.-) - nterobacter cloacae		81	72	306
4387	1	19	228	gi 460689	FWG [Thermoactinomyces vulgaris]		81	59	210
4191	1	581	306	gi 1524193	unknown [Mycobacterium tuberculosis]		81	67	276
4425	1	3	341	gi 143015	glucanase kinase (Bacillus subtilis)		81	66	339
9	1	1593	847	gi 1064786	function unknown (Bacillus subtilis)		80	62	747
17	1	544	311	gi 559164	helicase [Autographa californica nuclear polyhedrosis virus] sp P34307 V143 NPVAC HELICASE		80	40	234
45	2	1159	2448	gi 1109684	ProV (Bacillus subtilis)		80	63	1290
45	5	4032	4733	gi 1109687	ProZ (Bacillus subtilis)		80	55	702
54	8	10266	9502	gi 563952	glucanase permease (Bacillus licheniformis)		80	62	765
62	12	8852	7545	gi 854655	Na/H antiporter system (Bacillus alcalophilus)		80	62	1308
62	14	8087	8683	gi 559713	ORF (Homo sapiens)		80	68	597
67	16	13781	14122	gi 305002	ORF_F356 [Escherichia coli]		80	65	342
70	13	11495	10296	gi 1303995	YqkN (Bacillus subtilis)		80	64	1200
98	9	6336	7130	gi 467428	unknown (Bacillus subtilis)		80	68	795
98	10	7294	7833	gi 467430	unknown (Bacillus subtilis)		80	64	540
98	11	7820	8737	gi 467431	high level kanamycin resistance (Bacillus subtilis)		80	61	918
109	16	14154	14813	gi 580875	lpa-57d gene product (Bacillus subtilis)		80	63	660
112	15	14294	16636	gi 1072361	pyruvate-formate-lyase (Clostridium pasteurianum)		80	65	2343
119	1	1448	726	gi 506699	CapC (Staphylococcus aureus)		80	58	723
119	2	2179	1448	gi 506698	CapB (Staphylococcus aureus)		80	59	732
174	4	3271	2870	gi 1166242	aspartate 1-decarboxylase (Bacillus subtilis)		80	61	402

TABLE 2

S. aureus - putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
177	3	2102	2842	gi1467385	unknown [Bacillus subtilis]	80	70	741
184	6	6124	5912	gi1161953	85-kDa surface antigen [Trypanosoma cruzi]	80	46	213
186	4	5368	3875	gi1289282	glutaryl-CoA synthetase [Bacillus subtilis]	80	65	1494
205	30	15796	15140	gi140103	ribosomal protein L4 [Bacillus stearothermophilus]	80	66	657
207	1	140	1315	gi1460259	enolase [Bacillus subtilis]	80	67	1176
211	3	1078	1590	gi1410131	ORFX7 [Bacillus subtilis]	80	61	513
235	2	1962	2255	gi1143797	valyl-tRNA synthetase [Bacillus stearothermophilus] sp P11931 STV_BACST VALYL-TRNA SYNTHETASE (EC 6.1.1.9) VALINE--TRNA LIGASE (VALRS)	80	55	294
239	1	1	1263	gi1143000	proton glutamate symport protein [Bacillus stearothermophilus] pir S26247 S26247 glutamate/aspartate transport protein - Bacillus stearothermophilus	80	59	1263
272	5	2724	2461	gi1709993	hypothetical protein [Bacillus subtilis]	80	54	264
301	3	1446	1111	gi1467418	unknown [Bacillus subtilis]	80	58	336
310	4	5697	4501	gi1177686	acuC gene product [Staphylococcus xylosus]	80	67	1197
310	6	5258	7006	gi1348053	acetyl-CoA synthetase [Bacillus subtilis]	80	67	1749
310	7	7410	9113	gi1103865	formyl-tetrahydrofolate synthetase [Streptococcus mutans]	80	67	1704
325	3	1114	1389	gi1310325	outer capsid protein [Rotavirus sp.]	80	40	276
337	1	1268	636	gi1537049	ORF_0470 [Escherichia coli]	80	55	633
374	2	929	1228	gi1405448	YneP [Bacillus subtilis]	80	70	300
375	5	1062	3331	gi1467448	unknown [Bacillus subtilis]	80	68	270
388	1	267	587	gi11064791	function unknown [Bacillus subtilis]	90	65	321
394	1	9	659	gi1304976	matches PS00017: ATP_GTP_A and PS00301: EFATOR.GTP; similar to longation factor G, TetM/TetO tetracycline-resistance proteins [Escherichia coli]	80	65	651
456	1	625	1263	gi11146183	putative [Bacillus subtilis]	80	65	639
475	1	1	654	gi1288269	beta-fructofuranosidase [Staphylococcus xylosus]	80	66	654
544	2	1449	2240	gi1529754	speC [Streptococcus pyogenes]	80	50	792
622	4	1623	1871	gi11483545	unknown [Mycobacterium tuberculosis]	80	65	249
719	1	1	1257	gi11064791	function unknown [Bacillus subtilis]	80	68	1257
739	1	107	838	gi11666983	putative ATP binding subunit [Bacillus subtilis]	80	61	732

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
745	2	581	614	[gi11511600]	[coenzyme PQQ synthesis protein III [Methanococcus jannaschii]]	80	61	168
822	1	17	579	[gi1410141]	[ORFX17 [Bacillus subtilis]]	80	68	663
827	2	991	836	[gi1205301]	[leukotoxin secretion ATP-binding protein [Haemophilus influenzae]]	80	54	156
1044	1	3	149	[gi160632]	[vp2 [Marburg virus]]	80	55	147
1220	2	571	413	[pir161072]	[EPG6 [gallidermin precursor - Staphylococcus gallinarum]]	80	74	159
2519	1	75	275	[gi1147556]	[dpj [Escherichia coli]]	80	45	201
2947	1	503	279	[gi1184680]	[polynucleotide phosphorylase [Bacillus subtilis]]	80	62	225
3120	1	2	226	[gi1517205]	[67 kDa hyosin-crossreactive streptococcal antigen [Streptococcus pyogenes]]	80	65	225
3191	1	294	148	[gi151259]	[HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii]]	80	59	147
3560	2	285	434	[gi1217130]	[hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) [Pseudomonas sp.]]	80	70	150
3655	1	47	346	[gi1415855]	[photosystem I core protein B [Synechococcus vulcanus]]	80	56	300
3658	2	324	584	[gi1551531]	[deoxyribose aldolase [Mycoplasma hominis]]	80	54	261
3769	1	798	400	[gi1133950]	[2-nitropropane dioxygenase [Nillopsia saturnus]]	80	68	399
3781	1	692	348	[gi1166412]	[large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]]	80	62	345
3988	1	48	287	[gi1204695]	[NADH-glutamate synthase [Medicago sativa]]	80	69	240
4030	1	571	287	[gi1009366]	[fructose-permease IIBC component [Haemophilus influenzae]]	80	60	285
4092	1	547	275	[gi1370207]	[respiratory nitrate reductase [Bacillus subtilis]]	80	69	273
4103	1	680	342	[gi139956]	[orf6 [Lactobacillus sake]]	80	65	339
4231	1	692	348	[gi1289287]	[NADH-glucose pyrophosphorylase [Bacillus subtilis]]	80	65	345
4265	1	595	299	[gi1603768]	[UDP-glucose 5-proponate hydrolase [Bacillus subtilis]]	80	63	297
4504	1	498	250	[gi1133950]	[HutI protein, imidazolone-5-proponate hydrolase [Bacillus subtilis]]	80	68	249
2	6	5998	6798	[gi1535351]	[large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]]	79	63	801
4	7	8295	7057	[gi1603768]	[CodY [Bacillus subtilis]]	79	64	1245
25	6	5273	5515	[pir1A36728/A367]	[HutI protein, imidazolone-5-proponate hydrolase [Bacillus subtilis]]	79	65	243

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
59	2	1173	1424	gi 147923	threonine dehydratase 2 (EC 4.2.1.16) [Escherichia coli]	79	75	252
60	1	1	204	gi 666115	orf1 upstream of glucose kinase [Staphylococcus xylosum] pir[552351] [Staphylococcus xylosum]	79	60	204
81	1	3002	3590	gi 466882	ppa1; BA496_C2_189 [Mycobacterium leprae]	79	64	1413
85	7	7023	6505	gi 143364	phosphoribosyl aminimidazole carboxylase I (PUR-E) [Bacillus subtilis]	79	60	519
89	6	5660	4554	gi 144906	product homologous to E. coli thioesterin reductase; J. Biol. Chem. 1988; 263:9015-9019, and to P2a protein of alkyl hydroperoxide oxidase from S. typhimurium; J. Biol. Chem. (1990) 265:10333-10340; pen reading frame A [Clostridium pasteurianum]	79	35	1107
102	11	7489	8571	gi 143093	ketol-acid reductoisomerase [Bacillus subtilis] sp P37253 ILVC_BACSU_KETOL-ACID_REDUCTOISOMERASE (EC 1.1.1.86) ACETOHYDROXY-ACID ISOMEROREDUCTASE (ALPHA-KETO-BETA-HYDROXYLACIL EDUCOISOMERASE)	79	64	1083
102	14	11190	112563	gi 149428	putative [lactococcus lactis]	79	65	1374
127	9	7792	9372	gi 1458688	Pfrc/RF [Dichelobacter nodosus]	79	68	1581
139	3	2540	1983	gi 506697	CapA [Staphylococcus aureus]	79	55	558
144	2	1644	1156	gi 1498296	peptide methionine sulfoxide reductase [Streptococcus pneumoniae]	79	47	489
148	2	529	1098	gi 467457	hypoxanthine-guanine phosphoribosyltransferase [Bacillus subtilis] gi 467457 hypoxanthine-guanine phosphoribosyltransferase [Bacillus subtilis]	79	59	570
150	1	965	591	gi 755602	unknown [Bacillus subtilis]	79	61	375
176	1	1039	587	gi 297874	fructose-bisphosphate aldolase [Staphylococcus carnosus] pir A49943 A49943 fructose-bisphosphate aldolase (EC 4.1.2.13) - taphylococcus carnosus (strain TN300)	79	65	453
186	7	7584	6874	gi 1314298	ORF5; putative Sas protein; similar to Sas proteins from Haemophilus influenzae and Escherichia coli [Listeria monocytogenes]	79	64	711
205	16	8887	8498	gi 1044980	ribosomal protein L38 [Bacillus subtilis]	79	70	390
211	1	1	519	gi 1303994	YqkH [Bacillus subtilis]	79	62	519
223	2	4183	2801	gi 488430	alcohol dehydrogenase 2 [Entamoeba histolytica]	79	60	1383
243	8	8915	7896	gi 580883	lipa-8d gene product [Bacillus subtilis]	79	60	1020
279	4	3721	4329	gi 413930	lipa-6d gene product [Bacillus subtilis]	79	59	609
300	1	11	1393	gi 403372	glycerol 3-phosphate permease [Bacillus subtilis]	79	62	1383
307	3	2930	1935	gi 1950062	hypothetical yeast protein 1 [Mycoplasma capricolum] pir S48578 S48578 hypothetical protein - Mycoplasma capricolum SDC3 (fragment)	79	60	996

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
352	6	10106	8886	gi 216834	P47K [Pseudomonas chlororaphis]	79	59	1221
412	1	1153	578	gi 143177	putative [Bacillus subtilis]	79	51	576
481	3	621	1124	gi 786163	Ribosomal Protein L10 [Bacillus subtilis]	79	66	504
516	1	702	352	gi 805090	NisA [Lactococcus lactis]	79	48	351
525	2	2457	1426	gi 143371	[phosphoribosyl] aminimidazole synthetase (Pur-H) [Bacillus subtilis] pirH29326 ABSCU-phosphoribosylformylglycinamide cyclo-ligase BC 6.3.3.1 - Bacillus subtilis	79	61	1032
538	4	3448	2825	gi 1370207	orf6 [Lactobacillus sake]	79	67	624
570	1	2	421	gi 476160	arginine permease substrate-binding subunit [Lactaria monocytogenes]	79	61	420
645	8	2663	3241	gi 153898	transport protein [Salmonella typhimurium]	79	62	579
683	1	75	374	gi 1064795	function unknown [Bacillus subtilis]	79	62	300
816	3	4700	3987	gi 1407784	orf-1; novel antigen [Staphylococcus aureus]	79	62	714
2829	1	3	401	gi 1524397	glycine betaine transporter OpuD [Bacillus subtilis]	79	61	399
2937	1	357	202	pir S52915 S529	nitrate reductase alpha chain - Bacillus subtilis (fragment)	79	58	156
2940	1	768	385	gi 149429	putative [Lactococcus lactis]	79	72	384
2946	1	570	286	gi 143267	2-oxoglutarate dehydrogenase (odhA; EC 1.2.4.2) [Bacillus subtilis]	79	61	285
2999	1	3	212	gi 710020	nitrite reductase (nirB) [Bacillus subtilis]	79	59	210
3022	1	514	332	gi 450686	3-phosphoglycerate kinase [Thermotoga maritima]	79	61	183
3064	1	3	314	gi 1204436	pyruvate formate-lyase [Haemophilus influenzae]	79	60	312
3083	1	2	220	gi 1149662	hlypD gene product [Clostridium perfringens]	79	56	219
3126	1	701	411	gi 1339950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	79	55	291
3181	1	607	326	gi 1339950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	79	59	282
3345	1	3	476	gi 871784	Clp-like ATP-dependent protease binding subunit [Bos taurus]	79	63	474
3718	1	536	270	pir C36889 C368	leuB protein, inactive - Lactococcus lactis subsp. lactis (strain IL1403)	79	71	267
3724	2	159	401	gi 1009366	Respiratory nitrate reductase [Bacillus subtilis]	79	64	243
3836	1	608	312	gi 1524193	unknown [Mycobacterium tuberculosis]	79	65	297
3941	1	2	334	gi 415855	deoxyribose aldolase [Mycoplasma hominis]	79	54	313
4113	1	3	341	gi 143015	gluconate kinase [Bacillus subtilis]	79	63	339

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
4501	1	406	209	gi 1022726	unknown [Staphylococcus haemolyticus]	79	66	198
4612	1	2	218	gi 460689	TVG [Thermococcus vulgaris]	79	58	237
2	1	2	1213	gi 520753	DNA topoisomerase I [Bacillus subtilis]	78	64	1212
8	2	2266	1220	gi 216151	DNA polymerase (gene 1; ttg start codon) [Bacteriophage SP02] gi 579197 SP02 DNA polymerase (aa 1-648) [Bacteriophage SP02] pif A21698 DJ8P52 DNA-directed DNA polymerase (EC 2.7.7.7) - phage P02	78	72	1047
9	2	1340	1089	gi 1064787	function unknown [Bacillus subtilis]	78	57	252
32	8	6803	7702	gi 1146974	NH3-dependent NAD synthetase [Escherichia coli]	78	63	900
36	4	2941	3138	gi 290503	glutamate permease [Escherichia coli]	78	53	198
53	15	17684	16221	gi 1303941	YqjV [Bacillus subtilis]	78	58	1404
57	14	10520	12067	gi 1072418	glcA gene product [Staphylococcus carnosus]	78	65	1548
66	7	6798	5812	gi 1212729	YqjW [Bacillus subtilis]	78	67	987
67	4	4029	4376	gi 466612	nika [Escherichia coli]	78	71	348
91	9	10058	10942	gi 467380	stage 0 sporulation [Bacillus subtilis]	78	50	885
102	12	8574	10130	gi 149426	putative [Lactococcus lactis]	78	61	1557
112	6	3540	4463	gi 854234	cymC gene product [Klebsiella oxytoca]	78	56	924
124	2	1888	1061	gi 403622	unknown [Bacillus subtilis]	78	60	828
130	3	1805	2260	gi 1256636	putative [Bacillus subtilis]	78	71	456
133	1	751	377	gi 168060	lamB [Escherichia coli]	78	59	375
166	4	7125	6163	gi 451216	mannosephosphate isomerase [Streptococcus mutans]	78	63	963
186	1	1586	795	gi 289284	[cysteine]-tRNA synthetase [Bacillus subtilis]	78	63	792
195	4	2749	2315	gi 1353874	unknown [Rhodospirillum rubrum]	78	58	435
199	3	4279	3623	gi 143525	succinate dehydrogenase cytochrome b-558 subunit [Bacillus subtilis] pif A29843 DEBSC succinate dehydrogenase (EC 1.3.99.1) cytochrome b-558 - Bacillus subtilis	78	57	657
199	4	7209	5557	gi 142521	deoxyribodipyrimidine photolyase [Bacillus subtilis] pif A27192 A27192 uvrB protein - Bacillus subtilis sp p16951 UVRB-BACSU EXCINUCLEASE ABC SUBUNIT C	78	62	1653
223	3	3831	3523	gi 139596	[Escherichia coli] IS200 insertion sequence from ECOR63, partial 1, ene product [Escherichia coli]	78	47	309

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
299	4	1065	2149	gi1467439	temperature sensitive cell division [Bacillus subtilis]	78	62	285
321	9	7734	7315	gi1142979	ORF3 is homologous to an ORF downstream of the spor gene of E.coli; RFP [Bacillus stearothermophilus]	78	55	420
352	4	3714	3944	gi1349050	actin 1 [Pneumocystis carinii]	78	42	231
352	5	7592	6093	gi1903587	NADH dehydrogenase subunit 5 [Bacillus subtilis] sp139755 [NDH1, BACSU NADH DEHYDROGENASE SUBUNIT 5 (EC 1.6.5.3) NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5]	78	58	1500
376	1	2	583	gi1551693	dethiolobin synthase [Bacillus sphaericus]	78	34	582
424	2	1595	1768	gi11524117	alpha-acetolactate decarboxylase [Lactococcus lactis]	78	68	174
450	1	1914	988	gi11030068	[NAD(P)H oxidoreductase, isoflavone reductase homologue [Solanum tuberosum]	78	63	927
558	1	762	562	gi11511508	bi-functional protein [Methanococcus jannaschii]	78	60	201
670	3	1152	1589	gi1122759	unknown [Bacillus subtilis]	78	64	438
714	1	64	712	gi1143460	37 kd minor sigma factor (rpoF, sigB; tly start codon) [Bacillus subtilis]	78	57	659
814	1	1	368	gi11377833	unknown [Bacillus subtilis]	78	59	366
981	1	1381	692	gi1143802	GerC2 [Bacillus subtilis]	78	64	690
995	2	978	727	gi1296947	uridine kinase [Escherichia coli]	78	64	252
1045	1	3	401	gi11407784	orf-1; novel antigen [Staphylococcus aureus]	78	61	399
1163	2	368	186	gi11410117	glutaminolactate decarboxylase [Bacillus subtilis]	78	54	183
2191	1	794	399	gi1215098	excisionase [Bacteriophage 154a]	78	65	396
2933	1	2	181	gi11204436	pyruvate formate-lyase [Haemophilus influenzae]	78	73	180
3041	2	129	317	gi1624632	GLT [Escherichia coli]	78	53	189
3581	1	105	401	gi1763186	3-ketoacyl-coA thiolase [Saccharomyces cerevisiae]	78	55	297
3709	1	3	230	gi1460689	TVG [Thermactinomyces vulgaris]	78	58	228
3974	1	528	265	gi1558839	unknown [Bacillus subtilis]	78	65	264
3980	1	3	401	gi139956	1101c [Bacillus subtilis]	78	62	399
4056	1	647	354	gi11256635	dihydroxy-acid dehydratase [Bacillus subtilis]	78	55	294
4114	1	630	316	gi1809372	hypothetical protein - Trypanosoma brucei	78	62	315
4185	1	3	179	gi11339950	large subunit of NADH-dependent glutamate synthase [Plectonena boryanum]	78	58	177

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
4235	1	655	329	gi 558839	unknown [Bacillus subtilis]	78	60	327
4352	1	541	302	gi 603768	Hut1 protein, imidazolone-5-propionate hydrolase [Bacillus subtilis] gi 603768 Hut1 protein, imidazolone-5-propionate hydrolase [Bacillus subtilis]	78	63	240
4368	1	612	307	gi 1353678	heavy-metal transporting P-type ATPase [Proteus mirabilis]	78	59	306
4461	1	428	216	gi 1276841	glutamate synthase (GOGAT) [Porphyra purpurea]	78	36	213
4530	1	474	238	gi 139556	IGlc [Bacillus subtilis]	78	65	237
3	2	2969	2073	gi 1109684	ProV [Bacillus subtilis]	77	56	897
12	2	2426	1985	gi 467335	ribosomal protein L9 [Bacillus subtilis]	77	59	462
27	1	2	388	gi 1212728	YqhI [Bacillus subtilis]	77	63	387
39	2	590	1252	gi 40054	phenylalanyl-tRNA synthetase beta subunit (AA 1-804) [Bacillus subtilis]	77	60	663
42	6	2704	2931	gi 606241	30S ribosomal subunit protein S14 [Escherichia coli] sp P02370 RS14_ECOLI 30S RIBOSOMAL PROTEIN S14. (SUB 2-101)	77	65	228
46	18	15459	16622	gi 297798	mitochondrial formate dehydrogenase precursor [Solanum tuberosum] p1r J02272 J02272 formate dehydrogenase (EC 1.2.1.2) precursor. mitochondrial - potato	77	55	1164
100	4	4562	4002	gi 1340128	ORF1 [Staphylococcus aureus]	77	54	561
102	8	5378	5713	gi 1311482	acetolactate synthase [Thermus aquaticus]	77	57	336
109	7	4742	5383	gi 710637	unknown [Bacillus subtilis]	77	56	642
117	1	2	1228	gi 1237015	ORF4 [Bacillus subtilis]	77	53	1227
124	10	8323	7688	gi 405819	thymidine kinase [Bacillus subtilis]	77	63	636
147	3	1146	985	gi 849037	hypothetical 15.9-kDa protein [Bacillus subtilis]	77	37	162
152	10	7354	7953	gi 1205383	spermidine/putrescine transport ATP-binding protein [Haemophilus influenzae]	77	55	600
169	2	1004	1282	gi 473825	elongation factor EF-Ts' [Escherichia coli]	77	58	279
184	2	380	1147	gi 216314	esterase [Bacillus stearothermophilus]	77	60	768
189	7	3296	3668	gi 853809	ORF3 [Clostridium perfringens]	77	48	573
193	1	132	290	gi 1303788	VqgH [Bacillus subtilis]	77	54	159
195	8	8740	8414	gi 1499620	M. jannaschi predicted coding region M20798 [Methanococcus jannaschii]	77	44	327
205	8	5428	5204	gi 216340	ORF for adenylate kinase [Bacillus subtilis]	77	61	225

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match (1)	match gene name	% sim	% ident	length (nt)
205	29	14795	14502	gi1786155		Ribosomal Protein L23 [Bacillus subtilis]	77	62	294
211	5	1908	2084	gi1410132		ORFX8 [Bacillus subtilis]	77	47	177
217	5	3478	4416	gi146254		fibronectin/fibrinogen-binding protein (Streptococcus pyogenes)	77	54	939
232	1	267	998	gi1407784		orf-1; novel antigen (Staphylococcus aureus)	77	57	732
233	2	1819	1346	gi1467408		unknown [Bacillus subtilis]	77	61	474
243	3	2661	2299	gi1516155		unconventional myosin [Sus scrofa]	77	32	363
299	1	68	769	gi1467436		unknown [Bacillus subtilis]	77	54	702
301	4	1468	1283	gi1950071		ATP-bind. pyruvate kinase (Mycoplasma capricolum) p1r[S48605]S48605	77	48	186
302	5	2741	3211	gi1508980		hypothetical protein - Mycoplasma capricolum SCC3 (fragment)	77	57	471
302	7	3835	4863	gi1147783		pheB [Bacillus subtilis]	77	60	1029
307	9	5402	4797	gi1070015		ruvB protein [Escherichia coli]	77	60	606
312	1	99	1391	gi1143165		protein-dependent [Bacillus subtilis]	77	62	1293
312	2	1561	2443	gi11399855		malic enzyme (EC 1.1.1.38) [Bacillus stearothermophilus] p1r[A33107]DEBSXS	77	62	1293
312	3	1566	4596	gi139844		malate dehydrogenase oxaloacetate-decarboxylating (EC 1.1.1.38) - Bacillus stearothermophilus	77	62	1020
321	5	5666	4596	gi139844		carboxyltransferase beta subunit [Synechococcus PCC7942]	77	58	901
354	1	47	568	gi1154634		fumarate (citric) (aa 1-462) [Bacillus subtilis]	77	65	1071
365	1	2	1021	gi1143374		YmaB [Bacillus subtilis]	77	57	522
374	1	1	708	gi1405446		phosphoribosyl glycylamide synthetase (Pur-D; gtc start codon) Bacillus subtilis	77	62	1020
385	1	1128	565	gi1533099		transketolase [Bacillus subtilis]	77	61	708
392	2	594	1940	gi1556014		endonuclease III [Bacillus subtilis]	77	63	564
405	5	4079	3570	gi1303912		UDP-N-acetyl muramate-alanine ligase [Bacillus subtilis] sp1P40778[MURC_BACSU UDP-N-ACETYLURAMATE--ALANINE LIGASE (EC 3.2.8) (UDP-N- ACETYLURAMATE--L-ALANINE SYNTHETASE) (FRAGMENT)]	77	65	1347
487	4	1302	1472	gi1432427		YqjW [Bacillus subtilis]	77	64	510
522	1	2	562	gi1401179		ORF1 gene product [Acinetobacter calcoaceticus]	77	48	171
522	2	562	1472	gi1401179		tyrosine--tRNA ligase (EC 6.1.1.1) - Bacillus stearothermophilus	77	63	561

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
523	2	1587	1351	gi 1387979	44% identity over 302 residues with hypothetical protein from <i>Synechocystis</i> sp. accession D6006.C0; expression induced by environmental stress; some similarity to glycosyl transferases; two potential membrane-spanning helices [Bacillus subtilis]	77	48	237
536	2	983	612	gi 140366	adenylosuccinate lyase (Pur-B) (Bacillus subtilis) pir C99356 W28SDS adenylosuccinate lyase (EC 4.3.2.2) - Bacillus subtilis	77	61	372
548	2	339	872	gi 140387	aspartate transcarbamylase [Bacillus subtilis]	77	56	534
597	1	2	481	gi 904198	hypothetical protein [Bacillus subtilis]	77	33	480
633	2	1747	1313	gi 187577	ORF1A [Bacillus subtilis]	77	64	435
642	1	85	360	gi 46971	elip gene product [Staphylococcus epidermidis]	77	61	276
659	1	125	1219	gi 1072381	glutamy-aminopeptidase [Lactococcus lactis]	77	62	1095
670	4	1587	1820	gi 1122760	unknown [Bacillus subtilis]	77	58	234
789	1	2	391	gi 1377823	aminopeptidase [Bacillus subtilis]	77	65	390
815	1	10	573	gi 1303861	Yqgn [Bacillus subtilis]	77	49	564
890	1	1	225	gi 1303844	H ₁ influenza predicted coding region H10594 [Haemophilus influenzae]	77	55	225
1083	1	3	188	gi 460828	B969 [Saccharomyces cerevisiae]	77	66	186
1942	1	415	209	gi 160047	p101/acidic basic repeat antigen (Plasmodium falciparum) pir A29232 A29232 101K malaria antigen precursor - Plasmodium falciparum (strain Camp)	77	38	207
2559	1	1	171	gi 1499034	H ₁ jannaschii predicted coding region H30255 [Methanococcus jannaschii]	77	61	171
2913	2	243	401	gi 42370	pyruvate formate-lyase (AA 1-760) [Escherichia coli] ir S01788 S01788 formate C-acetyltransferase (EC 2.3.1.54) - Escherichia coli	77	72	159
2966	1	56	292	gi 1524397	glycine betaine transporter OpuD [Bacillus subtilis]	77	45	237
2976	1	614	309	gi 40003	oxoglutarate dehydrogenase (NADP+) [Bacillus subtilis] p P23125 O001_BACSU 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE)	77	60	306
2979	2	678	400	gi 1204354	spore germination and vegetative growth protein [Haemophilus influenzae]	77	61	279
2988	1	601	377	gi 438465	Probable operon with orf. Possible alternative initiation codon, aas 2151-2153. Homology with acetyltransferases; putative Bacillus subtilis	77	55	225
2990	1	331	167	gi 142562	ATP synthase epsilon subunit [Bacillus megaterium] pir B28595 PW85EN H+-transporting ATP synthase (EC 3.6.1.34) pailon chain - Bacillus megaterium	77	63	165
3032	1	3	389	gi 488430	alcohol dehydrogenase 2 [Entamoeba histolytica]	77	56	387
3057	1	1	195	gi 468764	mock gene product [Rhizobium meliloti]	77	50	195

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match	length (nt)	ident	align
4008	1	726	400	gi 603768	HutI protein, imidazole-5-propanone hydrolase (Bacillus subtilis) gi 603768 HutI protein, imidazole-5-propanone hydrolase (Bacillus subtilis)	327	52	77
4048	1	703	386	gi 216278	gramicidin S synthetase 1 (Bacillus brevis)	318	55	77
4110	1	3	368	gi 529215 S529	nitrate reductase alpha chain - Bacillus subtilis (fragment)	366	61	77
4115	1	1	348	gi 517205	67 kDa Myosin-crossreactive streptococcal antigen (Streptococcus pyogenes)	348	65	77
4225	1	590	297	gi 1322245	nevalonate pyrophosphate decarboxylase (Rattus norvegicus)	294	60	77
4611	2	494	327	gi 508979	GTP-binding protein (Bacillus subtilis)	168	57	77
4668	1	361	182	gi 529215 S529	nitrate reductase alpha chain - Bacillus subtilis (fragment)	180	61	77
25	1	2	1627	gi 1150620	HnsA (Streptococcus pneumoniae)	1626	58	76
38	5	1488	2537	gi A43577 A435	regulatory protein p10r - Clostridium perfringens	1050	57	76
52	5	2962	4041	gi 1161061	dioxigenase (Methylobacterium extorquens)	1080	62	76
56	20	27389	27955	gi 467402	unknown (Bacillus subtilis)	567	56	76
57	15	12046	12219	gi 1206040	weak similarity to keratin (Caenorhabditis elegans)	174	40	76
91	2	1062	2261	gi 475715	acetyl coenzyme A acetyltransferase (thiolase) (Clostridium acetobutylicum)	1200	57	76
98	2	818	1624	gi 467422	unknown (Bacillus subtilis)	807	62	76
98	5	2965	3228	gi 897793	ly8 gene product (Pediococcus acidilactici)	284	52	76
98	8	5922	6326	gi 467427	methionyl-tRNA synthetase (Bacillus subtilis)	405	53	76
104	3	1322	1885	gi 216151	DNA polymerase (gene L; ttg start codon) (Bacteriophage SP02) gi 579197 SP02 DNA polymerase (aa 1-648) (Bacteriophage SP02) p1r A21498 DUBPS2 DNA-directed DNA polymerase (EC 2.7.7.7) - phage P02	564	63	76
128	9	8134	7055	gi 853776	peptide chain release factor 1 (Bacillus subtilis) p1r S55437 S55437 peptide chain release factor 1 - Bacillus subtilis	1080	58	76
168	5	2832	3311	gi 1204976	prolyl-tRNA synthetase (Haemophilus influenzae)	480	53	76
168	2	2617	1841	gi 1177253	putative ATP-binding protein of ABC-type (Bacillus subtilis)	777	58	76
189	2	163	888	gi 467384	unknown (Bacillus subtilis)	726	63	76
235	3	2253	3518	gi 142936	folyl-polyglutamate synthetase (Bacillus subtilis) p1r B40646 B40646 folC - Bacillus subtilis	1266	53	76
236	1	335	925	gi 1146197	putative (Bacillus subtilis)	591	54	76
237	8	5323	5541	gi 1279261	PI3G3.6 (Caenorhabditis elegans)	219	47	76

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
263	5	5490	4585	gi 1510346	dihydrodipicolinate synthase [Methanococcus jannaschii]	76	49	906
304	3	1051	1794	gi 666982	putative membrane spanning subunit [Bacillus subtilis] pir S52382 S52382 probable membrane spanning protein - Bacillus subtilis	76	60	744
312	4	3611	4624	gi 143312	6-phospho-1-fructokinase [gtg start codon; EC 2.7.1.11] [Bacillus tearothermophilus]	76	56	1014
343	1	2	1016	gi 405956	yeaE [Escherichia coli]	76	59	1035
347	1	409	1701	gi 396304	acetylornithine decarboxylase [Escherichia coli]	76	72	1293
358	1	672	1907	gi 1146215	39.0% identity to the Escherichia coli S1 ribosomal protein; putative [Bacillus subtilis]	76	58	1236
371	3	1	222	gi 537084	alternate gene name mgt; CC Site No. 497 [Escherichia coli] pir S56468 S56468 mgtA protein - Escherichia coli	76	61	222
379	4	4331	4858	gi 143268	dihydrodipicolinate transsuccinylase [odhB; EC 2.3.1.61] [Bacillus subtilis]	76	60	528
404	5	4022	4492	gi 3303823	YqgG [Bacillus subtilis]	76	60	471
411	1	2	307	gi 186025	ORF YKL027W [Saccharomyces cerevisiae]	76	55	306
472	3	4356	2854	gi 1405464	AlaT [Bacillus subtilis]	76	57	1503
546	1	273	995	gi 153821	streptococcal pyrogenic exotoxin type C (speC) precursor Streptococcus pyogenes	76	36	723
588	1	1054	557	gi 1002520	NutS [Bacillus subtilis]	76	61	498
591	1	16	735	gi 885934	CtpB [Synecococcus sp.]	76	44	720
602	2	175	798	gi 1486422	OppD homologue [Rhizobium sp.]	76	52	624
619	2	547	290	gi 310613	major capsid protein [Human cytomegalovirus]	76	47	258
660	4	2568	3302	gi 904199	hypothetical protein [Bacillus subtilis]	76	55	735
677	1	452	228	gi 40177	hypothetical protein [Bacillus subtilis]	76	58	225
962	1	24	206	gi 142443	spoOF gene product [Bacillus subtilis]	76	67	183
					adenylosuccinate synthetase [Bacillus subtilis] sp 229726 PURA_BACSU ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) IMP--ASPARTATE LIGASE).			
978	1	1158	580	gi 1511333	M. jannaschii predicted coding region MJ1322 [Methanococcus jannaschii]	76	56	579
997	1	486	244	gi 467154	No definition line found [Mycobacterium leprae]	76	38	243
1563	1	529	266	gi 1303984	YqgK [Bacillus subtilis]	76	52	264
2184	1	361	182	gi 506706	CapJ [Staphylococcus aureus]	76	38	180
2572	1	1	387	gi 153898	transport protein [Salmonella typhimurium]	76	65	387

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
2942	1	29	400	gi 710020	nitrite reductase (nirB) (Bacillus subtilis)	76	59	372
2957	1	377	216	gi 1311251	hypothetical protein (SP-P42404) (Methanococcus jannaschii)	76	47	162
2980	1	554	279	gi 1403464	AlaT (Bacillus subtilis)	76	53	276
3015	1	649	326	gi 408115	ornithine acetyltransferase (Bacillus subtilis)	76	61	324
3124	1	13	174	gi 182705	ORF_0401 (Escherichia coli)	76	65	162
3179	1	3	161	gi 168477	ferredoxin-dependent glutamate synthase [Zea mays] pfr A38596 A38596 glutamate synthase (ferredoxin) (EC 1.4.7.1) - size	76	53	159
3789	1	2	379	gi 39956	IIGle (Bacillus subtilis)	76	55	378
3892	1	3	314	gi 1510398	ferripyochelin binding protein (Methanococcus jannaschii)	76	52	312
3928	1	798	400	gi 143016	permease (Bacillus subtilis)	76	59	399
4159	1	757	386	sp P80544 MRSP_	METHICILLIN-RESISTANT SURFACE PROTEIN (FRAGMENTS)	76	66	372
4204	1	17	331	gi 296464	ATPase (Lactococcus lactis)	76	56	315
4394	1	494	249	gi 987255	Menkes disease gene (Homo sapiens)	76	48	246
4506	1	2	313	gi 216746	D-lactate dehydrogenase (Lactobacillus plantarum)	76	47	312
4546	1	477	247	gi 133950	large subunit of NADH-dependent glutamate synthase (Plectonema boryanum)	76	61	231
4596	1	379	191	gi 560027	cellulose synthase (Acetobacter xylinum)	76	70	189
4	5	5257	4337	gi 682532	ORF_0294 (Escherichia coli)	75	59	921
6	1	164	952	gi 40960	OTCase (Escherichia coli)	75	56	789
12	3	5935	3944	gi 467336	unknown (Bacillus subtilis)	75	57	1992
23	18	18272	17310	gi 1296433	O-acetylserine sulphydrylase B (Alcaligenes eutrophus)	75	55	963
25	3	2356	1393	gi 1502419	Plax (Bacillus subtilis)	75	56	1038
36	8	5765	6037	gi 1256517	unknown (Schizosaccharomyces pombe)	75	45	273
46	13	11186	12058	gi 48972	nitrate transporter (Synechococcus sp.)	75	46	873
51	7	3474	3677	gi 143607	sporulation protein (Bacillus subtilis)	75	61	204
53	16	16850	16590	gi 143402	recombination protein (ttg start codon) (Bacillus subtilis) gi 1303923 NCBI (Bacillus subtilis)	75	51	261
74	3	3572	2568	gi 1204847	ornithine carbamoyltransferase (Haemophilus influenzae)	75	61	1005

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
85	3	4628	3930	gi1143368	phosphoribosylformyl glycylamide synthetase I (PUR-L; gtg start odon) (Bacillus subtilis)	75	63	699
85	5	5588	4878	gi1143367	phosphoribosyl aminolizole succinocarboxamide synthetase (PUR-C; tg start codon) (Bacillus subtilis)	75	55	711
85	8	6625	7530	gi11303916	Yqia (Bacillus subtilis)	75	53	906
87	3	2340	3590	gi11064813	homologous to sp:PHOR_BACSU (Bacillus subtilis)	75	56	1251
87	6	6084	6896	gi11064810	function unknown (Bacillus subtilis)	75	61	813
108	2	1844	1503	gi11001824	hypothetical protein (Synchocystis sp.)	75	51	342
110	3	1748	3727	gi11147593	putative ppGpp synthetase (Streptomyces coelicolor)	75	55	1980
110	7	4151	5252	gi11177251	cldD gene product (Bacillus subtilis)	75	75	900
120	14	11266	10649	gi11524394	ORF-2 upstream of gbaAB operon (Bacillus subtilis)	75	55	618
121	5	2050	4221	gi11154632	Nrde (Bacillus subtilis)	75	54	2172
124	1	283	143	gi1405622	unknown (Bacillus subtilis)	75	56	141
128	1	81	1139	gi1143316	[gap] gene products (Bacillus megaterium)	75	48	1059
130	8	5760	5903	gi11256654	54.8% identity with Neisseria gonorrhoeae regulatory protein PilQ; putative (Bacillus subtilis)	75	62	143
136	2	4480	3185	gi1467403	seryl-tRNA synthetase (Bacillus subtilis)	75	54	1296
161	10	5439	5798	gi11001195	hypothetical protein (Synchocystis sp.)	75	55	360
172	4	3819	2995	gi1755153	ATP-binding protein (Bacillus subtilis)	75	52	825
179	1	2024	1107	gi1143037	porphobilinogen deaminase (Bacillus subtilis)	75	58	918
195	10	9529	9374	gi1125745	HYPOTHETICAL PROTEIN IN PURB 5'REGION (ORF-15) (FRAGMENT)	75	60	156
200	4	2805	4596	gi1142440	ATP-dependent nuclease (Bacillus subtilis)	75	56	1992
206	3	6900	5620	gi11256135	ybbP (Bacillus subtilis)	75	53	1281
216	2	159	389	gi11052800	unknown (Schizosaccharomyces pombe)	75	58	231
229	1	29	847	gi11205958	branched chain aa transport system II carrier protein (Haemophilus influenzae)	75	49	819
230	2	518	1714	gi11971337	nitrite extrusion protein (Bacillus subtilis)	75	53	1197
231	1	2240	1122	gi11002521	HutL (Bacillus subtilis)	75	54	1119
233	3	1314	1859	gi1467405	unknown (Bacillus subtilis)	75	59	546

TABLE 2

A. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
269	1	325	164	gi11511246	methy coenzyme M reductase system, component A2 [Methanococcus jannaschii]	75	50	162
292	1	1389	772	gi11511604	M. jannaschii predicted coding region MJ1651 [Methanococcus jannaschii]	75	46	618
304	4	1773	2261	gi1205328	surfactin [Haemophilus influenzae]	75	55	489
312	3	2437	3387	gi1285621	undefined open reading frame [Bacillus stearothermophilus]	75	62	951
312	5	4622	6403	gi11041097	Pyruvate Kinase [Bacillus psychrophilus]	75	57	1782
319	1	353	877	gi11212728	YohI [Bacillus subtilis]	75	54	525
320	5	4321	5031	gi11070361	OMP decarboxylase [Lactococcus lactis]	75	56	711
320	6	5010	5642	gi1143394	OMP-PBP transferase [Bacillus subtilis]	75	60	633
337	4	1519	2088	gi1487433	citrate synthase II [Bacillus subtilis]	75	58	570
394	2	669	1271	gi1304976	matches PS00017; ATP-GTP A and PS00301; EFPACTOR-GTP; similar to longation factor G. TetH/TetO tetracycline-resistance proteins Escherichia coli	75	51	603
423	1	127	570	gi11183839	unknown [Pseudomonas aeruginosa]	75	59	444
433	2	1603	1929	gi1149211	acetolactate synthase [Klebsiella pneumoniae]	75	63	327
446	2	176	1540	gi1312441	dlhydroxylase [Bacillus caldolyticus]	75	62	1365
486	1	494	249	gi11149582	potP gene product [Clostridium perfringens]	75	55	246
496	1	3	794	gi1143582	spoIIIEA protein [Bacillus subtilis]	75	59	792
498	2	824	1504	gi1143328	phoP protein (put.); putative [Bacillus subtilis]	75	47	681
499	2	1061	1624	gi11387979	44% identity over 302 residues with hypothetical protein from Synchocystis sp. accession D6406.C0; expression induced by environmental stress; some similarity to glycosyl transferases; two potential membrane-spanning helices [Bacillus subtilis]	75	51	564
568	1	641	453	gi114310341	triacylglycerol lipase [EC 3.1.1.3] 2 - Mycoplasma mycoides subsp. mycoides [SC3]	75	50	189
613	2	430	233	gi1330993	tegument protein [Sialirine herpesvirus 2]	75	75	198
621	1	1	525	gi1529754	IspeC [Streptococcus pyogenes]	75	43	525
642	5	1809	2474	gi1176401	EnpG [Staphylococcus epidermidis]	75	51	666
646	2	454	657	gi1172402	ribonuclease P [Saccharomyces cerevisiae]	75	37	204
657	1	3	347	gi11842541	OMP_0236 [Escherichia coli]	75	47	345
750	1	1662	832	gi146971	leplP gene product [Staphylococcus epidermidis]	75	57	831

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
754	1	2	481	gi1103901	YnfR [Bacillus subtilis]	75	57	480
763	2	563	393	gi11205145	multidrug resistance protein [Haemophilus influenzae]	75	51	171
775	1	961	482	pir1036889 D168	LeuA protein, inactive - Lactococcus lactis subsp. lactis (strain IL1403)	75	63	480
793	1	1	180	gi1143116	[gap] gene products [Bacillus megaterium]	75	57	180
800	1	318	160	gi1509411	NPR1 protein [Asorhizobium caulinodans]	75	34	159
811	1	1117	560	gi1143434	Rho Factor [Bacillus subtilis]	75	60	558
940	1	493	329	gi11276985	arginase [Bacillus caldovelox]	75	50	165
971	2	37	252	gi11001373	hypothetical protein [Synchocystis sp.]	75	58	216
1059	1	384	232	gi1726480	L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus subtilis]	75	67	153
1109	2	219	374	gi1143331	alkaline phosphatase regulatory protein [Bacillus subtilis] pir1A27650 A27650 regulatory protein phoR - Bacillus subtilis sp123545 phoR_BACSU ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHO R (EC 2.7.3.-)	75	53	156
1268	1	271	137	gi1304135	ornithine acetyltransferase [Bacillus stearothermophilus] sp1007908 ARG1 BACST GLUTAMATE N-ACETYLTRANSFERASE (EC 2.3.1.35) ORNITHINE ACETYLTRANSFERASE (ORNITHINE TRANSACETYLASE) (ONTASE) / HMO-ACID ACETYLTRANSFERASE (EC 2.3.1.1) (N-ACETYLGLUTAMATE YNTHA	75	63	135
1500	1	324	163	gi11205488	excinuclease ABC subunit B [Haemophilus influenzae]	75	57	162
1529	1	798	400	gi11002521	MutL [Bacillus subtilis]	75	54	399
3010	1	770	387	gi11204635	pyruvate formate-lyase activating enzyme [Haemophilus influenzae]	75	54	384
3105	1	1	180	gi11041097	Pyruvate Kinase [Bacillus psychrophilus]	75	57	180
3117	1	45	212	gi1899317	peptide synthetase module [Microcystis aeruginosa] pir184911 S4911 probable amino acid activating domain - Microcystis aeruginosa (fragment) (SUB 144-528)	75	42	168
3139	2	119	345	gi1145294	adenine phosphoribosyl-transferase [Escherichia coli]	75	66	207
3880	1	618	310	gi11009366	Respiratory nitrate reductase [Bacillus subtilis]	75	58	309
3911	1	48	401	gi1433991	ATP synthase subunit beta [Bacillus subtilis]	75	68	354
3957	1	2	379	gi11016089 D168	3-isopropylmalate dehydratase (EC 4.2.1.33) chain Iuoc - Lactococcus lactis subsp. lactis (strain IL1403)	75	65	378
4005	1	5	259	gi1216746	D-lactate dehydrogenase [Lactobacillus plantarum]	75	48	255
4080	1	73	333	gi1415855	deoxyribose aldolase [Mycoplasma hominis]	75	59	261

TABLE 2

S. aureus - putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
4111	1	1	339	gi149405	putative [Lactococcus lactis]	75	57	339
4136	1	602	303	gi1450688	hsuM gene of Ecoprr1 gene product [Escherichia coli] p1r[S38437]S38437 hadM protein - Escherichia coli p1r[S09629]S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	75	56	300
4144	1	688	336	gi148972	nitrate transporter [Synchococcus sp.]	75	49	333
4237	1	664	374	gi1339950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	75	55	291
4306	2	73	318	gi1294260	major surface glycoprotein [Pneumocystis carinii]	75	68	246
4343	1	715	359	gi1204652	methylated-DNA--protein-cysteine methyltransferase [Haemophilus influenzae]	75	52	357
4552	1	620	312	gi1296464	ATPase [Lactococcus lactis]	75	55	309
38	9	5776	6126	gi1443793	RupC [Escherichia coli]	74	50	351
50	8	6910	6221	gi1239988	hypothetical protein [Bacillus subtilis]	74	55	690
56	9	10770	12221	gi11000451	Trap [Bacillus subtilis]	74	57	1452
64	2	2266	1622	gi141015	aspartate-tRNA ligase [Escherichia coli]	74	57	645
66	6	5063	4848	gi11212729	YqhJ [Bacillus subtilis]	74	47	216
67	18	14334	14897	gi11510631	endoglucanase [Methanococcus jannaschii]	74	52	564
102	15	12561	13136	gi149429	putative [Lactococcus lactis]	74	67	576
102	16	13121	14419	gi149435	putative [Lactococcus lactis]	74	57	1299
108	4	4873	3902	gi139478	ATP binding protein of transport ATPases [Bacillus firmus] lr[S15406]S15406 ATP-binding protein - Bacillus firmus p128946[YATR-BAC71]HYPOTHETICAL ATP-BINDING TRANSPORT PROTEIN	74	59	972
116	5	8574	7093	gi11205400	dipeptide transport system permease protein [Haemophilus influenzae]	74	49	1482
120	7	4342	4803	gi1146970	ribonucleoside triphosphate reductase [Escherichia coli] p1r[A47331]A47331 anaerobic ribonucleotide reductase - Escherichia coli	74	58	462
121	7	5961	6581	gi1107528	tetG start [Campylobacter coli]	74	51	621
128	3	2320	3531	gi1143318	phosphoglycerate kinase [Bacillus megaterium]	74	57	1212
130	7	5237	5791	gi11256653	DNA-binding protein [Bacillus subtilis]	74	60	555
136	3	6745	5150	gi1143076	histidase [Bacillus subtilis]	74	58	1596
145	2	664	1368	gi1407773	devA gene product [Anabaena sp.]	74	45	705
152	1	552	277	gi1377833	unknown [Bacillus subtilis]	74	54	276

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	Length (nt)
164	10	11064	11175	gi 580900	ORF3 gene product [Bacillus subtilis]	74	52	312
175	2	3109	2624	gi 642656	unknown [Mitsunobu meliloti]	74	36	486
175	9	6064	5612	gi 854656	[Na/H antiporter system ORF2 [Bacillus alcalophilus]	74	46	453
195	11	11346	10139	gi 1204430	hypothetical protein (SP:25745) [Haemophilus influenzae]	74	55	1008
205	17	9619	9059	gi 1044979	ribosomal protein L6 [Bacillus subtilis]	74	64	561
236	7	5574	6710	gi 1146207	putative [Bacillus subtilis]	74	63	1137
241	3	4521	3334	gi 694121	malate thiokinase [Methylobacterium extorquens]	74	52	1188
246	6	3305	2799	gi 467374	single strand DNA binding protein [Bacillus subtilis]	74	64	507
249	4	6551	5313	gi 1534397	glycine betaine transporter Opd [Bacillus subtilis]	74	55	1239
261	7	4389	4081	gi 809542	CbrB protein [Erwinia chrysanthemi]	74	42	309
278	6	5714	4665	gi 1204872	ATP-binding protein [Haemophilus influenzae]	74	54	1050
309	1	1220	666	gi 1205579	hypothetical protein (GB:U14003_302) [Haemophilus influenzae]	74	53	555
315	2	1473	862	gi 143398	quinol oxidase [Bacillus subtilis]	74	57	612
320	1	1	1065	gi 143389	glutaminase of carbamyl phosphate synthetase (Bacillus subtilis) p1r[E39845]E39845 carbamoyl-phosphate synthase glutamine-hydrolyzing (EC 6.3.5.5), pyrimidine-repressible, small hain - Bacillus subtilis	74	60	1065
380	2	382	1128	gi 534657	ATPase subunit a [Bacillus stearothermophilus]	74	56	747
405	2	1742	1311	gi 1303915	VqH2 [Bacillus subtilis]	74	65	432
433	5	2503	3270	gi 473902	alpha-acetolactate synthase [Lactococcus lactis]	74	56	768
452	1	1	942	gi 413982	lpa-58r gene product [Bacillus subtilis]	74	52	942
461	1	3	1193	gi 558494	homoserine dehydrogenase [Bacillus subtilis]	74	51	1191
461	2	1174	1407	gi 40211	threonine synthase (thiC) (AA 1-352) [Bacillus subtilis] tr[A25364]A25364	74	56	234
462	2	402	734	gi 142520	thioredoxin [Bacillus subtilis]	74	62	333
478	1	574	320	gi 1493005	glycyl-tRNA synthetase [Methanococcus jannaschii]	74	52	255
501	2	739	1740	gi 217040	acid glycoprotein [Streptococcus pyogenes]	74	58	1002
551	2	4083	2791	gi 143040	glutamate-1-semialdehyde 2,1-aminotransferase [Bacillus subtilis] p1r[pd2728]pd2728 glutamate-1-semialdehyde 2,1-aminotransferase (EC 4.3.8) - Bacillus subtilis	74	51	1293

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
573	1	1	477	gi 1006605	hypothetical protein (Synchocystis sp.)	74	45	477
596	2	1780	1298	gi 1303853	YqgP (Bacillus subtilis)	74	55	483
618	2	2924	1758	gi 1146237	21.4% of identity to trans-acting transcription factor of Saccharomyces cerevisiae; 25% of identity to sucrose synthase of Zea mays; putative (Bacillus subtilis)	74	55	1167
659	2	1269	1595	gi 1072380	ORF3 (Lactococcus lactis)	74	62	327
724	1	373	188	gi 143374	phosphoribosyl glycine synthetase (PUR-D; gta start codon) Bacillus subtilis	74	58	186
743	2	604	1209	gi 153833	ORF1; putative (Streptococcus parasanguis)	74	50	606
836	1	2	259	gi 143458	ORF V (Bacillus subtilis)	74	47	258
989	2	443	724	gi 1303994	YqgM (Bacillus subtilis)	74	46	282
1106	1	1	492	gi 146970	epiD gene product (Staphylococcus epidermidis)	74	54	492
1135	2	373	528	gi 1433948	ipa-24d gene product (Bacillus subtilis)	74	48	156
1234	1	817	472	gi 495245	recJ gene product (Erwinia chrysanthemi)	74	36	366
2586	1	2	238	gi 1149701	abcC gene product (Clostridium perfringens)	74	62	237
2959	1	798	400	gi 1405454	aconitase (Bacillus subtilis)	74	60	399
2962	1	650	363	gi 450886	1-phosphoglycerate kinase (Thermotoga maritima)	74	58	288
2983	1	3	191	gi 1303893	YqgL (Bacillus subtilis)	74	56	189
3018	1	2	223	gi 143040	glutamate-1-semialdehyde 2,1-aminotransferase (Bacillus subtilis) pir D42728 D42728 glutamate-1-semialdehyde 2,1-aminotransferase (EC 4.3.8) - Bacillus subtilis	74	56	222
3038	1	510	256	pir 552915 5529	nitrate reductase alpha chain - Bacillus subtilis (fragment)	74	57	255
3062	1	374	189	gi 1107528	ttg start (Campylobacter coli)	74	51	186
4035	1	184	360	gi 1022725	unknown (Staphylococcus haemolyticus)	74	64	177
4045	1	607	305	gi 1510977	M. jannaschii predicted coding region M30938 (Methanococcus jannaschii)	74	41	303
4283	1	471	304	gi 520844	orfe (Bacillus subtilis)	74	58	168
4449	1	3	221	gi 560910	peptide-synthetase ORF1 (Bacillus subtilis)	74	54	219
4587	1	458	231	gi 1370207	orf6 (Lactobacillus sake)	74	59	228

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	Length (nt)
4603	1	29	214	gi 146208	glutamate synthase large subunit (EC 2.6.1.53) [Escherichia coli] pif[A29617/A29617 glutamate synthase (NADPH) (EC 1.4.1.13) large chain - Escherichia coli	74	60	186
4670	1	366	184	gi 256135	ybbF [Bacillus subtilis]	74	61	183
5	10	7953	7162	gi 143727	putative [Bacillus subtilis]	73	42	792
11	2	2454	1372	gi 166338	dihydroorotate dehydrogenase [Agaricoba agerica]	73	55	1083
14	1	2024	1020	gi 143373	phosphoribosyl aminimidazole carboxy formyl ornyltransferase/inosine monophosphate cyclohydrolase (PUR-H(J)) [Bacillus subtilis]	73	54	1005
23	5	5426	4635	gi 1468939	meso-2,3-butanediol dehydrogenase (D-acetoin forming) [Klebsiella pneumoniae]	73	58	792
23	17	17379	16360	gi 297060	ornithine cyclodeaminase [Rhizobium meliloti]	73	37	1020
29	2	692	1273	gi 467442	stage V sporulation [Bacillus subtilis]	73	54	582
31	5	6467	4914	gi 414000	ipa-76d gene product [Bacillus subtilis]	73	55	1554
37	8	8658	7402	gi 429259	pept gene product [Bacillus subtilis]	73	59	1257
37	9	7738	7562	gi 168367	alpha-isopropylmalate isomerase (put-1); putative [Rhizomucor ircinellolides]	73	52	177
38	7	3931	4896	gi 405885	yeiN [Escherichia coli]	73	58	966
44	6	5041	4238	gi 580895	unknown [Bacillus subtilis]	73	53	804
44	11	7767	8306	gi 42009	mcnB gene product [Escherichia coli]	73	50	540
45	3	2439	3080	gi 1109685	ProW [Bacillus subtilis]	73	47	642
54	13	14016	13794	gi 413931	ipa-7d gene product [Bacillus subtilis]	73	61	243
59	4	1430	2248	gi 147923	threonine dehydratase 2 (EC 4.2.1.16) [Escherichia coli]	73	53	819
65	1	1458	730	gi 677944	AppF [Bacillus subtilis]	73	56	729
80	2	1375	860	gi 580932	murD gene product [Bacillus subtilis]	73	53	516
102	13	10124	11179	gi 580891	3-isopropylmalate dehydrogenase (AA 1 - 365) [Bacillus subtilis] pif[A26522/A26522 3-isopropylmalate dehydrogenase (EC 1.1.1.85) - subtilis	73	55	1056
109	2	3493	2600	gi 1510849	M. jannaschii predicted coding region M30775 [Methanococcus jannaschii]	73	40	894
120	8	4782	5756	gi 146970	ribonucleoside triphosphate reductase [Escherichia coli] pif[A47331/A47331 anaerobic ribonucleotide reductase - Escherichia coli	73	56	975
120	9	5726	6223	gi 1204333	anaerobic ribonucleoside-triphosphate reductase [Haemophilus influenzae]	73	62	498

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
132	5	4151	4363	gi1871048	HPSH2 - heavy chain potential motor protein [Giardia intestinalis]	73	43	213
140	6	5952	4324	gi1634107	kdpB [Escherichia coli]	73	59	1629
142	6	7060	5919	gi1410125	rflB gene product [Bacillus subtilis]	73	57	1132
149	4	1866	1717	gi1460892	heparin binding protein-44, HBP-44 (mice, Peptide, 360 aa) pit(JX0281/JX028) heparin-binding protein-44 precursor - mouse gi1220434 ORF [Mus musculus] (SUB 2-160)	73	53	150
158	1	1	1431	gi1882504	ORF_1560 [Escherichia coli]	73	57	1431
174	6	5352	4525	gi11146240	ketopantoate hydroxymethyltransferase [Bacillus subtilis]	73	55	828
175	8	5537	5178	gi1854657	Na/H antiporter system ORF [Bacillus alcalophilus]	73	56	360
186	5	6593	5493	gi1467477	unknown [Bacillus subtilis]	73	48	1101
249	6	6283	5729	gi11524397	glycine betaine transporter Opd [Bacillus subtilis]	73	56	555
265	4	1873	2280	gi139848	U3 [Bacillus subtilis]	73	41	408
270	1	328	582	gi1780461	220 kDa polypeptide [African swine fever virus]	73	53	255
278	4	4283	3618	gi11204965	hypothetical 23.3 kD protein [Escherichia coli]	73	49	666
279	3	4984	3593	gi11185288	isochorismate synthase [Bacillus subtilis]	73	58	1392
291	4	1207	1575	gi11511440	glutamine--fructose-6-phosphate transaminase [Methanococcus jannaschii]	73	63	369
299	2	735	1166	gi1467437	unknown [Bacillus subtilis]	73	58	432
299	5	2050	3234	gi1467439	temperature sensitive cell division [Bacillus subtilis]	73	53	1185
334	1	1237	728	gi1536655	ORF YBR244w [Saccharomyces cerevisiae]	73	43	510
336	2	1827	1036	gi1790943	urea amidolyase [Bacillus subtilis]	73	51	792
374	3	1389	1874	gi11405451	YneJ [Bacillus subtilis]	73	55	486
433	4	1916	2554	gi1473902	alpha-acetolactate synthase [Lactococcus lactis]	73	54	639
509	2	1795	1028	gi1467483	unknown [Bacillus subtilis]	73	56	768
513	1	1709	918	gi11146220	NAD+ dependent glycerol-3-phosphate dehydrogenase [Bacillus subtilis]	73	56	792
533	2	239	733	gi11510605	hypothetical protein (SP:P42297) [Methanococcus jannaschii]	73	44	495
546	2	1148	2815	gi141748	hadM protein (AA 1-520) [Escherichia coli]	73	52	1668
549	1	762	382	gi1114847	CinA [Bacillus subtilis]	73	57	381
567	1	1346	675	gi1410137	ORFX13 [Bacillus subtilis]	73	58	672

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
716	2	654	1112	gi 1256623	exodeoxyribonuclease (Bacillus subtilis)	73	56	459
772	1	3	677	gi 142010	Shows 70.2% similarity and 48.6% identity to the EnvM protein of almonella typhimurium (Anebaena sp.)	73	57	675
774	1	3	209	gi 409286	barU (Bacillus subtilis)	73	52	207
782	1	1	402	gi 143320	lgap1 gene products (Bacillus megaterium)	73	56	402
789	2	451	762	gi 1063266	low homology to P14 protein of Hemophilus influenzae and 14.2 kDa protein of Escherichia coli (Bacillus subtilis)	73	56	312
796	1	3	911	gi 853754	ABC transporter (Bacillus subtilis)	73	58	909
806	3	1209	949	gi 143786	cryptophary-tRNA synthetase (EC 6.1.1.2) (Bacillus subtilis)	73	51	261
816	2	4839	3097	gi 41748	hshK protein (AA 1-520) (Escherichia coli)	73	52	1743
839	1	798	400	gi 886906	argininosuccinate synthetase (Streptomyces clavuligerus) pIR S57659 S57659 argininosuccinate synthase (EC 6.3.4.5) - Streptomyces clavuligerus	73	59	399
857	1	3	290	gi 348052	acetoin utilization protein (Bacillus subtilis)	73	50	288
1008	1	790	398	gi 40100	rodC (tag) polypeptide (AA 1-746) (Bacillus subtilis) ir S06049 S06049 rodC protein - Bacillus subtilis p P3485 TAGF_BACSU TECHNIC ACID BIOSYNTHESIS PROTEIN F.	73	41	393
1018	1	1	213	gi 529357	No definition line found (Caenorhabditis elegans) sp P46975 STT3_CABEL OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT OHOLOG.	73	53	213
1011	1	3	491	gi 142706	comG1 gene product (Bacillus subtilis)	73	51	489
1174	1	395	204	gi 1149513	alpha3 subunit of laminin 5 (Homo sapiens)	73	60	192
1175	1	655	329	gi 473817	'ORF' (Escherichia coli)	73	57	327
1187	1	3	209	gi 580870	ipa-37d qoxA gene product (Bacillus subtilis)	73	52	207
1206	1	72	245	gi 144816	formyltetrahydrofolate synthetase (FMPS) (tgg start codon) (EC 3.4.3) (Moorella thermocetacea)	73	43	374
1454	1	423	241	gi 121253	unknown (Schizosaccharomyces pombe)	73	53	183
1469	1	517	260	gi 1303787	YqeG (Bacillus subtilis)	73	55	258
1761	1	374	189	gi 91135	Hat26Aa gene product (Drosophila simulans)	73	34	186
1849	1	467	243	gi 162307	DNA topoisomerase II (Trypanosoma cruzi)	73	60	225
2055	1	2	400	gi 559381	P47K protein (Rhodococcus erythropolis)	73	34	399
2556	1	2	244	gi 145925	fecB (Escherichia coli)	73	62	243

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
2947	2	549	400	gi 1184680	polynucleotide phosphorylase [Bacillus subtilis]	73	51	150
2956	1	746	375	gi 43397	quinol oxidase [Bacillus subtilis]	73	58	372
3037	1	655	329	gi 143091	acetolactate synthase [Bacillus subtilis]	73	55	327
3115	1	385	194	gi 323866	overlapping out-of-phase protein [eggplant mosaic virus]	73	53	192
3601	2	700	527	gi 143521	glutaryl-CoA dehydrogenase precursor [Mus musculus]	73	48	174
3743	1	798	400	gi 450688	hach gene of Ecopri gene product [Escherichia coli] pif[S28437]S28437 hach protein - Escherichia coli pif[S09629]S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	73	54	399
3752	1	840	359	gi 1524193	unknown [Mycobacterium tuberculosis]	73	59	282
3852	1	2	181	gi 216746	D-lactate dehydrogenase [Lactobacillus plantarum]	73	68	180
3914	1	475	239	gi 513490	Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Chicken (fragment)	73	53	237
3914	2	570	343	gi 528991	unknown [Bacillus subtilis]	73	38	228
4069	1	2	316	gi 40003	oxoglutarate dehydrogenase (NADP+) [Bacillus subtilis] pif[S21129]O001_BACSU 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE)	73	55	315
4165	1	715	365	gi 143521	glutaryl-CoA dehydrogenase precursor [Mus musculus]	73	48	351
4196	1	1	177	gi 809660	deoxyribose-phosphate aldolase [Bacillus subtilis] pif[S49455]S49455 deoxyribose-phosphate aldolase (EC 4.1.2.4) - acillus subtilis	73	60	177
4202	1	572	378	gi 528991	unknown [Bacillus subtilis]	73	38	195
4314	1	2	193	gi 436797	N-acyl-L-amino acid amidohydrolase [Bacillus stearothermophilus] sp[P37112]ANA_BACST N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 5.1.14) (AMINOACYLASE)	73	47	192
4393	1	3	263	gi 216267	ORF2 [Bacillus megaterium]	73	47	261
35	2	903	1973	gi 1146196	phosphoglycerate dehydrogenase [Bacillus subtilis]	72	53	1071
38	22	19094	17877	gi 602031	similar to trimethylamine DH [Mycoplasma capricolum] pif[S49950]S49950 probable trimethylamine dehydrogenase (EC 5.99.7) - Mycoplasma capricolum (SC3) (fragment)	72	54	1218
38	23	18114	15162	gi 413968	ipa-44d gene product [Bacillus subtilis]	72	54	1029
44	19	11895	12953	gi 516272	unknown [Bacillus subtilis]	72	49	1059
48	7	6248	7117	gi 43499	pyruvate synthase [Halobacterium halobium]	72	49	870
50	7	6560	5691	gi 1205399	proton glutamate symport protein [Haemophilus influenzae]	72	53	873

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
53	9	10521	9259	gi 1303956	YqjE [Bacillus subtilis]	72	52	1263
56	23	29549	29995	gi 467471	unknown [Bacillus subtilis]	72	67	447
69	4	5298	4123	gi 1354725	pfoS/R [Treponema pallidum]	72	46	1176
69	5	4377	4982	gi 904198	hypothetical protein [Bacillus subtilis]	72	43	606
73	1	2	856	gi 142997	glycerol uptake facilitator [Bacillus subtilis]	72	59	855
98	13	9371	10258	gi 467435	unknown [Bacillus subtilis]	72	50	888
127	1	1	1593	gi 217144	alanine carrier protein [thermophilic bacterium PS3] p1r[A45111][A45111]	72	56	1593
131	1	5197	2600	gi 153952	alanine transport protein - thermophilic acterium PS-3	72	53	2598
141	4	1040	1978	gi 1405446	polymerase III polymerase subunit (dnaE) [Salmonella typhimurium] p1r[A45915][A45915 DNA-directed DNA polymerase (EC 2.7.7.7) III lpha chain - Salmonella typhimurium]	72	53	2598
149	8	2819	2535	gi 606234	transketolase [Bacillus subtilis]	72	54	939
149	17	5472	5245	gi 1304472	secY [Escherichia coli]	72	44	285
154	1	1	210	gi 1205620	DNA polymerase [Unidentified phycodnavirus clone OT04]	72	55	228
155	1	2207	1320	gi 391610	ferritin like protein [Haemophilus influenzae]	72	40	210
180	1	2	328	gi 333630	[farnesyl diphosphate synthase [Bacillus stearothermophilus] p1r[JX0257][JX0257 geranyltransferase (EC 2.5.1.10) - Bacillus stearothermophilus]	72	57	888
184	3	1145	3553	gi 1205110	A180 [Saccharomyces cerevisiae]	72	62	327
195	2	1923	1279	gi 1001730	virulence associated protein homolog [Haemophilus influenzae]	72	49	2409
206	13	1646	15869	gi 1064807	hypothetical protein [Synecocystis sp.]	72	45	645
209	2	462	932	gi 1204666	ORTHINE AMINOTRANSFERASE [Bacillus subtilis]	72	50	1224
215	2	764	522	gi 881513	hypothetical protein [GB:X73124.53] [Haemophilus influenzae]	72	60	471
224	1	2	790	gi 949974	insulin receptor homolog [Drosophila melanogaster] p1r[S57245][S57245 insulin receptor homolog - fruit fly [Drosophila melanogaster] (SUB 46-2146)]	72	63	243
233	1	1526	765	gi 1408493	luciferase repressor [Staphylococcus xylosus]	72	54	789
240	1	220	1485	gi 537049	homologous to SwissProt:YIDA_ECOLI hypothetical protein [Bacillus subtilis]	72	52	762
245	1	3	1340	gi 1204578	ORF_0470 [Escherichia coli]	72	52	1286
					hypothetical protein [GB:006949.1] [Haemophilus influenzae]	72	46	1338

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
259	2	2108	1245	gi1140128	ORF1 [Staphylococcus aureus]	72	59	864
304	2	285	1094	gi1205130	glutamine-binding periplasmic protein [Haemophilus influenzae]	72	52	810
307	10	5326	5039	gi11070015	protein-dependent [Bacillus subtilis]	72	53	288
315	1	517	260	gi1143399	quinol oxidase [Bacillus subtilis]	72	55	258
316	11	9622	9308	gi11204445	hypothetical protein [SP27857] [Haemophilus influenzae]	72	52	315
317	3	926	1609	gi1487433	citrate synthase II [Bacillus subtilis]	72	55	684
364	7	12538	10493	gi11510643	ferrous iron transport protein B [Methanococcus jannaschii]	72	53	2046
409	2	340	1263	gi11402944	orfM1 gene product [Bacillus subtilis]	72	49	924
441	3	2177	1590	gi1312379	highly conserved among subacteria [Clostridium acetobutylicum] pir[S34312]S34312 hypothetical protein V - Clostridium acetobutylicum	72	48	588
453	6	2854	2505	gi1800601	antibacterial protein 3 - Staphylococcus haemolyticus	72	70	150
460	1	2	625	gi1016162	ABC transporter subunit [Cyanophora paradoxa]	72	51	624
463	1	3253	1628	gi1666014	The polymorphism (RFLP) of this gene is associated with susceptibility to essential hypertension. The SA gene product has light homology to acetyl-CoA synthetase (Homo sapiens)	72	60	1626
480	4	3047	3466	gi1433392	ATP synthase subunit epsilon [Bacillus subtilis]	72	53	420
502	1	1086	586	gi1310859	ORF2 [Synecococcus sp.]	72	50	501
519	1	81	1184	gi1303704	YrKE [Bacillus subtilis]	72	54	1104
559	1	3	746	gi1107530	caud gene product [Campylobacter coli]	72	56	744
575	1	1142	573	gi1303866	Yqgs [Bacillus subtilis]	72	56	570
671	1	2	592	gi1204497	protein-export membrane protein [Haemophilus influenzae]	72	44	591
679	2	295	1251	gi1563258	virulence-associated protein 2 [Dichelobacter nodosus]	72	52	957
687	2	295	957	gi11146214	44% identical amino acids with the Escherichia coli ambA suppressor; putative [Bacillus subtilis]	72	49	663
837	1	1	435	gi11146183	putative [Bacillus subtilis]	72	54	435
868	1	150	788	gi11377842	unknown [Bacillus subtilis]	72	55	639
922	1	130	432	gi11088269	unknown protein [Azotobacter vinelandii]	72	58	303
941	1	2	238	gi1153929	NADPH-sulfite reductase flavoprotein component [Salmonella typhimurium]	72	49	237
980	1	840	421	gi1853767	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis]	72	59	420

TABLE 2

5. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1209	1	383	213	gi1144735	neurotoxin type B [Clostridium botulinum]	72	44	171
1469	2	671	474	gi1205458	hypothetical protein (CB-D5652_47) [Haemophilus influenzae]	72	63	198
1956	1	727	365	gi154409	hexosephosphate transport protein [Salmonella typhimurium] pir[B41853]B41853 hexose phosphate transport system regulatory protein uhpB - Salmonella typhimurium	72	44	363
2101	1	3	401	gi11303950	YqjY [Bacillus subtilis]	72	50	399
2503	1	569	399	gi1149713	formate dehydrogenase (Methanobacterium formicicum) pir[A2712]A2712 formate dehydrogenase (EC 1.2.1.2) - ethanobacterium formicicum	72	56	171
2967	1	3	155	gi11212729	YqjJ [Bacillus subtilis]	72	46	153
3004	1	367	185	gi1665999	hypothetical protein [Bacillus subtilis]	72	55	183
3109	1	278	141	gi1413968	ipa-44d gene product [Bacillus subtilis]	72	45	138
3171	1	3	287	gi1515938	glutamate synthase (ferredoxin) [Synechocystis sp.] pir[S46957]S46957 glutamate synthase (ferredoxin) (EC 1.4.7.1) - Synechocystis sp.	72	52	285
3771	1	26	367	gi1408501	homologous to N-acyl-L-amino acid amidohydrolase of Bacillus stearothermophilus [Bacillus subtilis]	72	63	342
3951	1	1	222	gi11500409	M. jannaschii predicted coding region M31519 [Methanococcus jannaschii]	72	38	222
4190	1	721	362	gi139956	IIGlc [Bacillus subtilis]	72	57	360
4444	1	3	347	gi11009366	respiratory nitrate reductase [Bacillus subtilis]	72	55	345
6	2	911	1200	gi1537095	ornithine carbamoyltransferase [Escherichia coli]	71	56	270
11	15	11350	10859	gi1532309	25 kDa protein [Escherichia coli]	71	47	492
19	2	1248	2435	gi11244574	D-alanine:D-alanine ligase [Enterococcus hirae]	71	52	1188
21	2	898	1488	gi1149629	anthranilate synthase component 2 [Leptospira biflexa] pir[C32840]C32840 anthranilate synthase (EC 4.1.3.27) component II Leptospira biflexa	71	45	591
34	1	1	567	gi11303983	YqjP [Bacillus subtilis]	71	59	567
37	3	3192	2806	gi11209681	glutamate-rich protein [Bacillus firmus]	71	50	387
38	18	12250	112462	gi1927645	arginyl endopeptidase [Porphyromonas gingivalis]	71	50	213
39	3	1246	4431	pir[S09411]S094	spoIIIE protein - Bacillus subtilis	71	49	3186
53	14	15770	14760	gi1142611	branched chain alpha-keto acid dehydrogenase E1-alpha [Bacillus subtilis]	71	58	1011
54	11	113461	112625	gi1143014	lent repressor [Bacillus subtilis]	71	46	837

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
57	7	7152	5860	gi 508175	ETIC domain of PTS-dependent GAT transport and phosphorylation <i>Escherichia coli</i>	71	48	1293
57	18	11897	14314	gi 1063247	high homology to flavohemoprotein (Hemoglobin-like protein) of <i>Alcaligenes eutrophus</i> and <i>Saccharomyces cerevisiae</i> [<i>Bacillus subtilis</i>]	71	56	438
62	16	9831	10955	gi 1103926	YqjQ [<i>Bacillus subtilis</i>]	71	54	1125
70	12	8505	8966	gi 147198	phnA protein [<i>Escherichia coli</i>]	71	38	462
86	5	2384	2089	gi 904205	hypothetical protein [<i>Bacillus subtilis</i>]	71	51	306
96	7	7601	8269	gi 709991	hypothetical protein [<i>Bacillus subtilis</i>]	71	49	669
100	6	4822	5931	gi 1060848	Opine dehydrogenase [<i>Arthrobacter sp.</i>]	71	45	1110
103	1	1062	532	gi 143089	lep protein [<i>Bacillus subtilis</i>]	71	41	531
109	18	15312	15695	gi 413985	lpa-61d gene product [<i>Bacillus subtilis</i>]	71	57	384
113	1	630	316	gi 663254	probable protein kinase [<i>Saccharomyces cerevisiae</i>]	71	57	315
114	5	6598	5803	gi 143156	membrane bound protein [<i>Bacillus subtilis</i>]	71	40	996
133	2	3087	1723	gi 1303913	YqhX [<i>Bacillus subtilis</i>]	71	53	1365
149	19	6335	5895	gi 529650	G4OP [<i>Bacteriophage SP21</i>]	71	51	441
154	5	3635	3087	gi 425488	repressor protein [<i>Streptococcus sobrinus</i>]	71	47	549
164	11	11354	11689	gi 49318	ORF4 gene product [<i>Bacillus subtilis</i>]	71	52	316
169	5	1936	2745	gi 1403403	unknown [<i>Mycobacterium tuberculosis</i>]	71	56	810
193	2	272	1234	gi 1303788	YqgH [<i>Bacillus subtilis</i>]	71	49	963
205	1	1743	895	gi 1215694	GlnQ [<i>Mycoplasma pneumoniae</i>]	71	46	849
233	4	1849	2022	gi 633732	ORF1 [<i>Campylobacter jejuni</i>]	71	50	174
237	7	4501	5169	gi 149384	HistE [<i>Lactococcus lactis</i>]	71	54	669
272	4	2848	2273	gi 709993	hypothetical protein [<i>Bacillus subtilis</i>]	71	48	576
274	2	618	1496	gi 143035	NAD(P)H:glutamate-transfer RNA reductase [<i>Bacillus subtilis</i>] pir[AJ5252]AJ5252 5-aminolevulinic synthase (EC 2.3.1.37) - <i>ecillus subtilis</i>	71	53	879
276	5	3149	2720	gi 303562	ORF210 [<i>Escherichia coli</i>]	71	50	630
287	1	136	660	gi 110634	20 kDa protein [<i>Streptococcus gordonii</i>]	71	53	525
288	6	3322	2771	gi 1256625	putative [<i>Bacillus subtilis</i>]	71	47	552

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
301	6	3492	2461	gi1467417	similar to lysine decarboxylase [Bacillus subtilis]	71	57	1032
306	4	6607	5222	gi1256618	transport protein [Bacillus subtilis]	71	56	1386
307	2	1536	925	gi1622683	orfC [Mycoplasma capricolum]	71	45	612
310	5	5793	5146	gi1348052	acetoin utilization protein [Bacillus subtilis]	71	51	608
322	1	2	1303	gi11001819	hypothetical protein [Synechocystis sp.]	71	46	1302
331	4	4171	3995	gi1467473	unknown [Bacillus subtilis]	71	57	177
350	2	548	922	gi1551879	ORF 1 [Lactococcus lactis]	71	55	375
375	4	1860	3071	gi1467447	unknown [Bacillus subtilis]	71	57	1212
380	5	1560	2102	gi1142557	ATP synthase b subunit [Bacillus megaterium]	71	43	543
414	2	251	637	gi1580904	homologous to E.coli rnpA [Bacillus subtilis]	71	49	387
424	1	335	1354	gi1581305	L-lactate dehydrogenase [Lactobacillus plantarum]	71	57	1020
436	4	3701	3270	gi1467401 PNO5	phosphoribosylanthranilate isomerase (EC 5.3.1.24) - Bacillus subtilis (fragment)	71	66	432
482	1	3	1280	gi1401042	ORFX18 [Bacillus subtilis]	71	49	1278
525	3	2272	1844	gi1143370	phosphoribosylpyrophosphate amidotransferase (Pur-P, EC 2.4.2.14) Bacillus subtilis	71	56	429
529	4	2739	2047	gi1606150	ORF_1309 [Escherichia coli]	71	43	693
563	1	22	969	gi11237015	ORF4 [Bacillus subtilis]	71	53	948
581	1	506	255	gi11301730	72503.2 [Caenorhabditis elegans]	71	47	252
612	2	1068	913	gi1153968	[fimbriae 2 [Salmonella typhimurium]	71	55	156
613	1	1	654	gi1466778	lysine specific permease [Escherichia coli]	71	50	654
618	1	1243	623	gi1146238	[poly(A) polymerase [Bacillus subtilis]	71	52	621
630	1	1170	586	gi11466243	unknown [Bacillus subtilis]	71	53	585
691	1	1126	641	gi1289260	comE ORF1 [Bacillus subtilis]	71	51	486
694	2	149	427	gi112971	NADH dehydrogenase subunit V (AA 1-605) [Gallus gallus] (F1S10197)S10197 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain - chicken mitochondrion (SOG1)	71	47	279
715	2	169	777	gi11303830	YqfL [Bacillus subtilis]	71	53	609
746	2	1473	970	gi11377843	unknown [Bacillus subtilis]	71	52	504

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
748	1	1437	802	gi1403459	YnaS (Bacillus subtilis)	71	49	636
753	1	1018	524	gi1510189	M. jannaschii predicted coding region MJ0296 (Methanococcus jannaschii)	71	53	495
761	1	3	215	gi1475972	pentafunctional enzyme (Pneumocystis carinii)	71	47	213
783	1	1203	703	gi1536655	ORF YB244w (Saccharomyces cerevisiae)	71	52	501
800	3	1292	987	gi1204326	tRNA delta(2)-isopentenylpyrophosphate transferase (Haemophilus influenzae)	71	48	306
806	1	116	286	gi1419075	cbm gene product (Methanobacterium thermoautotrophicum)	71	50	171
931	1	973	488	gi1893358	PgaA (Bacillus subtilis)	71	56	486
1041	1	2	262	gi1408507	pyrimidine nucleoside transport protein (Bacillus subtilis)	71	45	261
1070	1	2	172	gi1709993	hypothetical protein (Bacillus subtilis)	71	46	171
1176	1	57	365	gi151259	HMG-CoA reductase (EC 1.1.1.88) (Pseudomonas mvaloni) p1r144756 (Pseudomonas sp.)	71	49	309
1181	1	366	184	gi146971	epip gene product (Staphylococcus epidermidis)	71	50	183
1281	1	3	290	gi153016	ORF 419 protein (Staphylococcus aureus)	71	50	288
1348	1	456	229	gi1602683	orfC (Mycoplasma capricolum)	71	48	228
2002	1	756	379	gi1008177	ORF YJL046w (Saccharomyces cerevisiae)	71	48	378
2119	1	2	217	gi1046088	arginyl-tRNA synthetase (Mycoplasma genitalium)	71	50	216
2418	1	3	320	gi1499771	M. jannaschii predicted coding region MJ0936 (Methanococcus jannaschii)	71	57	318
2961	1	2	187	gi1312443	carbamoyl-phosphate synthase (glutamine-hydrolysing) (Bacillus albidolycicus)	71	57	186
2999	2	67	306	gi1710020	nitrite reductase (nirB) (Bacillus subtilis)	71	43	240
3033	1	2	184	gi1262335	YnaA (Bacillus subtilis)	71	57	183
3584	1	3	338	gi1401716	beta-isopropylmalate dehydrogenase (Neurospora crassa)	71	55	336
3715	2	743	399	gi1563952	glucanate permease (Bacillus licheniformis)	71	59	345
3785	1	770	387	gi147382	acyl-CoA-dehydrogenase (Streptomyces purpurascens)	71	57	384
3875	1	541	272	gi1001541	hypothetical protein (Synecocystis sp.)	71	38	270
4135	1	637	320	gi142695	S-adenosyl-L-methionine:uroporphyrinogen III methyltransferase (Bacillus megaterium)	71	52	318
4249	1	63	239	gi1205363	deoxyribose aldolase (Haemophilus influenzae)	71	63	177
4508	1	530	267	gi1197667	vitellogenin (Anolis pulchellus)	71	46	264

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
6	3	1237	2721	gi 1321788	arginine ornithine antiporter [Clostridium perfringens]	70	54	1485
11	11	6572	7486	gi 216854	P47K [Pseudomonas chlororaphis]	70	41	915
12	1	2890	1481	gi 467330	replicative DNA helicase [Bacillus subtilis]	70	49	1410
15	1	1756	893	gi 451216	mannosephosphate isomerase [Streptococcus mutans]	70	46	864
15	2	1277	1050	gi 476092	unknown [Bacillus subtilis]	70	50	228
17	2	2132	1350	gi 145402	choline dehydrogenase [Escherichia coli]	70	52	783
21	1	2	925	gi 149516	anthranilate synthase alpha subunit [Lactococcus lactis] pir[S5124][S5124] anthranilate synthase [EC 4.1.3.27] alpha chain - actococcus lactis subsp. lactis	70	50	924
25	7	5580	6251	gi 1389549	ORF3 [Bacillus subtilis]	70	52	672
33	6	6071	7423	gi 1303875	YqjB [Bacillus subtilis]	70	51	1353
36	2	959	1594	gi 500755	methyl purine glycosylase [Mus musculus]	70	47	636
38	8	4901	5860	gi 1408507	pyrimidine nucleoside transport protein [Bacillus subtilis]	70	44	960
44	8	5312	5989	gi 1006620	hypothetical protein [Synchocystis sp.]	70	49	678
46	10	8950	10020	gi 1403126	lccD gene product [Alcaligenes eutrophus]	70	45	1071
52	2	2727	1900	gi 1486247	unknown [Bacillus subtilis]	70	53	828
52	6	4048	4656	gi 244501	esterase II-carboxylesterase [EC 3.1.1.1] [Pseudomonas fluorescens, optido, 218 aa]	70	50	609
56	8	8460	9962	gi 1339951	small subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	70	51	1503
62	1	48	290	gi 142702	A competence protein 2 [Bacillus subtilis]	70	47	243
64	1	1080	561	gi 1204377	molybdopterin biosynthesis protein [Haemophilus influenzae]	70	47	540
70	5	5139	3595	gi 1204834	2',3'-cyclic-nucleotide 2'-phosphodiesterase [Haemophilus influenzae]	70	47	1545
91	4	7793	5466	gi 886471	methionine synthase [Catharantus roseus]	70	56	2328
96	5	8754	7255	gi 89096 a390	alkaline phosphatase [EC 3.1.3.1] III precursor - Bacillus subtilis	70	54	1500
110	2	767	1300	gi 145294	adenine phosphoribosyl-transferase [Escherichia coli]	70	51	534
116	6	7026	7976	gi 143607	sporulation protein [Bacillus subtilis]	70	50	951
121	8	6401	6988	gi 1107528	ttg start [Campylobacter coli]	70	45	588
131	8	6842	7936	gi 1150454	prolidase PEP [Lactobacillus delbrueckii]	70	48	1095

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
135	1	2	1489	gi 311309	putative membrane-bound protein with four times repetition of ro-Sar-Ale at the N-terminus; function unknown [Alcaligenes utrophus]	70	49	1488
138	3	418	714	gi 904181	hypothetical protein [Bacillus subtilis]	70	46	297
164	8	9344	9874	gi 49315	ORF1 gene product [Bacillus subtilis]	70	47	531
164	16	15626	16618	gi 1205212	hypothetical protein (GB:D1048)_18 [Haemophilus influenzae]	70	50	993
205	2	2735	1803	gi 1215695	peptide transport system protein SapF homolog; SapF homolog [Mycobacterium tuberculosis]	70	47	933
209	3	910	1386	gi 1204665	hypothetical protein (GB:X73124_26) [Haemophilus influenzae]	70	48	477
246	3	340	756	gi 215098	excisionase [Bacteriophage 154a]	70	46	417
263	7	7876	6749	gi 142540	aspartokinase II [Bacillus sp.]	70	51	1128
268	3	3212	4117	gi 1340128	ORF1 [Staphylococcus aureus]	70	50	906
302	6	3201	3827	gi 147282	ruvA protein (95g start) [Escherichia coli]	70	46	627
302	10	5879	7051	gi C38530 C385	guanine RNA-ribosyltransferase (EC 2.4.2.29) - Escherichia coli	70	55	1173
313	1	2520	1414	gi 1205934	aminopeptidase a/i [Haemophilus influenzae]	70	46	1107
355	2	379	669	gi 1070013	protein-dependent [Bacillus subtilis]	70	48	291
403	1	1255	629	gi 733147	GuaF [Xanthomonas campestris]	70	33	627
444	10	8770	9273	gi 1204752	high affinity ribose transport protein [Haemophilus influenzae]	70	52	504
449	1	2	1243	gi 619724	MotE [Bacillus firmus]	70	44	1242
472	1	637	320	gi 727145	open reading frame; putative [Bacillus mytiliguelacensis] p1r[B29091 B29091] hypothetical protein (bglA region) - Bacillus mytiliguelacensis (fragment)	70	41	318
480	2	727	1608	gi 142560	ATP synthase gamma subunit [Bacillus megaterium]	70	44	882
524	1	2	307	gi 602292	RCH2 protein [Brassica napus]	70	45	306
525	1	823	413	gi 143372	phosphoribosyl glycineamide formyltransferase (Pur-N) [Bacillus subtilis]	70	52	411
565	4	3625	2552	gi 881434	ORFP [Bacillus subtilis]	70	51	1074
607	4	829	1284	gi 511524	hypothetical protein (SP:P37002) [Methanococcus jannaschii]	70	50	456
633	1	1383	703	gi 431231	luciferase [Bacillus caldolyticus]	70	53	681
646	3	1683	1309	gi 467340	unknown [Bacillus subtilis]	70	49	375
663	1	830	417	gi 1303873	Y-42 [Bacillus subtilis]	70	40	414

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
681	1	1488	781	gi 1001678	hypothetical protein [Synecocystis sp.]	70	53	708
708	1	2	448	sp P33940 YOH	HYPOTHETICAL 54.3 NO PROTEIN IN ECO-ALKB INTERGENIC REGION.	70	51	447
725	1	51	722	gi 1001644	hypothetical protein [Synecocystis sp.]	70	48	672
776	1	1371	787	gi 145165	putative [Escherichia coli]	70	47	585
834	1	250	783	gi 552971	NADH dehydrogenase (ndhF) [Vicia faba]	70	47	534
865	2	1585	1379	gi 1204636	ATP-dependent helicase [Haemophilus influenzae]	70	45	207
894	1	535	269	gi 467364	DNA binding protein (probable) [Bacillus subtilis]	70	41	267
919	1	3	317	gi 1314847	ClnA [Bacillus subtilis]	70	40	315
944	1	3	572	gi 709991	hypothetical protein [Bacillus subtilis]	70	44	570
988	2	772	605	gi 132441	ORF 3; putative [Bacillus subtilis]	70	50	168
1055	1	3	335	gi 529755	IspeC [Streptococcus pyogenes]	70	37	333
1093	1	2	904	gi 853754	ABC transporter [Bacillus subtilis]	70	49	903
1109	1	2	310	gi 1001827	hypothetical protein [Synecocystis sp.]	70	42	309
1220	1	488	235	pir S23416 S234	epiB protein - Staphylococcus epidermidis	70	40	234
1279	1	73	348	gi 153015	PemA protein [Staphylococcus aureus]	70	47	276
1336	1	195	542	sp P31776 PDBA	PENICILLIN-BINDING PROTEIN 1A (PBP-1A) [PENICILLIN-BINDING PROTEIN A]	70	50	348
1537	2	232	402	gi 1146181	putative [Bacillus subtilis]	70	50	171
1574	1	451	272	gi 219630	endothelin-A receptor [Homo sapiens]	70	47	180
1640	1	690	346	gi 1146243	22.4k identity with Escherichia coli DNA-damage inducible protein ...; putative [Bacillus subtilis]	70	46	345
2504	1	2	286	gi 495179	transmembrane protein [Lactococcus lactis]	70	51	285
3061	1	564	301	gi 508175	ETIC domain of PTS-dependent Gat transport and phosphorylation Escherichia coli	70	44	264
3128	1	2	199	gi 1340056	unknown [Mycobacterium tuberculosis]	70	51	198
3218	1	3	488	gi 515938	glutamate synthase (ferredoxin) [Synecocystis sp.] pir S46957 S46957	70	50	486
3323	1	794	399	gi 1154891	glutamate synthase (ferredoxin) (EC 1.4.7.1) - ynechocystis sp.	70	52	396
3679	1	599	399	gi 529385	ATP binding protein [Phoradendrum leucosum] chromosome condensation protein [Caenorhabditis elegans]	70	30	201

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	Length (nt)
3841	1	706	398	gi 1208965	hypothetical 23.3 kd protein [Escherichia coli]	70	47	309
3929	1	3	401	gi 149435	putative [Lactococcus lactis]	70	49	399
4044	1	595	374	gi 602031	similar to trimethylamine DH [Mycoplasma capricolum] pir[S49950]S49950 probable trimethylamine dehydrogenase [EC 5.99.7] - Mycoplasma capricolum (SQC3) (fragment)	70	40	222
4329	1	558	280	gi 1339951	small subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	70	49	279
4422	1	576	289	gi 296466	ATPase [Lactococcus lactis]	70	57	288
4647	1	361	200	gi 166412	NADH-glutamate synthase [Medicago sativa]	70	59	162
16	8	7571	9031	gi 1499620	M. jannaschii predicted coding region M30798 (Methanococcus jannaschii)	69	44	1461
16	9	9080	10033	gi 133197	thioredoxin reductase [Escherichia coli]	69	54	954
10	1	1452	727	gi 1204910	hypothetical protein (GI:14001_302) [Haemophilus influenzae]	69	52	726
38	4	1023	1298	gi 407773	devA gene product [Anabaena sp.]	69	41	276
44	9	5987	6595	gi 1205920	polyphosphate kinase system hydrophilic membrane-bound protein [Haemophilus influenzae]	69	45	609
62	15	9104	9475	gi 185178	unknown [Bacillus subtilis]	69	44	372
66	4	2402	2803	gi 1303893	YqjC [Bacillus subtilis]	69	51	402
67	15	14126	13627	gi 149647	ORF2 [Listeria monocytogenes]	69	37	498
67	17	14053	14382	gi 305002	ORF_1356 [Escherichia coli]	69	49	330
67	19	15130	15807	gi 1109684	ProV [Bacillus subtilis]	69	45	678
78	3	1447	2124	gi 1256633	putative [Bacillus subtilis]	69	53	678
78	4	4513	3725	gi 1103958	YqjG [Bacillus subtilis]	69	32	789
85	4	4521	4213	gi 1291261293	hypothetical protein (pur operon) - Bacillus subtilis	69	32	309
86	6	3253	2654	gi 973332	OrfC [Bacillus subtilis]	69	50	600
95	1	96	710	gi 786468	4All antigen, spore tail membrane antigen-putative sucrose-specific phosphotransferase enzyme-II homolog [rice, testis, peptide Partial, 72 aa]	69	43	615
100	7	6023	7426	gi 1203355	Na+/H+ antiporter [Haemophilus influenzae]	69	39	1404
102	2	2678	1650	gi 561690	sialoglycoproteinase [Pasteurella haemolytica]	69	47	1029
103	8	12241	8537	gi 1009366	Respiratory nitrate reductase [Bacillus subtilis]	69	54	3705
103	11	14987	12552	gi 1710020	Nitrite reductase (nirB) [Bacillus subtilis]	69	51	2436

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
112	11	8708	10168	gi 154411	hexosephosphate transport protein (Salmonella typhimurium) p1r D41853 D41853 hexose phosphate transport system protein uhpT - salmonella typhimurium	69	51	1461
112	16	16644	17414	gi 1204435	pyruvate formate-lyase activating enzyme (Haemophilus influenzae)	69	50	771
113	2	33	953	gi 290509	o307 [Escherichia coli]	69	43	921
114	2	1537	1058	pir A4271 A427	reticulocyte-binding protein 1 - Plasmodium vivax	69	39	480
121	6	4309	5310	gi 154633	NrdF [Bacillus subtilis]	69	53	1002
125	2	267	854	gi 413931	ipa-7d gene product [Bacillus subtilis]	69	43	588
149	27	10666	10400	pir 528089 5280	hypothetical protein A - yeast (Zygosaccharomyces bisporus) plasmid pSB1	69	39	267
161	1	1598	813	gi 1205538	hypothetical protein (G8-U14003_302) [Haemophilus influenzae]	69	47	786
165	4	2222	4633	gi 40054	phenylalanyl-tRNA synthetase beta subunit (AA 1-804) [Bacillus bacillus]	69	52	2412
169	3	1210	1761	gi 296031	elongation factor Ts (Spirulina platensis)	69	45	552
175	12	8686	8339	gi 732682	P1aE protein [Escherichia coli]	69	69	348
190	2	484	1671	sp P17731 H158	HISTIDINOL-PROPHATE AMINOTRANSFERASE (EC 2.6.1.9) (IMIDAZOLE ACETOL- PHOSPHATE TRANSAMINASE)	69	48	1188
206	1	5551	2777	gi 41750	hsdR protein (AA 1-1033) [Escherichia coli]	69	49	2775
206	4	6038	5796	gi 1256135	YbhF [Bacillus subtilis]	69	48	243
249	1	636	319	gi 1400456	YnuP [Bacillus subtilis]	69	40	118
302	8	4820	5776	gi 1001768	hypothetical protein (Synecocystis sp.)	69	48	957
324	2	7384	3893	gi 1256798	pyruvate carboxylase [Rizobium etli]	69	53	3492
351	3	2098	1808	gi 1491664	T04H1.4 [Caenorhabditis elegans]	69	30	291
369	3	2075	2305	gi 336458	ORP [Balaenoptera acutorostrata]	69	61	231
392	3	1999	2424	gi 556015	ORF1 [Bacillus subtilis]	69	45	426
410	1	87	779	gi 155611	phosphoglyceromutase [Zymomonas mobilis]	69	58	693
421	1	2085	1129	gi 1276905	arginase [Bacillus caldovelox]	69	54	957
444	8	6713	7741	gi 1221782	purine synthesis repressor [Haemophilus influenzae]	69	40	1029
453	1	828	415	gi 1122758	unknown [Bacillus subtilis]	69	57	414
469	2	3286	2246	gi 1458228	muty homolog [Homo sapiens]	69	44	1041

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	Length (nt)
509	3	1730	1371	gi 49224	Urf 4 (Synachococcus sp.)	69	39	360
520	5	3023	2823	gi 726427	similar to D. melanogaster MST101-2 protein (PIR:S34154) Caenorhabditis elegans	69	39	201
531	1	26	760	gi 509672	repressor protein (Bacteriophage Tuc2009)	69	33	735
589	1	107	253	gi 169101	17.9 kDa heat shock protein (hspl7.9) (Pium sativum)	69	52	147
594	2	597	1391	gi 142783	DNA photolyase (Bacillus firmus)	69	48	795
604	4	2476	2114	gi 413930	ipa-6d gene product (Bacillus subtilis)	69	45	363
607	1	2	313	gi 1236103	W08D2.3 (Caenorhabditis elegans)	69	47	312
607	2	590	312	gi 516715	ORF YBR275c (Saccharomyces cerevisiae)	69	39	279
734	1	864	433	gi 467327	unknown (Bacillus subtilis)	69	44	432
759	1	3	338	gi 1009367	Respiratory nitrate reductase (Bacillus subtilis)	69	50	336
761	2	392	586	gi 13508	Leucyl-tRNA synthetase (Cycloplasmic) (Saccharomyces cerevisiae) ORF YPL160w (Saccharomyces cerevisiae)	69	46	195
802	1	72	1013	gi 163044	ferrochelatase (Bacillus subtilis)	69	55	942
816	1	2573	1368	gi 1510268	restriction modification system S subunit (Methanococcus jannaschii)	69	45	1206
838	2	133	387	gi 1255371	coded for by C. elegans cDNA YK349.5; coded for by C. elegans cDNA YK349.3; similar to guanilate kinase (Xenopus laevis)	69	46	255
851	2	745	1005	gi 284998	secA gene product (Antilhamion sp.)	69	39	261
867	1	535	289	gi 1070014	protein-dependent (Bacillus subtilis)	69	47	267
995	1	954	478	gi 1205569	transcription elongation factor (Haemophilus influenzae)	69	53	477
999	1	1009	506	gi 899254	predicted trithorax protein (Drosophila virilis)	69	21	504
1127	1	1315	659	gi 1205434	H. influenzae predicted coding region H1191 (Haemophilus influenzae)	69	56	657
1138	1	248	460	gi 1510646	M. jannaschii, predicted coding region M0568 (Methanococcus jannaschii)	69	48	213
2928	1	3	401	gi 290503	glutamate permease (Escherichia coli)	69	41	399
3090	1	444	223	gi 1204987	DNA polymerase III, alpha chain (Haemophilus influenzae)	69	36	222
3817	1	2	400	gi 1483199	peptide-synthetase (Mycobacterium tuberculosis)	69	45	399
3833	1	667	335	gi 1524193	unknown (Mycobacterium tuberculosis)	69	46	333

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
4079	1	747	400	gi 546918	orf3 of comK [Bacillus subtilis, E26, Peptide Partial, 140 aa] pir S43612 S43612 hypothetical protein Y - Bacillus subtilis sp P40398 YHKD_BACSU HYPOTHETICAL PROTEIN IN COMK 3'REGION (ORFY FRAGMENT)	69	64	348
4115	2	215	400	gi 517205	67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes]	69	59	186
4139	1	1	333	gi 1208451	hypothetical protein [Synecocystis sp.]	69	36	333
4258	1	457	230	gi 496158	restriction-modification enzyme subunit M1 [Mycoplasma pneumoniae] pir S49395 S49395 HadM1 protein - Mycoplasma pneumoniae (SOC3)	69	43	228
4317	1	90	374	gi 413967	lda-43d gene product [Bacillus subtilis]	69	44	285
4465	1	3	293	gi 396256	similar to phosphotransferase system enzyme II [Escherichia coli] sp P32672 PNC_ECOLI PTS SYSTEM, FRUCTOSE-LIKE-2 IIC COMPONENT PHOSPHOTRANSFERASE ENZYME II, C COMPONENT)	69	49	291
3	1	2302	1193	gi 109685	ProM [Bacillus subtilis]	68	46	1110
15	4	2592	2074	gi 807973	unknown [Saccharomyces cerevisiae]	68	45	519
31	8	6328	8772	gi 290642	ATPase [Enterococcus hirae]	68	48	2445
40	2	1115	750	gi 606342	ORF_622; reading frame open far upstream of start; possible ranshift, linking to previous ORF [Escherichia coli]	68	55	166
46	9	6886	8415	gi 155276	aldehyde dehydrogenase [Vibrio cholerae]	68	44	1530
48	3	3643	3404	gi 285608	241k polyprotein [Apple stem grooving virus]	68	47	240
48	4	3536	4132	gi 1045937	M. genitalium predicted coding region M246 [Mycoplasma genitalium]	68	39	597
53	10	11671	10685	gi 1303952	VqJA [Bacillus subtilis]	68	46	987
70	9	7346	8155	gi 147198	phnE protein [Escherichia coli]	68	40	810
89	4	1899	2966	gi 145173	35 kDa protein [Escherichia coli]	68	43	1068
108	1	2187	1150	gi 38722	precursor (aa -20 to 381) [Acinetobacter calcoaceticus] ir A29277 A29277 aldose 1-epimerase (EC 5.1.3.3) - Acinetobacter calcoaceticus	68	57	1038
112	5	2686	3622	gi 153724	MalC [Streptococcus pneumoniae]	68	55	937
116	7	7865	8638	gi 143608	sporulation protein [Bacillus subtilis]	68	48	774
118	3	2484	3698	gi 1303805	VqER [Bacillus subtilis]	68	46	1215
120	2	1424	1594	sp P38038 CVSJ_	SULFITE REDUCTASE (NADPH) FLAVOPROTEIN ALPHA-COMPONENT (EC 1.8.1.2) (SIR- FP)	68	45	171
129	1	1	1011	gi 396307	argininosuccinate lyase [Escherichia coli]	68	50	1011

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
132	3	1867	2739	gi 16267	ORF2 (Bacillus megaterium)	68	48	873
134	2	848	1012	gi 147545	DNA recombinase [Escherichia coli]	68	50	165
141	2	372	614	gi 872116	lati (stress inducible protein) [Glycine max]	68	36	243
149	7	2454	2260	gi 145774	hap70 protein (dnaK gene) [Escherichia coli]	68	48	195
155	2	1776	1534	gi 216583	ORF1 [Escherichia coli]	68	36	243
158	3	1836	3289	sp P33940 VCJH_	HYPOTHEICAL 54.3 KD PROTEIN IN ECO-ALKB INTERGENIC REGION.	68	51	1468
169	6	2749	3318	gi 1401602	unknown [Mycobacterium tuberculosis]	68	46	570
175	10	9158	7365	gi 1072395	phaA gene product [Rhizobium molitoli]	68	51	1794
188	7	4184	5434	gi 1173843	3-ketoacyl-ACP synthase II [Vibrio harveyi]	68	48	1251
189	3	907	1665	gi 467383	DNA binding protein (probable) [Bacillus subtilis]	68	55	759
206	5	7683	6709	gi 1256138	YbbI [Bacillus subtilis]	68	48	975
206	8	10425	12176	gi 452687	pyruvate decarboxylase [Saccharomyces cerevisiae]	68	48	1752
212	8	3421	3648	gi 1369941	lci gene product [Bacteriophage B1]	68	39	228
214	8	5457	6482	gi 1420467	ORF YOR196c [Saccharomyces cerevisiae]	68	45	1026
237	4	2507	3088	gi 149381	HlsH [Lactococcus lactis]	68	46	582
243	5	5540	4542	gi 1235684	mevalonate pyrophosphate decarboxylase [Saccharomyces cerevisiae]	68	47	999
262	1	3	164	gi 150974	4-oxalacrylate tautomerase [Pseudomonas putida]	68	42	162
262	2	1984	1118	gi 1147744	PSR [Enterococcus hirae]	68	49	867
276	6	3702	3139	sp P30750 ABC_E	ATP-BINDING PROTEIN ABC (FRAGMENT)	68	50	564
306	6	6345	5725	gi 1256617	adenine phosphoribosyltransferase [Bacillus subtilis]	68	53	621
333	3	4599	3850	gi 467473	unknown [Bacillus subtilis]	68	45	750
365	6	5017	4838	gi 1130643	72283.3 [Caenorhabditis elegans]	68	45	180
376	2	549	1646	gi 1277026	DAPA aminotransferase [Bacillus subtilis]	68	51	1098
405	1	1741	872	gi 1303917	YqjB [Bacillus subtilis]	68	47	870
406	2	853	539	gi 1511513	ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]	68	44	315
426	6	3558	3391	gi 624632	GltL [Escherichia coli]	68	48	168
438	1	108	329	gi 146923	nitrogenase reductase [Escherichia coli]	68	43	222

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
443	1	476	240	gi 535810	hippuricase (Campylobacter jejuni)	68	42	237
443	2	518	1015	gi 1204742	H. influenzae predicted coding region HI0491 (Haemophilus influenzae)	68	48	498
443	5	4447	3779	gi 506660	deoxyribose-phosphate aldolase (Bacillus subtilis) pif[S49455]S49455	68	55	669
476	2	240	1184	gi 571345	unknown, similar to E. coli cardiolipin synthase (Bacillus subtilis) sp P45860 WME_BACSU HYPOTHETICAL 58.2 PROTEIN IN NNRI-ACDA INTERGENIC REGION.	68	45	945
486	2	1876	1046	gi 147328	transport protein (Escherichia coli)	68	41	831
517	3	1764	2084	gi 523809	orf2 (Bacteriophage A2)	68	64	321
572	1	2	571	sp P19237 Y05L	HYPOTHETICAL 6.8 KD PROTEIN IN NRDC-TK INTERGENIC REGION.	68	47	570
646	1	914	459	gi 413982	ipe-38c gene product (Bacillus subtilis)	68	52	456
659	3	1688	1901	gi 1107341	C33D9.8 (Caenorhabditis elegans)	68	36	234
864	5	1510	1716	gi 145774	hsp70 protein (dnaK gene) (Escherichia coli)	68	48	207
920	1	860	432	gi 1510416	hypothetical protein (SP:P31466) (Methanococcus jannaschii)	68	54	429
952	1	1096	611	gi 23456	reductase (Leishmania major)	68	46	486
970	1	91	402	gi 1354775	pfos/R (Treponema pallidum)	68	46	312
1028	1	1064	534	gi 10117	diaminopimelate decarboxylase (Bacillus subtilis)	68	47	531
1029	1	428	216	gi 1335714	Plasmodium falciparum mRNA for asparagine-rich antigen (clone 17C1)	68	31	213
1058	1	692	348	gi 281649	epic gene product (Staphylococcus epidermidis)	68	46	345
1096	2	665	465	gi 143434	Rho Factor (Bacillus subtilis)	68	43	201
1308	1	2	694	gi 169939	group B oligopeptidase-PepB (Streptococcus agalactiae)	68	50	693
1679	1	2	238	gi 17205	67 kDa Myosin-crossreactive streptococcal antigen (Streptococcus yogenes)	68	53	217
2039	1	3	383	gi 153898	transport protein (Salmonella typhimurium)	68	51	381
2077	1	3	326	pir C33496 C334	hisc homolog - Bacillus subtilis	68	47	324
2112	1	613	374	gi 64884	lamin LII (Xenopus laevis)	68	50	260
2273	1	793	398	gi 581648	epiB gene product (Staphylococcus epidermidis)	68	45	396
2948	1	2	385	gi 216869	branched-chain amino acid transport carrier (Pseudomonas aeruginosa) pir A2833 A28334 branched-chain amino acid transport protein braz Pseudomonas aeruginosa	68	41	384

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
2955	1	768	400	gi 1904179	hypothetical protein [Bacillus subtilis]	68	49	369
2981	1	572	288	gi 508979	GTP-binding protein [Bacillus subtilis]	68	48	285
3014	1	584	294	gi 1524394	ORF-2 upstream of gbaB operon [Bacillus subtilis]	68	45	291
3082	1	336	169	gi 1204696	fructose-permease IBC component [Haemophilus influenzae]	68	53	168
3108	1	103	258	gi 217855	heat-shock protein [Arabidopsis thaliana]	68	48	156
3639	1	919	461	gi 1510490	nitrate transport permease protein [Methanococcus jamaaschii]	68	47	459
3657	1	1	330	gi 155369	PTS enzyme-II fructose [Xanthomonas campestris]	68	46	320
3823	1	780	391	gi 603768	hutI protein, imidazole-5-propionate hydrolase [Bacillus subtilis]	68	54	390
3982	1	2	277	gi 149435	putative [Lactococcus lactis]	68	47	276
4051	1	1	342	gi 450688	hcdM gene of Ecoprr1 gene product [Escherichia coli] pir[S38437/S38437] hcdM protein - Escherichia coli pir[S09629/S09629] hypothetical protein A - Escherichia coli (SUB 40-520)	68	48	342
4089	1	12	209	gi 1353678	heavy-metal transporting P-type ATPase [Proteus mirabilis]	68	47	198
4143	1	47	187	gi 603769	HutU protein, uronase [Bacillus subtilis]	68	55	141
4148	1	2	352	gi 450688	hcdM gene of Ecoprr1 gene product [Escherichia coli] pir[S38437/S38437] hcdM protein - Escherichia coli pir[S09629/S09629] hypothetical protein A - Escherichia coli (SUB 40-520)	68	51	351
4173	1	2	382	gi 1041097	Pyruvate Kinase [Bacillus psychrophilus]	68	48	381
4182	1	498	250	gi 413968	lipa-44d gene product [Bacillus subtilis]	68	50	249
4362	2	148	318	gi 450688	hcdM gene of Ecoprr1 gene product [Escherichia coli] pir[S38437/S38437] hcdM protein - Escherichia coli pir[S09629/S09629] hypothetical protein A - Escherichia coli (SUB 40-520)	68	44	171
5	11	9493	8300	gi 163727	putative [Bacillus subtilis]	67	46	1194
31	11	10318	9833	gi 16746	D-lactate dehydrogenase [Lactobacillus plantarum]	67	41	486
32	3	1560	3155	gi 1098557	renal sodium/dicarboxylate cotransporter [Homo sapiens]	67	46	1596
32	5	4945	4145	gi 1510720	prephenate dehydratase [Methanococcus jamaaschii]	67	51	801
36	5	5350	4268	gi 146216	45% identity with the product of the ORF6 gene from the Erwinia herbicola carotenoid biosynthesis cluster; putative [Bacillus subtilis]	67	58	1083
44	7	6492	5304	gi 1006621	hypothetical protein [Synecocystis sp.]	67	43	813

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
56	7	3943	8481	gi 304131	glutamate synthase large subunit precursor (Azospirillum brasilense) p1r B46602 B46602 glutamate synthase (NADPH) (EC 1.4.1.13) alpha chain - Azospirillum brasilense	67	52	4539
56	12	13923	14678	gi 1000453	TraB (Bacillus subtilis)	67	48	756
62	8	5092	4757	gi 1113949	orf3 (Bacillus, C-125, alkali-sensitive mutant 18224, Peptide Mutant, 112 aa)	67	45	336
62	10	7570	6338	gi 154655	Na/H antiporter system (Bacillus alcalophilus)	67	49	1233
99	3	2119	3321	gi 1204349	hypothetical protein (GB:D90212.3) (Haemophilus influenzae)	67	50	1203
102	9	5695	7176	gi 149432	putative (Lactococcus lactis)	67	51	1482
103	13	14549	14049	gi 1408497	LPD gene product (Bacillus subtilis)	67	48	501
109	15	14821	13982	gi 413976	ipa-52r gene product (Bacillus subtilis)	67	49	840
109	17	14811	15194	gi 413983	ipa-59d gene product (Bacillus subtilis)	67	29	384
121	4	1713	2153	gi 1262335	YeaA (Bacillus subtilis)	67	54	441
122	1	1	1149	gi 143047	ORF8 (Bacillus subtilis)	67	35	1149
124	5	4060	3518	gi 556885	Unknown (Bacillus subtilis)	67	47	543
131	2	4584	3589	gi 1046081	hypothetical protein (GB:D6185_10) (Mycoplasma genitalium)	67	30	996
140	3	2899	2297	gi 146549	kdpC (Escherichia coli)	67	45	603
142	4	5409	4198	gi 1212775	GTP cyclohydrolase II (Bacillus amyloquifaciens)	67	55	1212
147	5	2913	2374	gi 1303709	YrkJ (Bacillus subtilis)	67	44	540
152	8	6341	6673	gi 1377841	Unknown (Bacillus subtilis)	67	48	331
161	4	2720	3763	gi 496319	SphX (Synechococcus sp.)	67	47	1044
163	6	1989	3428	gi 595681	2-oxoglutarate/malate translocator (Spinacia oleracea)	67	47	1440
193	3	1351	1626	gi 1511101	shikimate 5-dihydrogenase (Methanococcus jannaschii)	67	53	276
200	2	917	2179	gi 142439	ATP-dependent nuclease (Bacillus subtilis)	67	48	1263
206	10	12445	112801	sp p37347 VECD_	HYPOTHETICAL 21.8 KD PROTEIN IN ASP5 5' REGION.	67	47	357
206	11	13047	14432	gi 732813	branched-chain amino acid carrier (Lactobacillus delbrueckii)	67	46	1386
208	2	1321	809	gi 1033037	100 kDa heat shock protein (Hsp100) (Leishmania major)	67	36	513
238	3	1039	2052	gi 809542	CbrB protein (Erwinia chrysanthemi)	67	42	1014

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
246	2	176	367	gi 215098	excisionase (Bacteriophage 154a)	67	37	192
276	2	2260	1412	gi 303560	ORF271 (Escherichia coli)	67	50	849
297	6	2223	3056	gi 142784	IctA protein (Bacillus firmus)	67	46	834
307	7	5220	4186	gi 1070013	protein-dependent (Bacillus subtilis)	67	43	1035
316	1	36	1028	gi 1161061	dioxygenase (Methylobacterium extorquens)	67	57	993
324	3	5650	5030	gi 1469784	putative cell division protein (taw) (Enterococcus hirae)	67	49	621
336	1	524	264	gi 173122	urea amidolyase (Saccharomyces cerevisiae)	67	45	261
340	1	108	1394	gi 130053	HLSTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE--TRNA LIGASE) (HISRS)	67	47	1287
364	3	4890	3592	gi 151259	HMG-CoA reductase (EC 1.1.1.88) (Pseudomonas nevaloni) pir A44756 A44756 Pseudomonas sp.	67	46	1299
365	3	2940	2113	gi 1296823	hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88)	67	47	828
367	2	325	918	gi 1039479	orf2 gene product (Lactobacillus helveticus)	67	47	594
395	3	666	1271	gi 1204516	ORFU (Lactococcus lactis)	67	55	606
415	1	1800	901	gi 182579	hypothetical protein (GB:U00014_4) (Haemophilus influenzae)	67	46	900
419	1	1799	903	gi 520752	putative (Bacillus subtilis)	67	48	897
474	1	2	796	gi 486906	argininosuccinate synthetase (Streptomyces clavuligerus) pir S57659 S57659 argininosuccinate synthase (EC 6.3.4.5) - Streptomyces clavuligerus	67	49	795
485	2	1921	2226	gi 141434	Rho Factor (Bacillus subtilis)	67	43	306
596	1	1728	865	gi 1303853	VggF (Bacillus subtilis)	67	47	864
700	1	433	218	gi 1204628	hypothetical protein (SP:P21498) (Haemophilus influenzae)	67	47	216
806	2	249	647	gi 677947	AppC (Bacillus subtilis)	67	51	399
828	2	340	900	gi 777761	IrrA (Synchococcus sp.)	67	37	561
833	1	1407	916	gi 142596	regulatory protein (Bacillus subtilis)	67	41	492
856	1	1555	779	gi 780224	2K970.2 (Caenorhabditis elegans)	67	38	777
888	1	1614	850	gi 137315	77G start codon (Bacillus licheniformis)	67	40	765
1034	1	1190	597	gi 1205113	hypothetical protein (GB:L19201_15) (Haemophilus influenzae)	67	45	594
1062	1	636	319	gi 1303850	VggC (Bacillus subtilis)	67	41	318
1067	1	918	460	pir A32950 A329	probable reductase protein - Leishmania major	67	54	459

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1158	1	3	293	gi1001369	hypothetical protein (Synecocystis sp.)	67	44	291
2181	1	3	302	gi11510416	hypothetical protein (SP:P1486) (Methanococcus jannaschii)	67	48	300
3000	1	1	507	gi1517205	67 kDa Myosin-crossreactive streptococcal antigen (Streptococcus pyogenes)	67	56	507
3066	1	464	234	gi1308861	lgtG start codon (Lactococcus lactis)	67	46	231
3087	1	454	251	gi11205366	oligopeptide transport ATP-binding protein (Haemophilus influenzae)	67	44	204
3101	1	2	256	gi11531541	uroporphyrinogen III methyltransferase (Zea mays)	67	55	255
3598	1	728	393	gi1151259	HMG-CoA reductase (EC 1.1.1.88) (Pseudomonas mevaloni) p1r144756144756 Pseudomonas sp.	67	56	336
3765	2	584	366	gi1557489	memD (Bacillus subtilis)	67	45	219
3788	1	658	398	pir155293515529	nitrate reductase alpha chain - Bacillus subtilis (fragment)	67	45	261
3883	1	2	265	gi1704397	cytathionine beta-lyase (Arabidopsis thaliana)	67	46	264
3926	1	2	340	gi1483199	peptide-synthetase (Aerobacter aerogenes)	67	44	339
4417	1	82	396	gi11205337	ribonucleotide transport ATP-binding protein (Haemophilus influenzae)	67	46	315
2	3	3075	3989	gi1535348	CodY (Bacillus subtilis)	66	42	915
15	6	2273	2542	gi146491	SacB (Synecococcus PCT942)	66	37	270
31	9	8059	7826	gi1292046	mucin (Homo sapiens)	66	44	214
31	10	9034	9258	gi11204545	mercury scavenger protein (Haemophilus influenzae)	66	48	225
32	6	6347	5253	gi1998342	inducible nitric oxide synthase (Gallus gallus)	66	47	1095
44	13	8856	10124	gi11510751	molybdenum cofactor biosynthesis moaA protein (Methanococcus jannaschii)	66	46	1269
48	2	1276	2868	gi1150209	ORF 1 (Mycoplasma mycoides)	66	40	1593
58	8	7178	8428	gi1665999	hypothetical protein (Bacillus subtilis)	66	47	1251
62	7	5143	4370	gi11072398	phd gene product (Rhizobium meliloti)	66	40	774
70	14	11693	10998	gi1809660	deoxyribose-phosphate aldolase (Bacillus subtilis) p1r149455149455 deoxyribose-phosphate aldolase (EC 4.1.2.4) - acillus subtilis	66	55	696
76	1	1	1305	gi142440	ATP-dependent nuclease (Bacillus subtilis)	66	42	1305
91	6	9236	8205	gi1704397	cytathionine beta-lyase (Arabidopsis thaliana)	66	43	1032
102	5	3810	3265	gi11204323	hypothetical protein (SP:P1805) (Haemophilus influenzae)	66	41	546

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	Length (nt)
103	4	3418	2732	gi 371344	nitrate reductase gamma subunit [Bacillus subtilis] sp P42177 NAR_BACSU NITRATE REDUCTASE GAMMA CHAIN (EC 1.7.99.4). gi 1009369 Respiratory nitrate reductase [Bacillus subtilis] (SUB -160)	66	48	697
109	6	4243	4674	gi 170886	glucosamine-6-phosphate deaminase [Candida albicans] pir A46652 A46652 glucosamine-6-phosphate isomerase (EC 5.3.1.10) - east [Candida albicans]	66	45	432
112	17	17491	17712	gi 1323179	ORF YCR111W [Saccharomyces cerevisiae]	66	33	222
116	2	4667	2637	gi 1691813	gamma-glucanyltransferase [Bacillus subtilis]	66	43	2031
150	5	3189	2989	gi 1146224	putative [Bacillus subtilis]	66	30	201
172	5	3264	3462	gi 755152	highly hydrophobic integral membrane protein [Bacillus subtilis] sp P42953 TAGC_BACSU TETRAHYDROXY-4-ACID TRANSLOCATION PERMEASE PROTEIN AGG.	66	41	399
174	5	4592	3723	gi 1146241	pantothenate synthetase [Bacillus subtilis]	66	49	870
175	4	3209	2880	gi 642655	unknown [Rhizobium meliloti]	66	29	330
175	11	8743	7994	gi 854655	Na/H antiporter system [Bacillus alcalophilus]	66	43	750
190	5	7079	5727	gi 451072	di-tripeptide transporter [Lactococcus lactis]	66	40	1353
195	15	113919	11713	gi 1322411	unknown [Mycobacterium tuberculosis]	66	42	207
217	3	2822	2595	gi 1143542	alternative stop codon [Rattus norvegicus]	66	36	228
233	9	7133	6135	gi 1450327	F08P3.4 gene product [Caenorhabditis elegans]	66	47	999
238	1	41	1041	gi 809541	Chra protein [Klebsiella chrysanthii]	66	42	999
241	1	2102	1053	gi 153067	peptidoglycan hydrolase [Staphylococcus aureus]	66	53	1050
261	1	1178	648	gi 1510859	H. jannaschii predicted coding region M0790 [Methanococcus jannaschii]	66	40	531
263	3	3731	2973	gi 1205865	tetrahydrodipicolinate N-succinyltransferase [Haemophilus influenzae]	66	47	759
272	8	6548	5484	gi 882101	high affinity nickel transporter [Alcaligenes eutrophus] sp P23519 HOMU_ALCEU HIGH-AFFINITY NICKEL TRANSPORT PROTEIN.	66	44	1065
276	3	2805	2104	gi 1208965	hypothetical 23.3 kd protein [Escherichia coli]	66	47	702
278	2	2830	1784	gi 1488662	phosphatase-associated protein [Bacillus subtilis]	66	48	1047
278	3	3630	2952	gi 303560	ORF271 [Escherichia coli]	66	45	879
279	2	3894	2218	gi 1185289	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1- carboxylate synthase [Bacillus subtilis]	66	48	1677
288	4	2535	2275	gi 1256625	putative [Bacillus subtilis]	66	42	261
292	2	1133	942	gi 1511604	H. jannaschii predicted coding region M1651 [Methanococcus jannaschii]	66	30	192

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Coding ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
294	1	1116	559	gi 216314	esterase [Bacillus stearothermophilus]	66	45	558
297	4	2913	1978	gi 994794	cytochrome a assembly facto [Bacillus subtilis] sp p24009 COXK_BACSU PROBABLE CYTOCHROME C OXIDASE ASSEMBLY FACTOR.	66	45	936
316	4	2053	2682	gi 1107839	elginase lyase [Pseudomonas aeruginosa]	66	40	630
338	4	2460	2302	gi 520750	biotin synthetase [Bacillus sphaericus]	66	59	159
339	1	1214	785	gi 467468	7, 8-dihydro-6-hydroxymethylpterin-pyrophosphokinase [Bacillus subtilis]	66	52	480
363	1	3	863	gi 581649	epic gene product [Staphylococcus epidermidis]	66	47	863
366	2	232	483	gi 1103505	unknown [Schizosaccharomyces pombe]	66	53	252
367	4	2468	1845	sp p20692 TYRA_	PREPHENATE DEHYDROGENASE [EC 1.3.1.12] (PDH)	66	50	624
372	3	2150	1599	gi 467416	unknown [Bacillus subtilis]	66	38	552
378	1	212	1009	gi 147309	purine nucleoside phosphorylase [Escherichia coli]	66	50	798
401	1	1	462	gi 388263	p-aminobenzoic acid synthase [Streptomyces griseus] pir JN0531 JN0531 p-aminobenzoic acid synthase - Streptomyces riseus	66	46	462
404	7	4826	5254	gi 606744	cytidine deaminase [Bacillus subtilis]	66	51	429
411	2	1738	1103	gi 1460081	unknown [Mycobacterium tuberculosis]	66	44	636
420	1	2	543	gi 1046024	[Na+ ATPase subunit J] [Mycoplasma genitalium]	66	49	540
431	1	1	858	gi 1500008	M. jannaschii predicted coding region M2154 [Methanococcus jannaschii]	66	50	858
443	7	5679	5299	gi 852076	MrgA [Bacillus subtilis]	66	46	381
444	3	3405	2413	gi 153047	lysoastaphin (ttg start codon) [Staphylococcus simulans] pir A25881 A25881 lysoastaphin precursor - Staphylococcus simulans sp P10547 LSTP_STASI LYSOASTAPHIN PRECURSOR [EC 3.5.1.-]	66	51	993
561	1	956	480	gi 1204905	DNA-3-methyladenine glycosylase I [Haemophilus influenzae]	66	45	477
562	3	1066	1383	gi 1046082	M. genitalium predicted coding region M0372 [Mycoplasma genitalium]	66	52	318
576	1	11	724	gi 305014	ORF_0214 [Escherichia coli]	66	43	714
577	3	1190	903	gi 1001353	hypothetical protein [Synchocystis sp.]	66	52	288
584	1	2	331	sp p24204 YEB_A_	HYPOTHETICAL 46.7 KD PROTEIN IN MS88-RUVB INTERGENIC REGION (ORFU)	66	48	330
592	1	1410	706	gi 928839	ORF266; putative [Lactococcus lactis phage BK5-T]	66	51	705
601	1	1433	720	gi 1488695	novel antigen; orf-2 [Staphylococcus aureus]	66	55	714

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
619	3	468	845	gi 746573	similar to K. musculus transport system membrane protein, Hraap PIR:A07399 and S. cerevisiae SDF1 protein (PIR:A5154) Canorhabditis elegans	66	45	378
706	2	561	355	gi 804808	unknown protein [Rattus norvegicus]	66	46	207
734	2	673	512	gi 1519085	phosphatidylethanolamine binding immunoglobulin heavy chain IgH variable region [Mus musculus]	66	60	162
740	1	3	317	gi 1209272	argininosuccinate lyase [Campylobacter jejuni]	66	47	315
764	1	310	747	gi 435296	alkaline phosphatase like protein (Lactococcus lactis) pir S93339[S93339] alkaline phosphatase-like protein - Lactococcus actis	66	42	438
852	1	338	171	gi 536955	CG Site No. 361 [Escherichia coli]	66	43	168
886	1	3	158	gi 289272	tertrichrome-binding protein [Bacillus subtilis]	66	44	156
889	1	462	232	gi 833061	HCMVUL77 (AA 1-642) [Human cytomegalovirus]	66	66	231
893	1	2	247	gi 149008	putative [Helicobacter pylori]	66	45	246
900	1	1425	733	gi 580842	F3 [Bacillus subtilis]	66	51	693
906	2	2300	1473	gi 790945	eryl-alcohol dehydrogenase [Bacillus subtilis]	66	53	838
947	1	79	549	gi 410117	diaminopimelate decarboxylase [Bacillus subtilis]	66	47	471
950	1	1100	552	gi 48713	orf145 [Staphylococcus aureus]	66	35	549
955	2	89	475	gi 1204390	uridine kinase (uridine monophosphokinase) [Haemophilus influenzae]	66	50	387
981	2	1208	997	gi 457146	rhostry protein [Plasmodium yoelii]	66	38	312
986	1	25	315	gi 305002	ORF_4356 [Escherichia coli]	66	31	291
1057	1	3	203	gi 1303853	YqgP [Bacillus subtilis]	66	40	201
1087	1	1	294	gi 575913	unknown [Saccharomyces cerevisiae]	66	53	294
1105	1	1	231	gi 1045799	methylgalactoside permease ATP-binding protein [Mycoplasma genitalium]	66	46	231
1128	1	2	574	gi 1001493	hypothetical protein [Synecocystis sp.]	66	46	573
1150	1	498	250	gi 1499034	H. jannaschii predicted coding region M0255 [Methanococcus jannaschii]	66	40	249
1140	2	707	453	gi 215908	DNA polymerase [g43] [Bacteriophage T4]	66	46	255
1208	1	1123	587	gi 1256653	DNA-binding protein [Bacillus subtilis]	66	58	537
1342	1	1	402	gi 1208474	hypothetical protein [Synecocystis sp.]	66	53	402
1761	2	589	398	gi 215811	tail fiber protein [Bacteriophage T3]	66	50	192

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	meth gene name	% sim	% ident	length (nt)
1983	1	499	251	gi 1045915	[DNA helicase II (Mycoplasma genitalium)]	66	40	249
2103	2	176	400	gi 929798	[precursor for the major serotoxin surface antigens (Plasmodium alsciparum)]	66	46	225
2341	1	373	188	gi 1256623	[exodeoxyribonuclease (Bacillus subtilis)]	66	38	186
2458	1	325	164	gi 1019410	[unknown (Schistosoma haematodes)]	66	47	162
2505	1	468	235	gi 1510394	[putative transcriptional regulator (Methanococcus jannaschii)]	66	39	234
2525	1	558	280	gi 1000695	[cytotoxin L (Clostridium sordellii)]	66	44	279
2935	1	3	275	gi 765073	[autolysin (Staphylococcus aureus)]	66	47	273
3005	1	114	305	gi 1205784	[heterocyst maturation protein (Haemophilus influenzae)]	66	46	192
3068	1	80	277	gi 1303813	[Yqpw (Bacillus subtilis)]	66	42	198
3071	1	1	189	gi 1070014	[protein-dependent (Bacillus subtilis)]	66	41	189
3081	1	404	225	gi 984212	[unknown (Schistosoma haematodes)]	66	44	180
3090	2	580	386	gi 1204987	[DNA polymerase III, alpha chain (Haemophilus influenzae)]	66	48	195
3118	1	1	387	gi 1009366	[respiratory nitrate reductase (Bacillus subtilis)]	66	49	387
3739	1	798	400	gi 1109684	[proV (Bacillus subtilis)]	66	47	399
3796	1	402	202	gi 853760	[acyl-CoA dehydrogenase (Bacillus subtilis)]	66	60	201
4024	1	595	347	gi 563952	[glucanase (Bacillus licheniformis)]	66	46	249
4240	1	3	350	gi 151259	[HMG-CoA reductase (EC 1.1.1.88) (Pseudomonas mevalonii)]	66	51	348
					[hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) (Pseudomonas sp.)]			
4604	1	7	234	gi 126713	[hemocyanin subunit II - Atlantic horseshoe crab]	66	46	228
4	9	8845	9750	gi 145646	[cysR (Escherichia coli)]	65	35	906
6	5	2708	3565	gi 887824	[ORF_0310 (Escherichia coli)]	65	47	858
13	1	1993	998	gi 143402	[recombination protein (ttr start codon) (Bacillus subtilis)]	65	44	996
					[Bacillus subtilis]			
15	7	2493	3524	gi 1403126	[cicD gene product (Alcaligenes eutrophus)]	65	38	1032
18	3	1908	1372	gi 349187	[acyltransferase (Saccharomyces cerevisiae)]	65	50	537
21	3	1467	2492	gi 149518	[phosphoribosyl anthranilate transferase (Lactococcus lactis)]	65	52	1026
					[pir(S1516)(S1516) entranilate phosphoribosyltransferase (EC 4.2.18) - Lactococcus lactis subsp. lactis]			
25	4	3374	4312	gi 1502420	[melonyl-CoA:Acyl carrier protein transacylase (Bacillus subtilis)]	65	44	939

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
27	2	390	626	gi 1212729	yqhJ (Bacillus subtilis)	65	45	237
31	12	11040	10387	gi 509245	D-hydroxyacetate dehydrogenase (Lactobacillus delbrueckii)	65	41	654
38	24	19172	19528	gi 547...	H-protein (Pleurotus cornuicatus)	65	41	357
44	2	790	1746	gi 405882	yleK (Escherichia coli)	65	46	957
44	12	9356	8832	gi 1205905	polydum cofactor biosynthesis protein (Haemophilus influenzae)	65	50	525
45	8	6635	7588	gi 493074	ApbA protein (Salmonella typhimurium)	65	46	954
51	2	580	1503	gi 580897	OppB gene product (Bacillus subtilis)	65	45	924
52	1	225	953	gi 1205518	NAD(P)H-flavin oxidoreductase (Haemophilus influenzae)	65	45	729
55	4	1139	1058	gi 444591444	troponin T beta TnF-5 - rabbit	65	41	282
67	9	7421	8272	gi 143607	sporulation protein (Bacillus subtilis)	65	42	852
73	5	4446	5375	gi 1204896	lysophospholipase L2 (Haemophilus influenzae)	65	37	930
74	1	954	478	gi 1204844	H. influenzae predicted coding region H10594 (Haemophilus influenzae)	65	50	477
77	1	2	757	gi 1046082	H. genitalium predicted coding region H0372 (Mycoplasma genitalium)	65	46	736
77	2	795	1433	gi 1222116	permease (Haemophilus influenzae)	65	37	639
81	3	4728	3454	gi 1001708	hypothetical protein (Synechocystis sp.)	65	49	1275
91	7	8548	8357	gi 1399263	cystathionine beta-lyase (Escherichia nidulans)	65	40	132
98	3	1608	1988	gi 467423	unknown (Bacillus subtilis)	65	38	381
98	4	2250	2987	gi 467424	unknown (Bacillus subtilis)	65	45	738
102	3	2598	2119	gi 1511532	N-terminal acetyltransferase complex, subunit ARD1 (Methanococcus jannaschii)	65	39	480
102	4	3647	2862	gi 1204637	H. influenzae predicted coding region H10388 (Haemophilus influenzae)	65	32	786
103	9	10851	9841	gi 142695	S-adenosyl-L-methionine:uroporphyrinogen III methyltransferase Bacillus megaterium	65	47	1011
103	10	10439	10119	gi 1710021	nitrite reductase (nirD) (Bacillus subtilis)	65	51	321
106	2	262	1140	gi 39881	ORF 311 (AA 1-311) (Bacillus subtilis)	65	44	879
109	5	3909	4268	gi 1204399	glucosamine-6-phosphate deaminase protein (Haemophilus influenzae)	65	44	360
109	10	7165	8595	gi 1536955	CG Site No. 161 (Escherichia coli)	65	41	1431

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
110	4	3688	3915	gi 407881	stringent response-like protein [Streptococcus equisimilis] pIRJ59975/59975 stringent response-like protein - Streptococcus equisimilis	65	45	228
110	5	3882	4295	gi 407880	ORF1 [Streptococcus equisimilis]	65	50	414
110	6	4231	4380	gi 1139574	Orf2 [Streptomyces griseus]	65	56	150
112	10	9218	8640	gi 1204571	H. influenzae predicted coding region H10318 [Haemophilus influenzae]	65	52	579
112	12	12049	11288	gi 710496	transcriptional activator protein [Bacillus brevis]	65	32	762
125	1	2	202	gi 1151158	repeat organellar protein [Plasmodium chabaudi]	65	39	201
126	1	3	422	gi 37589	precursor [Homo sapiens]	65	46	420
127	11	10733	12658	gi 1064809	homologous to sp119RA_ECOLI [Bacillus subtilis]	65	41	1926
143	8	7543	7004	gi 216513	mutator mutT [AT-GC transversion] [Escherichia coli]	65	56	540
145	5	3587	3838	gi 1209768	D02_orf569 [Mycoplasma pneumoniae]	65	27	252
150	4	3482	2841	gi 1146225	putative [Bacillus subtilis]	65	37	642
166	1	3658	1948	gi 148304	beta-1,4-N-acetylmuramylhydrolase [Enterococcus hirae] pIRJ42296/A42296	65	50	1911
188	6	3195	4178	gi 151943	lysosome 2 [EC 3.2.1.-] precursor - Enterococcus faecalis (ATCC 9790)	65	46	984
189	9	4982	4785	gi 158812	ORF3; putative [Rhodobacter capsulatus]	65	40	198
195	6	7908	5272	gi 145220	ORF IV (AA 1-49) [Figueroa mosaic virus]	65	49	2637
195	7	10599	8104	gi 1882711	alanyl-tRNA synthetase [Escherichia coli]	65	38	2496
206	16	16896	18191	gi 408115	exonuclease V alpha-subunit [Escherichia coli]	65	53	1296
217	4	3844	3215	gi 1205974	ornithine acetyltransferase [Bacillus subtilis]	65	41	630
220	4	5265	3751	gi 580920	5'-guanylate kinase [Haemophilus influenzae]	65	40	1515
236	5	2327	3709	gi 1146200	rodB (gtaA) polypeptide (AA 1-673) [Bacillus subtilis] pIRJ506048/S06048	65	46	1381
237	3	1902	2513	gi 149379	probable rod protein - Bacillus subtilis sp P13484 PACR_BACSU PROBABLE POLY(GLYCEROL-PHOSPHATE) LPIA-GLUCOSYLTRANSFERASE [EC 2.4.1.52] [TECHOIC ACID BIOSYNTHESIS ROUTIN E]	65	46	612
241	4	4968	4195	gi 1205308	DNA or RNA helicase, DNA-dependent ATPase [Bacillus subtilis]	65	50	774
252	1	1278	940	gi 1204989	ribonuclease HII [EC 3.1.26.4] (RNase HII) [Haemophilus influenzae]	65	40	339
261	5	4780	3794	gi 145927	hypothetical protein (GB:U00022.9) [Haemophilus influenzae]	65	43	987
					[fecD [Escherichia coli]]			

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
274	1	3	278	gi1496558	orfX (Bacillus subtilis)	65	42	276
301	2	982	815	gi1-57418	unknown (Bacillus subtilis)	65	45	168
307	4	3586	2864	gi1070014	protein-dependent (Bacillus subtilis)	65	40	723
335	2	2286	1399	gi1146913	N-acetylglucosamine transport protein (Escherichia coli) p1r1829895 p08C2N phosphotransferase system enzyme II (EC 7.1.69), N-acetylglucosamine-specific - Escherichia coli sp p09323 PTAA_ECOLI PTS SYSTEM, N-ACETYLGLUCOSAMINE-SPECIFIC IIABC ONPONENT (ETIA)	65	50	888
338	5	4120	3170	gi11277029	biotin synthase (Bacillus subtilis)	65	49	951
343	3	1490	2800	gi1143264	membrane-associated protein (Bacillus subtilis)	65	48	1311
344	4	2761	2531	gi11050540	tRNA-glutamine synthetase (Lupinus luteus)	65	34	231
358	3	3421	3621	gi11146220	NAD+ dependent glycerol-3-phosphate dehydrogenase (Bacillus subtilis)	65	47	201
364	1	238	699	gi11340128	ORF1 (Staphylococcus aureus)	65	51	462
379	1	1	576	gi1143331	alkaline phosphatase regulatory protein (Bacillus subtilis) p1r1A27650 A27650 regulatory protein phoR - Bacillus subtilis sp p23545 PHOR_BACSU ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN HOR (EC 2.7.3.-)	65	40	576
379	3	3666	4346	gi1143268	dihydrolipoamide transsuccinylase (odhB; EC 2.3.1.61) (Bacillus subtilis)	65	50	681
428	1	187	483	gi11420465	ORF YOR195w (Saccharomyces cerevisiae)	65	45	297
438	2	272	838	gi1143498	degS protein (Bacillus subtilis)	65	38	567
444	11	9280	10215	gi11204756	ribokinase (Haemophilus influenzae)	65	47	936
449	2	1241	1531	gi11599848	Ha/H antiporter homolog (Lactococcus lactis)	65	41	291
478	2	1452	865	gi11045942	glycyl-tRNA synthetase (Mycoplasma genitalium)	65	39	588
479	1	1032	517	gi11498192	putative (Pseudomonas aeruginosa)	65	40	516
480	6	4312	5637	gi11415662	UDP-N-acetylglucosamine 1-carboxyvinyl transferase (Acinetobacter calcoaceticus)	65	48	1326
484	1	2	430	gi11746551	transmembrane protein (kdpB) (Escherichia coli)	65	44	429
499	1	54	932	gi1603456	reductase (Leishmania major)	65	53	879
505	1	914	459	gi11518853	Osfa (Salmonella typhimurium)	65	39	456
571	2	1509	883	gi149399	open reading frame upstream glnE (Escherichia coli) tr1S37754 S37754 hypochemical protein XE (glnE 5' region) - Escherichia coli	65	44	627
611	2	506	270	gi110961	RAP-2 (Plasmodium falciparum)	65	40	237

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
705	1	564	283	gi 710020	nitrite reductase (nirB) [Bacillus subtilis]	65	52	282
712	1	1	177	gi 289272	ferrichrome-binding protein [Bacillus subtilis]	65	37	177
712	2	196	354	gi 289272	ferrichrome-binding protein [Bacillus subtilis]	65	37	159
743	1	2	631	gi 310631	ATP binding protein [Streptococcus gordonii]	65	45	630
749	2	393	779	gi 467374	single strand DNA-binding protein [Bacillus subtilis]	65	29	387
762	1	1698	850	gi 160399	multidrug resistance protein [Plasmodium falciparum]	65	48	849
788	1	85	315	gi 1128096	unknown protein [Bacillus sp.]	65	35	231
850	1	1	408	gi 1006604	hypothetical protein [Synecocystis sp.]	65	37	408
908	1	1	444	gi 1199546	[2362] [Saccharomyces cerevisiae]	65	46	444
925	1	1	174	gi 1256653	DNA-binding protein [Bacillus subtilis]	65	54	174
1031	1	26	232	gi 238657	AppCacyochrome d oxidase, subunit 1 homolog [Escherichia coli, K12, aptide, 514 aa]	65	47	207
1037	1	414	262	gi 1491813	gamma-glutamyltranspeptidase [Bacillus subtilis]	65	46	153
1053	1	348	175	gi 642655	unknown [Rhizobium meliloti]	65	34	174
1149	1	1399	752	gi 1162980	ribulose-5-phosphate 3-epimerase [Spinacia oleracea]	65	48	668
1214	1	881	495	gi 1205959	lactam utilization protein [Haemophilus influenzae]	65	45	387
1276	1	476	276	pir S35493 S354	site-specific DNA-methyltransferase Stel (EC 2.1.1.-) - Streptococcus sanguis	65	36	201
1276	2	900	577	gi 473794	ORF' [Escherichia coli]	65	34	324
2057	1	272	138	gi 633699	TreH [Yersinia enterocolitica]	65	21	135
2521	1	336	169	gi 1045789	hypothetical protein (CB:U14003_76) [Mycoplasma genitalium]	65	41	168
2974	1	590	297	gi 152052	enantiomerase-selective amidase [Rhodococcus sp.]	65	45	294
3031	1	306	154	hit JQ1024 JQ10	hypothetical JOK protein (LmH140 5' region) - fruit fly (Drosophila melanogaster)	65	45	153
3069	1	3	278	gi 144906	product homologous to E.coli thioredoxin reductase; J.Biol.Chem. 1988) 263:9015-9019, and to F52a protein of alkyl hydroperoxide oxidase from S. typhimurium; J.Biol.Chem. (1990) 265:10535-10540; pen reading frame A [Clostridium pasteurianum]	65	46	276
3146	1	282	142	gi 49315	ORF1 gene product [Bacillus subtilis]	65	47	141
3170	1	679	341	gi 1507711	indolepyruvate decarboxylase [Erwinia herbicola]	65	44	339

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	-match gene name	% sim	% ident	length (nt)
3546	1	1	303	gi 450688	hsdM gene of E. coli product [Escherichia coli] pir[S38437]S38437 hsdM protein - Escherichia coli pir[S09629]S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	65	42	303
3782	1	2	328	gi 166412	NADH-glutamate synthase (Medicago sativa)	65	42	327
3990	1	374	189	gi 1009366	Respiratory nitrate reductase [Bacillus subtilis]	65	53	186
4032	1	613	308	gi 1323127	ORF YCR087c [Saccharomyces cerevisiae]	65	50	306
4278	2	726	364	gi 1197667	vitellogenin [Anolis pulchellus]	65	42	363
19	4	4259	5518	gi 165727	dead [Escherichia coli]	64	45	1260
19	6	7639	6926	gi 1016232	ycf27 gene product [Cyanophora paradoxa]	64	36	714
20	8	7053	6454	gi 765073	autolysin [Staphylococcus aureus]	64	47	600
31	13	12706	11537	gi 414009	ipa-85d gene product [Bacillus subtilis]	64	45	1170
33	4	2388	4364	gi 1204696	fructose-permease IIBC component [Haemophilus influenzae]	64	47	1977
36	3	1871	3013	gi 290503	glutamate permease [Escherichia coli]	64	40	1143
37	6	4065	4409	gi 39815	orf 2 gene product [Bacillus subtilis]	64	46	345
45	9	7852	8760	gi 1230585	nucleotide sugar epimerase [Vibrio cholerae O139]	64	53	909
53	3	1540	1899	gi 1303961	YqjJ [Bacillus subtilis]	64	50	360
56	6	4793	3855	gi 457514	glcC [Bacillus subtilis]	64	45	919
56	24	30002	30247	gi 470331	similar to zinc fingers [Caenorhabditis elegans]	64	42	246
62	4	2759	2421	gi 642655	unknown [Rhizobium meliloti]	64	28	339
85	6	7178	6027	gi 457702	5-aminimidazole ribonucleotide-carboxylase [Pichia methanolica] pir[S3912]S3912 phosphoribosylaminimidazole carboxylase (EC 1.1.2.1) - yeast [Pichia methanolica]	64	46	1152
96	9	9251	10030	gi 1511513	ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]	54	42	780
100	1	1	600	gi 765073	autolysin [Staphylococcus aureus]	64	44	600
106	5	3868	4854	gi 466778	lysine specific permease [Escherichia coli]	64	46	987
123	2	838	554	gi 467484	unknown [Bacillus subtilis]	64	47	285
127	8	7514	7810	gi 210061	serotype-specific antigen [African horse sickness virus] pir[S27891]S27891 capsid protein VP2 - African horse sickness virus	64	28	297
131	7	7134	6721	gi 1511160	M. jannaschii predicted coding region NJ1163 [Methanococcus jannaschii]	54	46	414

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
142	5	5455	4817	gi 1173517	riboflavin synthase alpha subunit (Actinobacillus pleuropneumoniae)	64	44	639
143	1	708	356	pic A32950 A329	probable reductase protein - Leishmania major	64	52	354
149	10	3555	3295	gi 398151	major surface antigen MSG2 (Pneumocystis carinii)	64	44	261
154	4	3134	2307	gi 1984587	DinP (Escherichia coli)	64	50	828
161	5	3855	4880	gi 903304	ORF72 (Bacillus subtilis)	64	37	1036
165	1	33	791	gi 467483	unknown (Bacillus subtilis)	64	38	759
175	6	6355	4714	gi 1072398	phad gene product (Rhizobium meliloti)	64	42	1512
188	3	2042	2500	gi 1001961	MHC class II analog (Staphylococcus aureus)	64	45	459
195	14	13667	13446	gi 396380	No definition line found (Escherichia coli)	64	47	222
206	15	16429	16938	gi 304134	argC (Bacillus stearothermophilus)	64	49	510
215	1	560	282	gi 142359	ORF 6 (Azotobacter vinelandii)	64	39	279
243	7	7818	6928	gi 414014	ipe-90d gene product (Bacillus subtilis)	64	49	891
258	2	1330	845	gi 664754	P17 (Listeria monocytogenes)	64	38	486
259	1	462	232	gi 1499663	M. jannaschii predicted coding region M0837 (Methanococcus jannaschii)	64	52	231
263	6	6565	5567	gi 142828	aspartate semialdehyde dehydrogenase (Bacillus subtilis) sp Q04797 NHAS_BACSU ASPARTATE-SEMIALDEHYDE DEHYDROGENASE [EC 2.1.11] (ASA DEHYDROGENASE)	64	48	999
271	1	3	1163	gi 467091	hclX; B2235_C2_202 (Mycobacterium leprae)	64	44	1161
280	1	173	1450	gi 1303839	YqfR (Bacillus subtilis)	64	43	1278
293	1	2532	1267	gi 147345	primoanal protein n' (Escherichia coli)	64	45	1266
295	2	742	1488	gi 459266	Potential membrane spanning protein (Staphylococcus hominis) pir S42932 S42932 potential membrane spanning protein - taphylococcus hominis	64	39	747
301	5	1625	1446	gi 580835	lysine decarboxylase (Bacillus subtilis)	64	35	180
315	4	5064	3949	gi 143396	quinol oxidase (Bacillus subtilis)	64	45	1116
321	1	1264	635	gi 710496	transcriptional activator protein (Bacillus brevis)	64	41	630
333	5	4520	4239	gi 1316295	ORF2: putative 39 kDa protein (Listeria monocytogenes)	64	43	282
342	1	1	549	gi 142940	ftsA (Bacillus subtilis)	64	38	549
353	3	2878	2324	gi 537049	ORF_0470 (Escherichia coli)	64	44	555

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
379	2	827	3658	gi 525295 A128	oxoglutarate dehydrogenase (liponamide) (EC 1.2.4.2) - Bacillus subtilis	64	47	2832
404	6	4429	4839	pir A36933 A369	diacylglycerol kinase homolog - Streptococcus mutans	64	35	411
407	1	2020	1133	gi 969026	OrfX (Bacillus subtilis)	64	41	888
425	1	1109	591	gi 1146177	phosphotransferase system glucose-specific enzyme II (Bacillus subtilis)	64	44	519
443	6	4082	4798	gi 147309	purine nucleoside phosphorylase [Escherichia coli]	64	51	717
450	2	1035	1604	gi 106376	ORF_0162 [Escherichia coli]	64	38	570
470	5	1680	6107	gi 1369948	host interacting protein (Bacteriophage B1)	64	45	4428
486	4	1911	1471	gi 1205582	spermidine/putrescine transport system permease protein (Haemophilus influenzae)	64	35	441
497	1	2217	1159	sp P36929 PMU_E	PMU PROTEIN	64	38	1059
501	1	3	410	gi 142450	ahrc protein (Bacillus subtilis)	64	38	408
514	1	3	290	gi 1204496	H. influenzae predicted coding region H10238 (Haemophilus influenzae)	64	34	288
551	4	3162	3323	gi 1204511	bacterioferritin comigratory protein (Haemophilus influenzae)	64	41	162
603	4	759	936	gi 755623	RAHR dehydrogenase F (Streptococcus americana)	64	35	198
653	2	940	746	gi 1213234	dicarboxylic amino acids Dap5p permease (Saccharomyces cerevisiae)	64	41	195
660	1	3401	2257	sp P46133 VDAL	HYPOTHEICAL PROTEIN IN OCT 5' REGION (FRAGMENT)	64	39	1345
695	1	11	502	gi 1001383	hypothetical protein (Synchocystis sp.)	64	41	492
702	1	3	752	gi 142865	DNA primase (Bacillus subtilis)	64	46	750
826	1	1	339	gi 971336	arginyl tRNA synthetase (Bacillus subtilis)	64	50	339
838	1	1831	917	gi 1334775	pfoS/R (Treponema pallidum)	64	41	915
864	3	675	944	gi 139833	cyclomaltodextrin glucanotransferase (Bacillus stearothermophilus) i 19835	64	47	270
867	1	3	677	gi 153002	enterotoxin type 2 precursor (Staphylococcus aureus) pir A28179 A28179	64	46	675
					enterotoxin E precursor - Staphylococcus aureus sp P12593 ETX_E STAU			
					ENTEROTOXIN TYPE E PRECURSOR (SEE)			
928	2	1172	963	gi 111976	fibrinogen-binding protein (Staphylococcus aureus) pir S34270 S34270	64	41	210
					fibrinogen-binding protein - Staphylococcus aureus			
1049	2	800	606	gi 1049115	Pap60 (Bacillus subtilis)	64	42	195
1067	2	999	748	gi 1151072	HhaA precursor (Haemophilus ducreyi)	64	50	252

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1120	1	50	202	gi 142439	ATP-dependent nuclease [Bacillus subtilis]	64	30	153
1125	1	751	377	gi 581648	lepiB gene product [Staphylococcus epidermidis]	64	44	375
1688	1	402	214	pir A01365 TKNS	transforming protein K-rae - mouse	64	47	189
2472	1	2	358	gi 487282	Na ⁺ -ATPase subunit J [Enterococcus hirae]	64	36	357
2989	1	520	356	gi 304134	argC [Bacillus stearothermophilus]	64	50	165
3013	1	630	352	gi 551699	cytochrome oxidase subunit I [Bacillus firmus]	64	51	279
3034	1	546	274	gi 1204349	hypothetical protein (CB:CB.D90212_3) [Haemophilus influenzae]	64	50	273
3197	1	613	308	gi 1009366	respiratory nitrate reductase [Bacillus subtilis]	64	46	306
3303	1	90	362	gi 1107839	arginate lyase [Pseudomonas aeruginosa]	64	43	273
3852	2	82	288	gi 216746	D-lactate dehydrogenase [Lactobacillus plantarum]	64	42	207
3868	1	1	312	gi 149435	putative [Lactococcus lactis]	64	48	312
3918	1	660	311	gi 5532	acetyl-CoA acyltransferase [Yarrowia lipolytica]	64	46	330
4000	1	112	378	gi 941688	unknown [Saccharomyces cerevisiae]	64	44	267
4009	1	81	368	gi 39372	gras gene product [Bacillus brevis]	64	41	288
4166	1	2	349	gi 149435	putative [Lactococcus lactis]	64	46	348
4366	1	2	307	gi 216267	ORF2 [Bacillus megaterium]	64	44	306
4457	1	2	400	gi 1197667	Vitellogenin [Anolis pulchellus]	64	43	399
11	3	1539	2438	gi 438228	ORF C [Staphylococcus aureus]	63	32	900
24	7	5611	5423	gi 1369943	al gene product [Bacteriophage B1]	63	34	189
29	1	1	390	gi 467441	expressed at the end of exponential growth under conditions in which the enzymes of the TCA cycle are repressed [Bacillus subtilis] gi 467441	63	43	390
					expressed at the end of exponential growth under conditions in which the enzymes of the TCA cycle are repressed [Bacillus subtilis]			
31	6	6329	5712	gi 496943	ORF [Saccharomyces cerevisiae]	63	47	618
44	23	14669	15019	pir A04446 OQEC	hypothetical protein P-92 - Escherichia coli	63	36	351
48	6	4403	6250	gi 43498	pyruvate synthase [Halobacterium halobium]	63	42	1848
50	5	3869	4738	gi 413967	ipa-43d gene product [Bacillus subtilis]	63	43	870
53	6	6764	5742	gi 474176	regulator protein [Staphylococcus xylosus]	63	49	1023

TABLE 2

2. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match gene name	Accession	Sim	Ident	Length (nt)
56	14	15880	17607	DNA polymerase III subunit [Bacillus subtilis]	gi1467409	63	44	1728
57	11	7945	7376	ORF_0158 [Escherichia coli]	gi1137036	63	39	570
62	3	2479	2114	Unknown [Rhizobium meliloti]	gi142656	63	41	366
70	8	6562	7353	PhoC [Rhizobium meliloti]	gi11399821	63	46	792
75	2	223	927	HISG [Lactococcus lactis]	gi1149376	63	45	705
78	5	4912	4403	Ipa-26d gene product [Bacillus subtilis]	gi1411950	63	42	510
91	5	9076	7220	meth2; B2126-CL157 [Mycobacterium leprae]	gi1466997	63	41	1857
91	8	10566	9448	Cystathionine gamma-synthase [Haemophilus influenzae]	gi11204344	63	45	1119
120	1	21	1508	sulfite reductase (NADPH) [Escherichia coli]	gi1882657	63	46	1488
120	4	2722	4125	hypothetical protein [Bacillus subtilis]	gi1665994	63	34	1404
127	7	6064	7566	murE gene product [Bacillus subtilis]	gi140162	63	44	1503
149	6	2321	2106	dnaK [Escherichia coli]	gi1148503	63	40	216
149	126	10445	10170	ORF 2, has similarity to DNA polymerase (Saccharomyces kluyveri) r[S15961]S15961 hypothetical protein 2 - yeast (Saccharomyces yverli) plasmid pSKL	gi14870	63	42	276
164	2	507	1298	CDP-diglyceride synthetase [Escherichia coli]	gi115476	63	44	792
166	6	9909	8164	fructose 6-phosphate 1-phosphotransferase [Rhodospirillum rubrum]	gi1151912	61	41	1746
169	4	1704	1886	elongation factor Ts (tsf) [Spiroplasma citri]	gi1152886	63	48	183
188	5	3145	2951	GIY COI 114 grp 18 protein [Podospira anserina]	gi1131457	63	42	195
195	13	11767	12804	ORF_0335 [Escherichia coli]	gi1606100	63	40	1038
201	2	607	2283	arginyl-tRNA synthetase [Corynebacterium glutamicum] pIR[A49936]A49936 arginine-tRNA ligase (EC 6.1.1.19) - corynebacterium glutamicum	gi1433534	63	46	1677
206	14	15893	16489	N-acetyl-glutamate-gamma-semialdehyde dehydrogenase [Bacillus subtilis]	gi1580828	63	49	597
220	5	7769	5766	secA protein [Bacillus subtilis]	gi1216334	63	42	2004
221	1	74	907	AppA [Bacillus subtilis]	gi1677945	63	42	834
227	3	944	1708	cobryc acid synthase [Methanococcus jannaschii]	gi11510538	63	46	765
261	2	804	1070	ORF_YNR054c [Saccharomyces cerevisiae]	gi1486511	63	45	267
269	2	3606	1960	DNA-dependent ATPase, DNA helicase (Escherichia coli) pIR[J50137]J50137 recQ protein - Escherichia coli	gi1148221	63	42	1647

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
278	8	7417	8176	gi 599273	cystathionine gamma-synthase [Mycobacterium leprae] sp P46807 HETB_MYCLE CYSTATHIONINE GAMMA-SYNTASE (EC 4.2.99.9) O-SUCCINYLHOMOSERINE (THIOL)- LYASE)	63	41	1242
287	2	738	1733	gi 405133	putative [Bacillus subtilis]	63	38	996
295	1	2	748	gi 1239883	hypothetical protein [Bacillus subtilis]	63	41	747
328	3	2148	3134	gi 45302	carrier protein (AA 1 - 437) [Pseudomonas aeruginosa] tr S11497 S11497 branched-chain amino acid tr: sport protein brab - eudomonas aeruginosa	63	36	987
362	2	1226	1216	sp P35136 SERA_	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) (PCDH)	63	38	411
404	1	326	1051	gi 1303816	YqeZ [Bacillus subtilis]	63	35	726
405	3	2101	1715	gi 1303914	YqjV [Bacillus subtilis]	63	42	387
406	1	451	227	gi 142152	sulfate permease (gtg start codon) [Synecococcus PCC6301] pir A30301 GRYCS7 sulfate transport protein - Synecococcus sp. PCC 7942)	63	43	225
415	2	1048	2718	gi 1205402	transport ATP-binding protein [Haemophilus influenzae]	63	41	1671
426	4	3575	2679	gi 393268	29-kilodalton protein [Streptococcus pneumoniae] sp P42362 P29K_STRPW 29 MD MEMBRANE PROTEIN IN PSAA 5' REGION ORF1)	63	39	897
505	3	1347	2195	gi 1418999	orf4 [Lactobacillus sake]	63	40	849
507	1	2	574	gi 546917	comK [Bacillus subtilis, E26, Peptide, 192 aa]	63	35	573
562	2	146	1084	gi 43985	infS-like gene [Lactobacillus delbrueckii]	63	45	939
675	1	427	215	gi 1510994	serine aminotransferase [Methanococcus jannaschii]	63	29	213
686	1	3	230	gi 517356	nitrate reductase (NADH) [Lotus japonicus]	63	52	228
701	1	3	392	gi 881940	NorO protein [Paracoccus denitrificans]	63	41	390
720	1	2	400	gi 47168	open reading frame [Streptomyces lividans]	63	35	399
779	1	571	287	gi 1261932	unknown [Mycobacterium tuberculosis]	63	41	285
907	1	22	321	gi 149445	ORF1 [Lactococcus lactis]	63	27	300
972	1	794	399	gi 1511235	M. jannaschii predicted coding region M1232 [Methanococcus jannaschii]	63	27	396
1085	1	1154	618	gi 1204277	hypothetical protein (CB:000019_14) [Haemophilus influenzae]	63	38	537
1094	1	3	542	gi 790943	urea amidolyase [Bacillus subtilis]	63	39	540
1108	1	3	482	pir S49892 S498	regulation protein - Bacillus subtilis	63	44	480
1113	1	1231	617	gi 493017	endocarditis specific antigen [Enterococcus faecalis]	63	45	615

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
1300	1	3	695	[sp J33940 YQH_	HYPOTHETICAL 54.3 KD PROTEIN IN ECO-ALMB INTERGENIC REGION.	63	46	693
1325	1	1	204	[gi 928989	ip100 protein [Borrelia burgdorferi]	63	30	204
1814	1	3	245	[gi 1303914	Yqhy [Bacillus subtilis]	63	34	243
2021	1	498	250	[pir C33496 C334	hisc homolog - Bacillus subtilis	63	46	249
2325	1	2	193	[gi 436132	product is similar to TnpA of transposon Tn554 from Staphylococcus aureus [Clostridium butyricum]	63	40	192
2335	1	1	195	[gi 1184298	flagellar NS-ring protein [Borrelia burgdorferi]	63	47	195
2406	1	451	227	[gi 1041785	phoptry protein [Plasmodium yoelii]	63	33	225
2961	2	136	360	[gi 312443	carbamoyl-phosphate synthase (glutamine-hydrolysing) [Bacillus aldolyticus]	63	52	225
2965	1	1	402	[gi 1407784	orf-1: novel antigen [Staphylococcus aureus]	63	50	402
2987	1	583	293	[gi 1224069	amidase [Moraxella catarrhalis]	63	35	291
2994	1	266	125	[gi 183646	phosphoribosylformimino-praic ketolismomerase [Rhodobacter phaeoidea]	63	51	132
3043	1	440	252	[gi 1480237	phenylacetalddehyde dehydrogenase [Escherichia coli]	63	40	189
3078	1	609	400	[gi 1487982	intrinsic membrane protein [Mycoplasma hominis]	63	36	210
3139	1	2	217	[gi 439126	glutamate synthase (NADPH) [Xospiroillum brasiliense] pir A49916 A49916	63	47	216
1625	1	79	198	[gi 623073	ORF100: putative [Bacterium lupanoid 14-11]	63	48	196
3658	1	1	199	[gi 1303697	Yrka [Bacillus subtilis]	63	37	399
3659	1	3	395	[gi 1256135	YbbP [Bacillus subtilis]	63	48	393
3783	1	720	361	[gi 1256902	pyruvate decarboxylase isozyme 2 (Swiss Prot. accession number P16467) [Saccharomyces cerevisiae]	63	36	360
3900	1	338	171	[sp J10537 ANYB_	BETA-AMYLASE (EC 3.2.1.2) (1.4-ALPHA-D-GLUCAN MALTOTRIOLASE)	63	54	168
4309	1	3	176	[pir A37967 A379	neural cell adhesion molecule NG-CAM precursor - chicken	63	57	174
4367	1	1	195	[gi 1321932	Per6p gene product [Pichia pastoris]	63	30	195
4432	1	1	312	[gi 131259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas nevaloni] pir A44756 A44756	63	51	312
					hydroxymethylglutaryl-CoA reductase (EC-1.1.1.88) Pseudomonas sp.			
4468	1	6	308	[gi 296464	ATPase [Lactococcus lactis]	63	36	303
33	3	1411	2400	[gi 153675	tagatase 6-P Kinase [Streptococcus mutans]	62	44	990
36	9	5985	6218	[gi 1490521	INH3 [Homo sapiens]	62	51	234

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	Length (nt)
37	1	2	721	gi 1107531	ceuE gene product (Campylobacter coli)	62	33	720
38	15	110912	11589	gi 1222058	H. influenzae predicted coding region HIN1279 (Haemophilus influenzae)	62	38	678
38	35	19526	20329	gi 695280	ORF2 (Alcaligenes eutrophus)	62	41	806
57	2	2523	1780	gi 171234	orf1 (Haemophilus influenzae)	62	55	744
57	9	6646	6350	gi 508174	eltB domain of PTS-dependent Gat transport and phosphorylation Escherichia coli	62	35	297
58	1	2	559	gi 755152	highly hydrophobic integral membrane protein (Bacillus subtilis) sp P42953 TAGC_BACSU TEICHOIC ACID TRANSLLOCATION PERMEASE PROTEIN AGG.	62	34	558
67	10	8250	9014	gi 470683	Shows similarity with ATP-binding proteins from other ABC-transport proteins. Swiss Prot Accession Numbers P24137, P08007, P04285, P24136 Escherichia coli	62	34	765
69	8	8315	7494	gi 46816	lactVA 4 gene product (Streptomyces coelicolor)	62	44	822
80	3	1793	1320	gi 39593	UDP-N-acetyluramoylalanine-D-glutamate ligase (Bacillus subtilis)	62	43	474
87	7	7034	9205	gi 217191	5'-nucleotidase precursor (Vibrio parahaemolyticus)	62	48	2172
100	3	4051	3089	gi 1511047	phosphoglycerate dehydrogenase (Methanococcus jannaschii)	62	42	963
102	1	2	520	gi 153655	mismatch repair protein (Streptococcus pneumoniae) pir(C28667)C28667 DNA mismatch repair protein hexA - Streptococcus pneumoniae	62	34	519
112	2	466	1068	gi 153741	ATP-binding protein (Streptococcus mutans)	62	37	603
114	7	6855	7562	gi 1204866	lu-fucose operon activator (Haemophilus influenzae)	62	38	708
116	4	6823	5633	gi 677947	AppC (Bacillus subtilis)	62	37	1191
124	8	6855	6004	gi 653777	product similar to E.coli PRF2 protein (Bacillus subtilis) pir S55438 S55438 ynfK protein - Bacillus subtilis sp P45873 HEMK_BACSU POSSIBLE PHOTOPHOSPHORYLATION OXIDASE (EC 3.3.-)	62	44	852
148	1	24	554	gi 467456	unknown (Bacillus subtilis)	62	30	531
149	20	7591	6725	gi 1205807	replicative DNA helicase (Haemophilus influenzae)	62	41	867
163	3	1503	1153	gi 40067	X gene product (Bacillus sphaericus)	62	42	351
164	15	14673	15632	gi 42219	P35 gene product (AA 1 - 314) (Escherichia coli)	62	38	960
165	2	1166	1447	gi 403936	[phenylalanyl-tRNA synthetase alpha subunit (Gly294 variant) unidentified cloning vector]	62	38	282
166	2	2084	5089	gi 1308861	CTC start codon (Lactococcus lactis)	62	43	1006
171	1	1225	614	gi 1046053	hypothetical protein (SP:P32049) (Mycoplasma genitalium)	62	41	612

TABLE 2

5. aureus - putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
181	1	2521	1310	gi1143045	henY (Bacillus subtilis)	62	45	1212
200	1	3	956	gi1142439	ATP-dependent nuclease (Bacillus subtilis)	62	32	954
237	2	935	1966	gi1141695	hisC protein (Escherichia coli)	62	44	1032
261	3	4008	2605	gi1143121	ORF A; putative (Bacillus firmus)	62	42	1404
299	8	4477	4719	gi11467441	expressed at the end of exponential growth under conditions in which he enzymes of the TCA cycle are repressed (Bacillus subtilis) gi11467441 expressed at the end of exponential growth under conditions in which the enzymes of the TCA cycle are repressed Bacil	62	47	243
304	6	3018	3819	gi1153015	Fema protein (Staphylococcus aureus)	62	43	1200
324	1	2	262	gi1142717	Cytochrome aa3 controlling protein (Bacillus subtilis) pir(A33960)A33960 cta protein - Bacillus subtilis sp P12946 CTAA_BACSU CYTOCHROME AA3 CONTROLLING PROTEIN	62	30	261
325	2	289	1207	gi11581088	(methionyl)-S-TRIA formyltransferase (Escherichia coli)	62	39	939
332	6	4894	4631	gi11499960	uridine 5'-monophosphate synthase (Methanococcus jennaschii)	62	36	264
355	1	2	370	gi1145925	fecB (Escherichia coli)	62	32	369
365	8	6628	6804	gi11413843	ipe-19d gene product (Bacillus subtilis)	62	54	177
369	2	2744	1626	pir(A43577)A435	regulatory protein pfor - Clostridium perfringens	62	42	1119
370	1	34	264	gi1140665	pute-glucosidase (Clostridium thermocellum)	62	37	231
415	3	2709	3176	gi11203401	transport ATP-binding protein (Haemophilus influenzae)	62	35	468
429	1	1578	790	gi11046024	[Na ⁺ ATPase subunit J (Mycoplasma genitalium)	62	40	789
444	2	704	1369	gi11581510	modulation gene; integral membrane protein; homology to Rhizobium eguminosarum nodi (Rhizobium loti)	62	37	666
477	2	751	1869	pir(A18440)A484	ring-infected erythrocyte surface antigen 2, RESA-2 - Plasmodium falciparum	62	44	1119
485	1	241	1707	gi117934	betaine aldehyde dehydrogenase (Beta vulgaris)	62	43	1467
487	3	1141	1311	gi1149445	ORF1 (Lactococcus lactis)	62	31	171
494	2	1134	1313	gi1166835	ribulose biphosphate carboxylase/oxygenase activase (Arabidopsis thaliana)	62	37	180
518	1	193	882	gi1153491	O-methyltransferase (Streptomyces glaucescens)	62	39	690
534	2	369	2522	gi11480429	putative transcriptional regulator (Bacillus stearothermophilus)	62	35	2154
551	6	4371	4820	gi1151113	ferric uptake regulation protein (Campylobacter jejuni)	62	37	450
574	1	1	570	gi1153000	enterotoxin B (Staphylococcus aureus)	62	43	570

TABLE 2

5 aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
590	2	344	1171	gi 40367	ORF6 (Clostridium acetobutylicum)	62	37	828
655	1	396	830	gi 147195	phnB protein (Escherichia coli)	62	44	435
656	1	2	478	gi 1205451	cell division inhibitor (Haemophilus influenzae)	62	36	477
676	1	692	348	gi 1511613	methyl coenzyme M reductase system, component A2 (Methanococcus jannaschii)	62	36	365
687	1	493	248	gi 49272	asparaginase (Bacillus licheniformis)	62	48	246
700	2	267	944	gi 1205822	hypothetical protein (GB:X75627.4) (Haemophilus influenzae)	62	40	678
840	2	1715	1041	gi 1045865	M. genitalium predicted coding region MG181 (Mycoplasma genitalium)	62	36	675
864	4	898	1491	gi 1144332	deoxyuridine nucleotidohydrolase (Homo sapiens)	62	38	594
916	1	35	400	gi 413931	lipa-7d gene product (Bacillus subtilis)	62	45	366
1071	1	1	771	gi 1510649	aspartokinase I (Methanococcus jannaschii)	62	40	771
1084	1	19	609	gi 488011	Agx-1 antigen (human, infertile patient, testis, Peptide, 505 aa)	62	39	591
1103	1	3	203	gi 581261	ORF homologous to E. coli mobA (Mycoplasma genitalium) p1r S14030 S14030	62	51	201
1217	1	463	233	gi 460025	ORF2, putative (Streptococcus pneumoniae)	62	41	231
1533	1	644	414	gi 413968	lipa-44d gene product (Bacillus subtilis)	62	48	231
1537	1	3	257	gi 1510641	elanyl-CNA synthetase (Methanococcus jannaschii)	62	23	255
2287	1	3	161	gi 485956	mapC gene product (Proteus mirabilis)	62	45	159
2386	1	3	245	gi 285708	nontoxic component (Clostridium botulinum)	62	31	243
2484	1	331	167	gi 142092	DNA-repair protein (recA) (Anabaena variabilis)	62	35	165
2490	1	798	400	gi 581648	lepis gene product (Staphylococcus epidermidis)	62	42	399
3016	1	596	300	gi 710022	uroporphyrinogen III (Bacillus subtilis)	62	51	297
3116	1	1	213	gi 466883	nlfs; B1496_C2_193 (Mycobacterium leprae)	62	44	213
3297	1	823	413	gi 475715	acetyl coenzyme A acetyltransferase (thiolase) (Clostridium acetobutylicum)	62	42	411
3609	1	31	276	gi 1408501	homologous to N-acetyl-L-amino acid amidohydrolase of Bacillus stearothermophilus (Bacillus subtilis)	62	48	246
3665	2	584	402	gi 151259	HMG-CoA reductase (EC 1.1.1.88) (Pseudomonas mvalonii) p1r A44756 A44756	62	40	183
3733	1	3	374	gi 1351197	hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	62	42	372

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3898	1	1	237	gi 153675	lactatase 6-P kinase [Streptococcus mutans]	62	45	237
4027	1	283	143	gi 330705	homologue to gene 30 (aa 1-59); putative [Bovine herpesvirus 4]	62	43	141
4109	1	727	365	gi 41748	hscM protein (AA 1-520) [Escherichia coli]	62	45	363
4303	1	1	303	gi 1303813	Yqew [Bacillus subtilis]	62	43	303
4380	1	530	267	gi 1235684	invasionate pyrophosphate decarboxylase [Saccharomyces cerevisiae]	62	55	264
4494	1	2	256	gi 510692	enterotoxin H [Staphylococcus aureus]	62	34	255
4598	1	411	223	gi 763513	ORF4; putative [Streptomyces violaceoruber]	62	45	189
4624	1	1	222	gi 41748	hscM protein (AA 1-520) [Escherichia coli]	62	45	222
5	5	4288	3912	gi 928831	ORF5; putative [Lactococcus lactis phage HK5-T]	61	36	357
11	1	320	162	gi 33356[CJ33]	prothymosin alpha homolog (clone 32) - human (fragment)	61	33	159
16	11	10991	11938	gi 1205391	hypothetical protein (SP-P31995) [Haemophilus influenzae]	61	44	948
32	1	281	801	gi 1066504	exo-beta 1,3 glucanase [Cocciobolus carbonum]	61	50	519
38	3	616	1107	gi 1510864	glutamine transport ATP-binding protein Q [Methanococcus jannaschii]	61	41	492
45	4	3082	4038	gi 1109686	ProX [Bacillus subtilis]	61	45	957
48	8	7118	7504	gi 498839	ORF2 [Clostridium perfringens]	61	33	387
51	9	4605	5570	gi 380269	trac [Plasmid pAD1]	61	42	966
60	6	1689	2243	gi 1205893	hypothetical protein (GB:U00011.3) [Haemophilus influenzae]	61	32	555
62	9	5559	5122	gi 854656	Na/H antiporter system ORP2 [Bacillus alcalophilus]	61	38	438
67	5	4330	5646	gi 466612	nika [Escherichia coli]	61	36	1317
74	2	2400	1504	gi 1204846	carbamate kinase [Haemophilus influenzae]	61	40	897
85	1	2198	1101	gi 1498756	amidophosphoribosyltransferase PurP [Rhizobium etli]	61	41	1098
86	4	1995	1582	gi 1499931	H. jannaschii predicted coding region HJ1083 [Methanococcus jannaschii]	61	44	414
97	1	74	649	gi 1518679	orf [Bacillus subtilis]	61	44	576
99	2	2454	1990	gi 413958	lpa-34d gene product [Bacillus subtilis]	61	18	465
124	7	6223	5123	gi 556881	Similar to Saccharomyces cerevisiae SUP4 protein [Bacillus subtilis] pir S4938 S4938 ipc-230 protein - Bacillus subtilis sp P31933 THUC_BACSU HYPOTHETICAL 37.0 KD PROTEIN IN SPO1R-GLYC MTERGENIC REGION.	61	46	1101
125	4	1668	2531	gi 1491643	OREA gene product [Chloroflexus aurantiacus]	61	43	864

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
112	1	1250	627	gi 1400259 P002	hypothetical protein 1 - Enterococcus faecalis plasmid pAM-beta-1 (fragment)	61	43	624
149	9	3617	3075	gi 1144332	deoxyuridine nucleotidylhydrolase (Homo sapiens)	61	40	543
149	122	8690	7869	gi 160047	PI01/acidic basic repeat antigen (Plasmodium falciparum) pIR/A29222[A29222] PI01K malaria antigen precursor - Plasmodium falciparum (strain Camp)	61	35	822
168	3	1915	2361	gi 1499694	HIT protein, member of the HIT-family (Methanococcus jannaschii)	61	41	447
171	9	9675	7948	gi 467416	similar to SpoVB (Bacillus subtilis)	61	38	1728
174	3	1042	2340	gi 216374	glucaryl 7-ACA acylase precursor (Bacillus laterosporus)	61	49	1299
190	4	5034	4111	gi 409286	bmrU (Bacillus subtilis)	61	37	924
216	1	2	190	gi 415861	eukaryotic initiation factor 2 beta (eif-2 beta) (Oryctolagus unicolor)	61	29	189
227	7	4161	5048	gi 216341	ORF for methionine amino peptidase (Bacillus subtilis)	61	41	888
238	4	1959	3047	gi 409543	Cbrc protein (Erwinia chrysanthemi)	61	38	1089
247	1	2	694	gi 537231	ORF 4579 (Escherichia coli)	61	38	693
247	2	678	1034	gi 142226	clwD protein (Agrobacterium tumefaciens)	61	40	357
257	2	3523	2627	gi 699379	glvr-1 protein (Mycobacterium leprae)	61	40	897
268	2	3419	3051	gi 40364	ORF1 (Clostridium acetobutylicum)	61	41	369
275	4	4621	4827	gi 1204848	hypothetical protein (GP:M87049.57) (Haemophilus influenzae)	61	36	207
277	1	1	1945	gi 794897	beta-N-acetylhexosaminidase (Streptococcus pneumoniae) pIR/A56390[A56390] mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - streptococcus pneumoniae	61	45	1845
278	9	8003	7032	gi 467462	cysteine synthetase A (Bacillus subtilis)	61	43	972
278	10	9878	8535	gi 1205919	Na+ and Cl- dependent gamma-aminobutyric acid transporter (Haemophilus influenzae)	61	38	1344
283	1	1	366	gi 755607	polyA polymerase (Bacillus subtilis)	61	36	366
288	2	1918	1496	gi 368108	cell wall enzyme - enterococcus faecalis	61	43	423
291	1	86	334	gi 454265	F8P3 (Petunia hybrida)	61	38	249
318	1	1104	694	gi 290531	similar to beta-glucoside transport protein (Escherichia coli) sp P31451 PTIB_ECOLI PTS SYSTEM, ARBITRIN-LIKE IIB COMPONENT PHOSPHOTRANSFERASE ENZYME II, B COMPONENT (EC 2.7.1.69)	61	47	411
330	2	1912	1190	gi 1001805	hypothetical protein (Synecocystis sp.)	61	41	723

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
385	2	1513	1025	gi 533098	DnaD protein [Bacillus subtilis]	61	42	489
426	1	794	399	gi 1303853	Yqef [Bacillus subtilis]	61	44	396
438	3	810	1421	gi 1293660	AbaA2 [Streptomyces coelicolor]	61	36	612
454	1	1580	792	gi 733522	phosphatidylinositol-4,5-diphosphate 3-kinase [Dictyostelium discoideum]	61	30	789
464	2	784	560	gi 1123120	C53B7.5 gene product [Caenorhabditis elegans]	61	38	235
470	8	6077	7357	gi 623073	ORF360; putative [Bacteriophage LU-H]	61	47	1281
509	1	554	279	gi 467484	unknown [Bacillus subtilis]	61	45	276
555	3	1916	1296	gi 141800	anthranilate synthase glutamine amidotransferase [Acinetobacter alcoaceticus]	61	42	621
589	1	1711	857	gi 467090	B2335_C2_195 [Mycobacterium leprae]	61	47	855
585	2	961	803	sp P3686 SURE_	SURVIVAL PROTEIN SURE HOMOLOG (FRAGMENT)	61	33	159
592	3	1694	1422	gi 1221602	immunity repressor protein [Hemophilus influenzae]	61	32	273
603	1	43	357	gi 507738	Ilp [Vibrio parahaemolyticus]	61	33	315
669	1	2467	1235	gi 1146243	22.4% identity with Escherichia coli DNA-damage inducible protein ... putative [Bacillus subtilis]	61	37	1233
675	3	805	1101	gi 403373	glycerophosphoryl diester phosphodiesterase [Bacillus subtilis] p1r[S17251 S17251 glycerophosphoryl diester phosphodiesterase - subtilis	61	36	297
701	1	1656	829	gi 537181	ORF_670 [Escherichia coli]	61	32	828
728	1	1628	816	gi 806281	DNA polymerase I [Bacillus stearothermophilus]	61	39	813
821	1	61	318	gi 709992	hypothetical protein [Bacillus subtilis]	61	38	258
856	2	2313	1567	gi 609310	portal protein gp3 [Bacteriophage HK97]	61	40	747
923	1	1081	542	gi 143213	putative [Bacillus subtilis]	61	38	540
1124	1	59	370	gi 1107541	C3JD9.8 [Caenorhabditis elegans]	61	26	312
1492	1	548	276	gi 406397	unknown [Mycoplasma genitalium]	61	32	273
1602	1	46	318	gi 733522	phosphatidylinositol-4,5-diphosphate 3-kinase [Dictyostelium discoideum]	61	34	273
2500	1	577	290	gi 1045964	hypothetical protein (CB-U14003.297) [Mycoplasma genitalium]	61	31	288
2968	1	2	808	gi 397526	clumping factor [Staphylococcus aureus]	61	55	807
3076	1	3	248	gi 149373	ORF 1 [Lactococcus lactis]	61	41	246

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3609	2	207	401	gi 1408501	homologous to N-acetyl-L-amino acid amidohydrolase of <i>Bacillus stearothermophilus</i> [Bacillus subtilis]	61	39	195
3662	1	1477	740	gi 1303813	Yqgw [Bacillus subtilis]	61	42	738
3672	1	2	442	gi 784897	beta-N-acetylhexosaminidase (Streptococcus pneumoniae) pir A56390 A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	50	441
3724	1	2	220	gi 1009366	Respiratory nitrate reductase [Bacillus subtilis]	61	41	219
3728	1	3	398	gi 677943	Appd [Bacillus subtilis]	61	46	396
3884	1	3	401	gi 784897	beta-N-acetylhexosaminidase (Streptococcus pneumoniae) pir A56390 A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	47	399
3971	1	3	383	gi 784897	beta-N-acetylhexosaminidase (Streptococcus pneumoniae) pir A56390 A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	45	381
4038	1	661	359	gi 1339970	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	61	24	303
4041	1	546	274	gi 413953	lme-29d gene product [Bacillus subtilis]	61	48	273
4047	1	1	402	gi 528991	unknown [Bacillus subtilis]	61	42	402
4102	1	1	345	gi 976025	Hrsa [Escherichia coli]	61	46	345
4155	1	1	336	gi 784897	beta-N-acetylhexosaminidase (Streptococcus pneumoniae) pir A56390 A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	50	336
4268	1	463	233	gi 450688	hadH gene of Ecoor1 gene product [Escherichia coli] pir S38437 S38437 hadH protein - Escherichia coli pir S09629 S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	61	38	231
4374	1	542	273	gi 784897	beta-N-acetylhexosaminidase (Streptococcus pneumoniae) pir A56390 A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	50	270
4389	1	2	172	gi 147516	ribokinase [Escherichia coli]	61	35	171
4621	1	2	268	gi 784897	beta-N-acetylhexosaminidase (Streptococcus pneumoniae) pir A56390 A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	47	267
4663	1	27	227	gi 976025	Hrsa [Escherichia coli]	61	50	201
4	6	663	5536	gi 1408501	homologous to N-acetyl-L-amino acid amidohydrolase of <i>Bacillus stearothermophilus</i> [Bacillus subtilis]	60	43	1128

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
11	6	3426	3725	gi 410748	ring-infected erythrocyte surface antigen (Plasmodium falciparum) pfrA2556/A2556 ring-infected erythrocyte surface antigen recuor - Plasmodium falciparum (strain FC7/Papua New Guinea) sp P13830 RESA_PLAFF RING-INFECTED ERYTHROCYTE SURFACE ANTIGEN RE	60	24	300
11	14	11035	10313	gi 1217651	carboxyl reductase (NADPH) (Rattus norvegicus)	60	28	723
16	12	11917	12930	gi 1001453	hypothetical protein (Synchocystis sp.)	60	37	1014
33	1	26	469	gi 388109	regulatory protein (Enterococcus faecalis)	60	41	444
37	13	10414	9834	gi 133656	Orf1 (Bacillus subtilis)	60	40	981
39	4	4364	4522	gi 4872	ORF 4 (Saccharomyces kluyveri)	60	47	159
41	1	2047	1025	gi 142822	O-alanine racemase cde (Bacillus subtilis)	60	39	1023
43	4	2474	3607	gi 468046	para-nitrobenzyl esterase (Bacillus subtilis)	60	40	1134
44	10	6756	7769	gi 414234	thif (Escherichia coli)	60	52	1014
45	10	8874	9074	gi 343949	var1(40.0) (Saccharomyces cerevisiae)	60	44	201
56	18	27842	26430	gi 468764	moaB gene product (Rhizobium meliloti)	60	35	1413
60	2	173	388	gi 1303864	YggO (Bacillus subtilis)	60	33	216
63	2	357	1619	gi 467124	ureD; B229_C1_234 (Mycobacterium leprae)	60	43	1263
69	1	787	395	gi 1518853	OafA (Salmonella typhimurium)	60	36	193
88	1	1	1188	gi 1480429	putative transcriptional regulator (Bacillus stearothermophilus)	60	30	1188
92	6	4735	3881	gi 349227	transmembrane protein (Escherichia coli)	60	37	855
92	7	5996	4923	gi 466613	nlkB (Escherichia coli)	60	38	1074
93	1	949	476	gi 1510925	coenzyme F420-reducing hydrogenase, beta subunit (Methanococcus jannaschii)	60	27	474
96	6	7166	7478	gi 472715	accessory protein (Mycobacterium placentiae)	60	30	213
98	6	3212	4069	gi 467425	unknown (Bacillus subtilis)	60	42	858
102	10	7158	7430	gi 141092	acetolactate synthase small subunit (Bacillus subtilis) sp P37252 ILVNBACSU ACETOLACTATE SYNTHASE SMALL SUBUNIT (EC 1.3.18) (NHS) (ACETONHYDROXY-ACID SYNTHASE SMALL SUBUNIT) (ALS)	60	37	273
109	11	9127	10515	gi 1255259	O-succinylbenzoic acid (OSB) CoA ligase (Staphylococcus aureus)	60	28	1389
109	12	10499	11656	gi 141954	beta-ketothiolase (Alcaligenes eutrophus)	60	41	1158
119	2	4630	3134	gi 1524280	unknown (Mycobacterium tuberculosis)	60	45	1497

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
121	9	6957	7846	gi1107529	lecC gene product [Campylobacter coli]	60	35	690
140	7	7704	6013	gi146547	kdpA [Escherichia coli]	60	45	1692
145	1	2	703	gi1460077	unknown [Mycobacterium tuberculosis]	60	23	702
150	3	2809	2216	gi1146220	putative [Bacillus subtilis]	60	40	594
157	2	1389	961	gi1303975	YqjX [Bacillus subtilis]	60	30	429
158	5	5125	4769	gi1449288	unknown [Mycobacterium tuberculosis]	60	36	357
159	1	511	257	gi1580932	murD gene product [Bacillus subtilis]	60	43	255
160	1	159	1187	gi1204512	hypothetical protein (GB:U19201.29) [Haemophilus influenzae]	60	34	1029
161	14	8249	7866	gi1496003	ORF3: PopV, putative oligoendopeptidase based on homology with Lactococcus lactis PopV (GenBank Accession Number 232522) [Caldicellulosiruptor saccharolyticus]	60	34	384
172	3	1331	2110	gi1485280	28.2 kDa protein [Streptococcus pneumoniae]	60	33	780
173	2	4082	2460	gi1524397	glycine betaine transporter Opd [Bacillus subtilis]	60	41	1623
173	4	5963	4953	gi1100737	NAUP dependent leukotoxin b4 12-hydroxydehydrogenase [Sus scrofa]	60	44	1011
198	1	3	995	gi1413943	lpa-19d gene product [Bacillus subtilis]	60	42	993
201	4	3641	4573	sp137028 YADP	HYPOTHEICAL 29.4 KD PROTEIN IN HENL-PPS INTERGENIC REGION PRECURSOR.	60	37	933
203	3	3269	2415	gi1927798	[D9719.34p; CA1: 0.14 [Saccharomyces cerevisiae]	60	43	835
206	9	12234	12515	sp137347 YEC0	HYPOTHEICAL 21.8 KD PROTEIN IN ASP5 5'REGION.	60	47	282
212	4	1213	1410	gi1332711	hemagglutinin-neuraminidase fusion protein [Human parainfluenza virus 3]	60	34	198
214	1	65	1153	gi1204366	hypothetical protein (GB:U14003.130) [Haemophilus influenzae]	60	36	1089
237	1	2	937	gi1149377	HisD [Lactococcus lactis]	60	40	936
241	6	5696	4998	gi11046160	hypothetical protein (GB:U00021.5) [Mycoplasma genitalium]	60	37	699
260	6	5919	6485	gi1431950	similar to a B.subtilis gene (GB: DACHEM9.5) [Clostridium astreum]	60	35	567
264	1	2432	1218	gi1397526	clumping factor [Staphylococcus aureus]	60	53	1215
267	1	3	1409	gi1148316	NaN-antiporter protein [Enterococcus hirae]	60	27	1407
275	3	3804	4595	gi136889 F168	leuB 3'-region hypothetical protein - Lactococcus lactis subsp. lactis [strain U1403]	60	35	792
291	3	860	1198	gi1208889	coded for by C. elegans cDNA yk10612.5; contains C2H2-type zinc fingers [Caenorhabditis elegans]	60	33	339

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
307	6	3421	3176	gi 1070014	protein-dependent [Bacillus subtilis]	60	36	246
316	8	4957	5823	gi 413952	ipe-28d gene product [Bacillus subtilis]	60	41	867
328	4	2996	3484	gi 1204484	membrane-associated component, branched amino acid transport system [Haemophilus influenzae]	60	39	489
332	5	4887	4363	gi 1205449	colicin V production protein (pur regulon) [Haemophilus influenzae]	60	37	525
357	1	1062	532	gi 887842	single-stranded DNA-specific exonuclease [Escherichia coli]	60	41	531
375	2	96	362	gi 1057	adenylate cyclase gene product [Saccharomyces kluyveri] r[301145]OBYK	60	47	267
397	1	66	416	gi 709999	glucuronate dehydratase [Bacillus subtilis]	60	37	351
409	1	2	163	gi 499700	glycogen phosphorylase [Saccharomyces cerevisiae]	60	35	162
453	4	914	1237	gi 1196899	unknown protein [Staphylococcus aureus]	60	36	324
453	7	1838	3620	sp P1222 VCP1_HYPOTHETICAL 226 KD PROTEIN (ORF 1501)		60	31	219
470	2	622	945	pir S30782 S307	integrin homolog - yeast [Saccharomyces cerevisiae]	60	31	324
500	1	118	606	gi 467407	unknown [Bacillus subtilis]	60	36	489
503	3	752	982	gi 167835	leucosin heavy chain [Dictyostelium discoideum]	60	34	231
505	4	2238	3563	gi 1510732	NADH oxidase [Methanococcus jannaschii]	60	26	1326
523	1	3	1043	gi 143331	alkaline phosphatase regulatory protein [Bacillus subtilis] pir A27650 A27650 regulatory protein phoA - Bacillus subtilis sp P23345 PHO_A27650 ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN IOR (EC 2.7.3.-)	60	41	1041
543	1	1	465	gi 1511103	cobalt transport ATP-binding protein O [Methanococcus jannaschii]	60	40	465
545	1	1	726	gi 1498192	putative [Pseudomonas aeruginosa]	60	40	726
556	1	2	1054	gi 1477402	tox gene product [Bordetella pertussis]	60	42	1053
578	1	974	489	gi 1205129	H. influenzae predicted coding region H10882 [Haemophilus influenzae]	60	42	486
594	1	1	624	gi 1212755	adenylate cyclase [Aeromonas hydrophila]	60	45	624
604	1	3	530	gi 145925	fecB [Escherichia coli]	60	42	528
620	1	926	465	gi 1205483	bicyclic resistance protein [Haemophilus influenzae]	60	33	462
630	2	871	1122	gi 1486242	unknown [Bacillus subtilis]	60	41	252
645	2	574	425	gi 1205136	serine hydroxymethyltransferase [serine methylase] [Haemophilus influenzae]	60	28	150

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
684	1	1082	843	gi 1205538	hypothetical protein [GB:U14003_302] (Haemophilus influenzae)	60	39	240
786	1	967	485	gi 1402944	orfRw1 gene product [Bacillus subtilis]	60	46	483
844	1	588	346	gi 790943	urea amidolyase [Bacillus subtilis]	60	40	243
851	1	1	726	gi 159661	GMP reductase [Ascaris lumbricoides]	60	41	726
871	1	1746	874	gi 1001493	hypothetical protein [Synechocystis sp.]	60	39	873
896	1	1558	839	gi 604926	NADH dehydrogenase, subunit 5 [Escherichia coli] sp P50369 NUSH_SCHCO	60	39	720
908	2	448	753	gi 662880	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 6.5.3)	60	31	306
979	1	2	595	gi 1429255	novel hemolytic factor [Bacillus cereus]	60	30	594
1078	1	669	502	gi 581055	putative; orf1 [Bacillus subtilis]	60	40	168
1112	1	1150	620	gi 407885	inner membrane copper tolerance protein [Escherichia coli] gi 871029	60	34	531
1135	1	484	275	gi 1171407	disulphide isomerase like protein [Escherichia coli] pif S47295 S47295	60	36	210
1146	1	17	562	gi 1233981	inner membrane copper tolerance protein - scherichia coli	60	36	546
1291	1	716	360	pif S57530 S575	carboxyl esterase - Acinetobacter calcoaceticus	60	30	357
1332	1	336	169	gi 1222056	aminotransferase [Haemophilus influenzae]	60	44	168
1429	1	3	146	gi 1205619	ferritin like protein [Haemophilus influenzae]	60	39	144
1722	1	570	286	gi 240052	dihydroflavonol-4-reductase, DFR [Hordeum vulgare-barley, cv. Gula, eptide 356 aa]	60	36	285
2350	1	385	200	gi 497626	ORF 1 [Plasmid pHQ1]	60	20	186
2936	1	519	310	gi 508981	prephenate dehydratase [Bacillus subtilis]	60	48	210
3027	1	568	302	gi 1146199	putative [Bacillus subtilis]	60	37	267
3084	1	20	208	gi 1407784	orf-1, novel antigen [Staphylococcus aureus]	60	51	189
3155	1	2	226	gi 1046097	cytadherence-accessory protein [Mycoplasma genitalium]	60	34	225
3603	1	368	186	gi 510108	mitochondrial long-chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit [Rattus norvegicus]	60	42	183
3665	1	486	244	gi 151259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pif A44756 A44756	60	42	243
3747	1	3	146	gi 474192	hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	60	36	144

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3912	1	3	335	gi 488695	novel antigen: orf-2 [Staphylococcus aureus]	60	44	333
4072	1	3	272	gi 405879	yeiH [Escherichia coli]	60	33	270
4134	1	510	352	gi 780656	chemoreceptor protein [Rhizobium leguminosarum bv. viciae] gi 780656	60	28	159
4207	2	677	402	gi 602031	similar to trimethylamine DH [Mycoplasma capricolum] pir[S49950]S49950 probable trimethylamine dehydrogenase (EC 5.99.7) - Mycoplasma capricolum (SGC3) (fragment)	60	41	276
4243	1	127	324	gi 899117	peptide synthetase module [Microcystis aeruginosa] pir[S49111]S49111 probable amino acid activating domain - Microcystis aeruginosa (fragment) (SUB 144-528)	60	42	198
4710	1	624	313	gi 304980	pheB [Bacillus subtilis]	60	28	312
4345	1	343	173	gi 510108	mitochondrial long-chain enoyl-CoA hydratase/3-hydroxacyl-CoA dehydrogenase alpha-subunit [Rattus norvegicus]	60	42	171
4382	1	498	280	gi 47382	acyl-CoA-dehydrogenase [Streptomyces purpurascens]	60	48	219
4474	1	53	223	gi 510108	mitochondrial long-chain enoyl-CoA hydratase/3-hydroxacyl-CoA dehydrogenase alpha-subunit [Rattus norvegicus]	60	42	171
23	4	4518	3523	gi 426446	VipB protein [Salmonella typhi]	59	39	996
33	2	707	1483	pir[S48604]S486	hypothetical protein - Mycoplasma capricolum (SGC3) (fragment)	59	33	777
33	5	4651	5853	gi 6721	P5982.3 [Caenorhabditis elegans]	59	33	1203
17	2	1228	2299	gi 142813	ORF2 [Bacillus subtilis]	59	37	910
38	21	16784	16593	gi 912576	BIP [Phaeodactylum tricornutum]	59	40	192
52	3	2648	2349	gi 536972	ORF_090a [Escherichia coli]	59	44	300
54	12	14181	13402	gi 483940	transcription regulator [Bacillus subtilis]	59	37	780
57	3	4397	3339	gi 508176	[Gat-1-P-DH, NAD dependent [Escherichia coli]	59	40	1059
66	1	986	495	gi 1303901	Yqht [Bacillus subtilis]	59	34	492
67	7	6552	7460	gi 912461	nlxK [Escherichia coli]	59	37	909
70	7	5383	6366	gi 1399822	PhoD precursor [Rhizobium meliloti]	59	46	984
78	1	1	1449	gi 971345	unknown, similar to E. coli cardiolipin synthase [Bacillus subtilis] sp P45860 WIE_BACSU HYPOHETICAL 58.2 PROTEIN IN NANI-ACDA HYPERGENIC REGION.	59	39	1449
82	10	14329	15534	gi 490328	[ORF P (unidentified)]	59	44	1206

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
89	2	1602	958	gi 642801	unknown (Saccharomyces cerevisiae)	59	32	645
96	4	4940	5473	gi 1333802	protein of unknown function (Rhodobacter capsulatus)	59	33	534
98	1	2	820	gi 467421	similar to B. subtilis DnaH (Bacillus subtilis)	59	34	819
119	1	166	1557	gi 143122	ORF B; putative (Bacillus firmus)	59	36	1392
120	10	6214	6756	gi 15354	ORF 55.9 (Bacteriophage T4)	59	39	543
120	16	12476	13510	gi 1086575	Beth (Rhizobium meliloti)	59	44	1035
123	1	386	195	gi 984737	catalase (Campylobacter jejuni)	59	38	192
130	1	170	645	gi 125634	25.8% identity over 120 aa with the Synenococcus sp. NpV protein; putative (Bacillus subtilis)	59	31	276
131	4	5278	5712	gi 1510655	hypothetical protein (SP:P42297) (Methanococcus jannaschii)	59	39	435
164	1	3	509	gi 1001342	hypothetical protein (Synchocystis sp.)	59	41	507
164	4	1529	2821	gi 1205165	hypothetical protein (SP:P37764) (Haemophilus influenzae)	59	35	1293
164	19	19643	21376	gi 1001381	hypothetical protein (Synchocystis sp.)	59	34	1734
173	3	4727	3717	gi 1184121	leucin-induced protein (Vigna radiata)	59	50	1011
179	2	2218	1688	gi 143036	unidentified gene product (Bacillus subtilis)	59	33	531
195	12	12669	11503	gi 762778	NIFS gene product (Anabaena azollae)	59	41	1167
201	5	4702	5670	gi 1510240	hemolysase (Methanococcus jannaschii)	59	32	969
201	7	5719	6315	gi 1511456	M. jannaschii predicted coding region M31437 (Methanococcus jannaschii)	59	34	597
209	1	102	461	gi 1204666	hypothetical protein (GB:X73124.53) (Haemophilus influenzae)	59	42	360
214	3	1050	2234	gi 551531	2-nitropropane dioxygenase (Willopsia saturnus)	59	36	1185
214	5	3293	4135	gi 1303709	YrkJ (Bacillus subtilis)	59	32	843
217	2	3183	2167	gi 290489	dtp (CG Site No. 18430) (Escherichia coli)	59	44	1215
237	5	3078	3785	gi 149182	YlIA (Lactococcus lactis)	59	38	708
251	2	376	960	gi 1303791	YqoJ (Bacillus subtilis)	59	34	585
286	1	1621	812	gi 146551	transmembrane protein (kdp) (Escherichia coli)	59	31	810
316	5	4978	3860	gi 405879	YeiH (Escherichia coli)	59	32	1119
370	3	600	761	gi 1303794	YqeM (Bacillus subtilis)	59	35	162

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
382	1	1009	506	gi 547513	orf3 [Haemophilus influenzae]	59	34	504
391	3	1620	1273	gi 152901	orf3 [Spirochaeta aurantia]	59	37	348
406	3	2805	1705	gi 709992	hypothetical protein [Bacillus subtilis]			
426	5	3802	3245	gi 1204610	iron(III) diethrate transport ATP-binding protein PECE [Haemophilus influenzae]	59	36	558
439	2	1513	1148	gi 1064809	homologous to sp-HTRA_ECOLI [Bacillus subtilis]	59	42	366
460	2	708	1301	gi 466882	ppsl_81496_C2_189 [Mycobacterium leprae]	59	37	594
461	4	2212	3135	gi 1498295	homoserine kinase homolog [Streptococcus pneumoniae]	59	37	928
473	1	2929	1607	gi 147989	trigger factor [Escherichia coli]	59	40	1323
480	8	5862	6110	gi 1205311	(3R)-hydroxymyristol acyl carrier protein dehydrase [Haemophilus influenzae]	59	40	249
521	1	14	1354	pir A25620 A256	staphylococcalase - Staphylococcus aureus (fragment)	59	32	1341
534	4	2994	4073	gi 153746	mannitol-phosphate dehydrogenase [Streptococcus mutans] pir C44798[C44798 mannitol-phosphate dehydrogenase MCD - treptococcus mutans]	59	36	1080
535	1	1	954	gi 1469939	group B oligopeptidase PepB [Streptococcus agalactiae]	59	33	954
551	3	2836	3186	gi 1204511	bacterioferritin comigratory protein [Haemophilus influenzae]	59	45	351
573	2	449	940	gi 386681	ORF YAL022 [Saccharomyces cerevisiae]	59	36	492
650	1	5	748	gi 396400	similar to eukaryotic Na+/H+ exchangers [Escherichia coli] sp P32703 YJCE_ECOLI HYPOTHEICAL 60.5 KD PROTEIN IN SOXN-ACS INTERGENIC REGION (0349)	59	30	744
664	1	566	285	gi 1262748	LukP-PV like component [Staphylococcus aureus]	59	33	282
670	1	3	455	gi 112758	unknown [Bacillus subtilis]	59	42	453
674	3	543	929	gi 293033	integrase [Bacteriophage phi-LC3]	59	46	387
758	1	349	176	gi 1500472	M. jannaschii predicted coding region MJ1577 [Methanococcus jannaschii]	59	37	174
771	2	2270	1461	gi 522150	bromoperoxidase BPO-A1 [Streptomyces aureofaciens] sp P31912 BPAL_STRAU NON-HAEM BROMOPEROXIDASE BPO-A1 (EC 1.11.1.-) BROMIDE PEROXIDASE (BPO1), (SUB 2-275)	59	44	810
825	1	2191	1097	gi 397526	clumping factor [Staphylococcus aureus]	59	47	1095
1052	2	1094	723	gi 289262	comE ORF3 [Bacillus subtilis]	59	36	372
1152	1	373	168	gi 1127668	ORF238 gene product [Porphyra purpurea]	59	37	186

TABLE 2

S. aureus - putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
1198	1	492	247	gi 142439	ATP-dependent nuclease [Bacillus subtilis]	59	26	246
1441	1	468	235	gi 1045942	glycyl-tRNA synthetase [Mycoplama genitalium]	59	37	234
2103	1	1	186	gi 1459250	trilacylglycerol lipase [Galactomyces geotrichum]	59	33	186
2205	1	793	398	gi 1303794	Yqem [Bacillus subtilis]	59	38	396
2578	1	484	284	gi 258003	insulin-like growth factor binding protein complex acid-labile subunit [rats, liver, peptide, 603 aa]	59	48	201
2967	2	145	348	gi 1212730	Yqhk [Bacillus subtilis]	59	44	204
3012	1	3	248	gi 173571	neurofilament protein NF70 [Helix aspersa]	59	31	246
3544	1	3	401	gi 1055218	crotonase [Clostridium acetobutylicum]	59	42	399
3548	1	3	401	gi 1055218	crotonase [Clostridium acetobutylicum]	59	42	399
3580	1	698	351	gi 1055218	crotonase [Clostridium acetobutylicum]	59	42	348
3720	1	722	363	gi 1408494	homologous to penicillin acylase [Bacillus subtilis]	59	36	360
4171	1	3	276	gi 1055218	crotonase [Clostridium acetobutylicum]	59	42	294
4305	1	618	310	gi 1524193	unknown [Mycobacterium tuberculosis]	59	39	309
18	1	1242	622	gi 146913	N-acetylglucosamine transport protein [Escherichia coli] pir 829895 WQBC2H phosphotransferase system enzyme II (EC 7.1.69), N-acetylglucosamine-specific - Escherichia coli gp p09323 PTAA_ECOLI PTS SYSTEM, N-ACETYLGLUCOSAMINE-SPECIFIC IIAC COMPONENT [E1A]	58	43	621
20	7	7020	5845	gi 50302	collagen alpha chain precursor (AA -27 to 1127) [Mus musculus]	58	50	1176
21	5	3234	3626	gi 1034860	phosphoribosyl anthranilate isomerase [Thermotoga maritima]	58	32	393
23	2	2841	1669	gi 1276880	Epac [Streptococcus thermophilus]	58	29	1173
23	10	9301	8090	pir A31133 A311	diaminopimelate decarboxylase (EC 4.1.1.20) - Pseudomonas aeruginosa	58	37	1212
38	29	22555	22884	gi 1973249	vestitone reductase [Medicago sativa]	58	37	330
44	1	2	406	gi 289272	ferrichrome-binding protein [Bacillus subtilis]	58	33	405
45	1	1	552	gi 29464	embryonic myosin heavy chain (1085 AA) (Homo sapiens) tr S12460 S12460 myosin beta heavy chain - human	58	33	552
55	2	759	538	gi 158852	glucose regulated protein [Echinococcus multilocularis]	58	32	222
62	13	8493	8068	gi 1975353	kinase-associated protein B [Bacillus subtilis]	58	35	426
63	3	1553	1717	gi 166926	[Arabidopsis thaliana unidentified mRNA sequence, complete cds.]_ene product [Arabidopsis thaliana]	58	35	165

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
67	13	12017	11229	gi 1228083	NADH dehydrogenase subunit 2 (Chorthippus parallelus)	58	41	789
96	8	8208	9167	gi 709992	hypothetical protein (Bacillus subtilis)	58	42	960
107	2	2065	1364	gi 806327	Escherichia coli hcrA gene for A protein similar to yeast Prp16 and Prp22 (Escherichia coli)	58	37	702
112	7	4519	5613	gi 135568	glucose-fructose oxidoreductase (Zymomonas mobilis) pfr A42289 A42289 glucose-fructose oxidoreductase (EC 1.1.1.-) reductase - Zymomonas mobilis	58	38	1095
114	6	7118	6503	gi 1377843	unknown (Bacillus subtilis)	58	38	816
143	2	2261	1395	gi A45605 A456	mature-parasite-infected erythrocyte surface antigen HESA - Plasmodium falciparum	58	31	867
151	2	717	950	gi 1370261	unknown (Mycobacterium tuberculosis)	58	31	234
154	6	6015	4627	gi 1209277	PCTHm1 gene product (Chlamydia trachomatis)	58	41	1389
154	16	14281	13541	gi 146613	DNA ligase (EC 6.5.1.2) (Escherichia coli)	58	39	741
155	3	2269	1892	gi 1303917	YqjB (Bacillus subtilis)	58	34	378
174	1	1056	539	gi 904198	hypothetical protein (Bacillus subtilis)	58	26	528
189	4	1533	1769	gi 467383	DNA binding protein (probable) (Bacillus subtilis)	58	25	237
201	3	2869	3307	gi 1511453	endonuclease III (Methanococcus jannaschii)	58	34	639
208	1	2	238	gi 1276729	phycobilisome linker polypeptide (Porphyra purpurea)	58	29	237
220	11	14575	13058	gi 397526	clumping factor (Staphylococcus aureus)	58	51	1518
231	3	1629	1474	gi 3002520	HutS (Bacillus subtilis)	58	45	156
233	6	4201	3497	gi 1463023	No definition line found (Caenorhabditis elegans)	58	39	705
243	10	9303	10082	gi 537207	ORF_277 (Escherichia coli)	58	32	780
257	1	331	1143	gi 1340128	ORF1 (Staphylococcus aureus)	58	44	813
302	2	460	801	gi 40174	ORF X (Bacillus subtilis)	58	34	342
307	31	6984	6127	gi 1303842	YqjU (Bacillus subtilis)	58	30	858
321	3	1914	2747	gi 1239996	hypothetical protein (Bacillus subtilis)	58	41	834
342	4	2724	3497	gi 456838	ORF 6; putative (Pseudomonas aeruginosa)	58	41	774
348	1	1	663	gi 467478	unknown (Bacillus subtilis)	58	36	663
401	2	384	605	gi 143407	para-aminobenzoic acid synthase, component 1 (pab) (Bacillus subtilis)	58	53	222

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
437	1	325	1554	gi 1303866	yqps [Bacillus subtilis]	58	35	1230
445	1	105	1442	gi 581583	protein A [Staphylococcus aureus]	58	32	1338
453	3	789	965	gi 1009455	unknown [Schizosaccharomyces pombe]	58	34	177
453	5	2748	2047	gi 537214	yjg gene product [Escherichia coli]	58	40	702
479	2	731	1444	gi 1256621	26.7% of identity in 165 aa to a Thermophilic bacterium hypothetical protein 6; putative [Bacillus subtilis]	58	36	714
490	1	909	547	gi 580920	rodd (gaa) polypeptide (AA 1-673) [Bacillus subtilis] pif 506048 506048 probable rodd protein - Bacillus subtilis sp P3484 PAGE_BACSU PROBABLE POLY(GLYCEROL-PHOSPHATE) LPH-GLUCOSYLTRANSFERASE (EC 2.4.1.52) (TECHNOIC ACID BIOSYNTHESIS ROBIN E1)	58	36	363
517	1	1	1164	sp P47264 Y018_	HYPOTHETICAL HELICASE MG018	58	30	1164
517	6	4182	4544	gi 453422	orf288 gene product [Mycoplasma hominis]	58	29	363
546	3	2802	4019	gi 886052	restriction modification system 5 subunit [Spiroplasma citri] gi 886052 restriction modification system 5 subunit [Spiroplasma citri]	58	37	1218
562	1	3	179	gi 41831	inf5 protein (AA 1-400) [Klebsiella pneumoniae]	58	34	177
600	2	1347	1156	gi 1181839	unknown [Pseudomonas aeruginosa]	58	48	192
604	2	1231	1001	gi 1001353	hypothetical protein [Synecocystis sp.]	58	41	231
619	1	1	504	gi 903748	integral membrane protein [Homo sapiens]	58	43	504
625	1	2	364	gi 1208474	hypothetical protein [Synecocystis sp.]	58	43	363
635	1	1492	755	gi 1510995	transaldolase [Methanococcus jannaschii]	58	41	738
645	1	1	846	gi 677882	ileal sodium-dependent bile acid transporter [Rattus norvegicus] gi 677882 ileal sodium-dependent bile acid transporter [Rattus norvegicus]	58	33	846
645	3	906	1556	gi 1239999	hypothetical protein [Bacillus subtilis]	58	41	651
665	1	771	532	gi 1204262	hypothetical protein (GB:U0128.61) [Haemophilus influenzae]	58	39	240
674	1	635	327	gi 498817	ORF8; homologous to small subunit of phage terminases [Bacillus subtilis]	58	39	309
675	2	1312	806	gi 42181	osac gene product [Escherichia coli]	58	28	507
745	1	618	310	gi 1205432	coenzyme PQQ synthesis protein III (pqqIII) [Haemophilus influenzae]	58	32	309
799	2	242	1174	gi 1204669	collagenase [Haemophilus influenzae]	58	36	933
800	2	1096	614	gi 171963	tRNA isopentenyl transferase [Saccharomyces cerevisiae] sp P07888 P005_YEAST tRNA ISOPENTENYLTRANSFERASE (EC 2.5.1.8) ISOPENTENYL-DIPHOSPHATE: tRNA ISOPENTENYLTRANSFERASE (IPP RANSEASE) (IPPT)	58	37	483

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
854	1	1108	605	gi 466778	lysine specific peptidase [Escherichia coli]	58	44	504
885	1	481	242	gi 861199	protoporphyrin IX Mg-chelatase subunit precursor [Hordaea vulgare]	58	33	240
891	1	3	527	gi 1293660	AbaA2 [Streptomyces coelicolor]	58	31	525
942	1	931	467	gi 405567	trnH [Plasmodium falciparum]	58	30	465
1002	1	952	521	gi 577649	proLUMK [Staphylococcus aureus]	58	34	432
1438	1	1	261	gi 581558	isoleucyl tRNA synthetase [Staphylococcus aureus] sp P41368 SYIP-STAAU ISOLEUCYL-TRNA SYNTHETASE, MUPIROICIN RESISTANT EC 6.1.1.51 (ISOLEUCINE--TRNA LIGASE) (ILERS) (MUPIROICIN RESISTANCE ROTENIN)	58	30	261
1442	1	2	463	gi 971394	similar to Acc No. D26185 [Escherichia coli]	58	34	462
1473	1	480	241	gi 1339951	small subunit of NADH-dependent glutamate synthase [Plectonoma boryanum]	58	38	240
1876	1	3	158	gi 529216	No definition line found [Caenorhabditis elegans] sp P46503 YLA7_CAREL HYPOTHETICAL 7.3 NO PROTEIN F3JF12.7 IN HRODSOME III	58	33	156
1989	1	108	401	gi 1405458	YneR [Bacillus subtilis]	58	29	394
2109	1	3	401	gi 1001801	hypothetical protein [Synecococcus sp.]	58	31	399
2473	1	288	145	gi 510140	lipoendopeptidase F [Lactococcus lactis]	58	38	144
2523	1	452	228	gi 644873	catabolic dehydroquinase dehydratase [Acinetobacter calcoaceticus]	58	37	225
3041	1	2	211	gi 1205367	oligopeptide transport ATP-binding protein [Haemophilus influenzae]	58	39	210
3094	1	3	263	gi 1185288	isochorismate synthase [Bacillus subtilis]	58	38	261
3706	1	3	383	gi 456614	mevalonate kinase [Arabidopsis thaliana]	58	48	381
3854	1	1	402	gi 808869	human gcp372 [Homo sapiens]	58	32	402
4082	1	51	224	gi 508551	ribulose-1,5 biphosphate carboxylase large subunit -methyltransferase [Pisum sativum]	58	37	174
4278	1	3	206	gi 180189	cerebellar-degeneration-related antigen (CDR34) [Homo sapiens] gi 182737 cerebellar degeneration-associated protein [Homo sapiens] p1r A29770 A29770 cerebellar degeneration-related protein - human	58	37	204
19	7	7818	7363	gi 1001516	hypothetical protein [Synecococcus sp.]	57	31	456
23	11	9663	8872	gi 606066	ORF_1256 [Escherichia coli]	57	29	792
31	1	4801	2402	gi 153146	ORF3 [Streptomyces coelicolor]	57	32	2400
38	14	11611	10796	gi 144859	ORF B [Clostridium perfringens]	57	31	816
46	14	112063	13046	gi 1001319	hypothetical protein [Synecococcus sp.]	57	25	984

TABLE 2

5 aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
51	3	1411	1187	gi 131856 B338	hypothetical 80K protein - <i>Bacillus sphaericus</i>	57	38	225
54	1	1	453	gi 684950	staphylococcal accessory regulator A [<i>Staphylococcus aureus</i>]	57	31	453
75	1	3	239	gi 1000470	C27B7.7 [<i>Caenorhabditis elegans</i>]	57	42	237
92	5	3855	3061	gi 143607	sporulation protein [<i>Bacillus subtilis</i>]	57	35	795
96	3	4006	4773	gi 144297	acetyl esterase (Xyc) [<i>Caldocellum saccharolyticum</i>] p1c B37202 B37202 acetyl esterase (EC 3.1.1.6) (Xyc) - <i>Caldocellum saccharolyticum</i>	57	34	768
107	3	1480	2076	gi 1460955	TagE [<i>Vibrio cholerae</i>]	57	42	597
109	8	5340	5933	gi 1438846	unknown [<i>Bacillus subtilis</i>]	57	41	594
112	9	6679	7701	gi 1468250	unknown [<i>Bacillus subtilis</i>]	57	33	1023
114	4	6384	4108	gi 1871456	putative alpha subunit of formate dehydrogenase [<i>Methanobacterium thermoautotrophicum</i>]	57	37	2277
126	2	430	1053	gi 288301	ORF2 gene product [<i>Bacillus megaterium</i>]	57	37	624
131	5	6537	6277	gi 1511160	M. jannaschii predicted coding region MJ1163 [<i>Methanococcus jannaschii</i>]	57	38	261
133	3	2668	2201	gi 1303912	YqjW [<i>Bacillus subtilis</i>]	57	40	468
133	4	3383	2784	gi 1221884	{urea?} amidolyase [<i>Mamophilus influenzae</i>]	57	37	600
147	4	2164	1694	gi 1467469	unknown [<i>Bacillus subtilis</i>]	57	33	471
160	2	1293	1060	gi 558604	Chitin synthase 2 [<i>Neurospora crassa</i>]	57	28	234
163	8	5687	4764	gi 145580	rarD gene product [<i>Bacillus coli</i>]	57	38	924
168	6	4336	5325	gi 139782	33kDa lipoprotein [<i>Bacillus subtilis</i>]	57	32	990
170	5	3297	3455	gi 1603404	Yer154p [<i>Saccharomyces cerevisiae</i>]	57	37	159
221	6	8026	6809	gi 1136221	carboxypeptidase [<i>Sulfolobus solfataricus</i>]	57	32	1218
228	3	1348	1791	gi 288969	fibronectin binding protein [<i>Streptococcus dysgalactiae</i>] p1c S33850 S33850 fibronectin-binding protein - <i>Streptococcus dysgalactiae</i>	57	32	444
263	4	4411	3686	gi 1185002	dihydrodipicolinate reductase [<i>Pseudomonas syringae</i> pv. tabaci]	57	42	726
276	1	494	255	gi 396380	No definition line found [<i>Escherichia coli</i>]	57	40	240
283	2	335	1324	gi 773349	B1A protein [<i>Bacillus subtilis</i>]	57	32	990
297	1	489	236	gi 1334820	reading frame V [<i>Cauliflower mosaic virus</i>]	57	46	234
342	3	1993	2805	gi 1204431	hypothetical protein (SP:P33644) [<i>Mamophilus influenzae</i>]	57	35	813

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
375	6	3340	3741	gi 385177	cell division protein [Bacillus subtilis]	57	26	402
433	6	3286	4011	gi 1524117	alpha-acetolactate decarboxylase [Lactococcus lactis]	57	40	726
470	3	903	1145	gi 804819	protein serine/threonine kinase [Toxoplasma gondii]	57	30	243
487	5	1391	1723	gi 507323	ORF1 [Bacillus stearothermophilus]	57	28	333
498	1	274	852	gi 1334549	IMAD-ubiquitinone oxidoreductase subunit 4L [Podospira anserina]	57	34	579
503	1	343	173	gi 1502283	organic cation transporter OCT2 [Rattus norvegicus]	57	30	171
505	2	1619	1284	gi 466884	B1496_C2_194 [Mycobacterium leprae]	57	40	336
519	2	1182	2549	gi 1303707	YrXH [Bacillus subtilis]	57	34	1368
522	2	3234	1945	gi 1064809	homologue to sp:HTRA_ECOLI [Bacillus subtilis]	57	36	1290
538	2	909	1415	gi 153179	phosphorothioic N-acetyltransferase [Streptomyces coelicolor] p1rJH0246JH0246 phosphothioic N-acetyltransferase (EC 2.3.1.-) Streptomyces coelicolor	57	40	507
547	1	968	486	gi 467340	unknown [Bacillus subtilis]	57	50	483
599	1	1062	532	sp P20692 TYRA_	PREPHENATE DEHYDROGENASE (EC 1.1.1.12) (PDR)	57	41	531
620	2	757	572	gi 1107894	unknown [Schizosaccharomyces pombe]	57	38	186
622	2	1600	1130	gi 173028	thiorodoxin II [Saccharomyces cerevisiae]	57	39	471
625	2	362	1114	gi 1262366	hypothetical protein [Mycobacterium leprae]	57	34	753
680	1	1	204	gi 143544	RNA polymerase sigma-30 factor [Bacillus subtilis] p1r/A28625/A28625 transcription initiation factor sigma H - actillus subtilis	57	30	204
690	1	3	629	gi 466520	pocr [Salmonella typhimurium]	57	29	627
696	1	2	433	gi 413972	ipa-48r gene product [Bacillus subtilis]	57	33	432
704	1	36	638	gi 1499931	M. jannaschii predicted coding region MJ1083 [Methanococcus jannaschii]	57	36	603
712	1	2316	1621	gi 1438999	orf4 [Lactobacillus sake]	57	37	696
746	1	451	227	gi 392973	Rab3 [Aplysia californica]	57	42	225
757	1	20	466	gi 43979	L. curvatus small cryptic plasmid gene for rep protein [Lactobacillus curvatus]	57	45	447
862	1	2	295	gi 1303827	Vqf1 [Bacillus subtilis]	57	21	294
1049	1	907	455	gi 1510108	ORF-1 [Agrobacterium tumefaciens]	57	35	453
1117	1	1387	695	gi 896286	HH2 terminus uncertain [Leishmania tarentolae]	57	28	693

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
1136	1	2	322	gi11303853	YggF [Bacillus subtilis]	57	38	321
1144	2	1033	611	gi11310083	voltage-activated calcium channel alpha-1 subunit [Rattus orvegicus]	57	46	423
1172	1	1472	738	gi11511146	H. jennaschii predicted coding region M114 [Methanococcus jannaschii]	57	28	735
1500	2	746	558	gi1142780	putative membrane protein; putative [Bacillus subtilis]	57	35	189
1676	1	659	399	gi11313777	uracil permease [Escherichia coli]	57	31	261
2481	1	2	400	gi11237015	ORF4 [Bacillus subtilis]	57	23	399
3099	1	3	230	gi11204540	isochlorimate synthase [Haemophilus influenzae]	57	39	228
3123	1	360	181	gi1882472	ORF_0464 [Escherichia coli]	57	40	180
3560	1	2	361	gi1153490	tetracycline C resistance and export protein [Streptomyces laevis]	57	37	360
3850	1	856	434	gi1155588	glucose-fructose oxidoreductase [Zymomonas mobilis] p1r[A42289]A42289	57	40	423
3931	1	704	354	gi1413953	glucose-fructose oxidoreductase (EC 1.1.1.88) [Pseudomonas mevalonii] p1r[A44756]A44756	57	36	351
3993	1	1	384	gi1151259	hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) [Pseudomonas sp.]	57	39	384
4065	1	793	398	gi11300377	nitrate reductase (EC 1.7.99.4) alpha chain - Escherichia coli	57	31	396
4100	1	596	300	gi11086633	T06C10.5 gene product [Caenorhabditis elegans]	57	47	297
4163	1	571	287	gi121512	polatin [Solanum tuberosum]	57	50	285
4267	2	631	335	gi11000365	Spotting [Bacillus subtilis]	57	38	297
4358	1	3	302	gi1298032	IEF [Streptococcus suis]	57	32	300
4389	2	108	290	gi1405894	1-phosphofructokinase [Escherichia coli]	57	37	183
4399	1	2	232	gi11481603	pristinamycin I synthase I [Streptomyces pristinaespiralis]	57	35	231
4481	1	572	288	gi1405879	yleH [Escherichia coli]	57	44	285
4486	1	512	258	gi1515938	glutamate synthase (ferredoxin) [Synchocystis sp.] p1r[S46957]S46957	57	42	255
4510	1	481	242	gi1205301	leukotoxin secretion ATP-binding protein [Haemophilus influenzae]	57	38	240
4617	1	468	256	gi1511222	restriction modification enzyme, subunit M1 [Methanococcus jannaschii]	57	35	213
4	11	12201	11524	gi1149204	histidine utilization repressor G [Klebsiella aerogenes] p1r[A36730]A36730	56	31	678
					hutG protein - Klebsiella pneumoniae (fragment) ep1p19452[HUTG_KLEAE			
					FORMINOGLUTAMINASE (EC 3.5.3.8) FORMINOGLUTAMINATE HYDROLASE (HISTIDINE			
					UTILIZATION PROTEIN G) FRAGMENT)			

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
22	8	4248	5177	gi11322222	RACH1 (Homo sapiens)	56	33	930
38	28	21179	22264	gi11480705	lipote-protein ligase (Mycoplasma capricolum)	56	34	1086
44	3	1863	2421	gi1490320	Y gene product (unidentified)	56	31	561
44	15	10103	10606	gi11203099	hypothetical protein (GB-L19201_1) (Haemophilus influenzae)	56	39	504
50	6	4820	5161	gi1209311	fiber protein (Human adenovirus type 5)	56	48	342
53	4	2076	2972	gi1623476	transcriptional activator (Providencia stuartii) sp P43463 AARP_PROST TRANSCRIPTIONAL ACTIVATOR AARP.	56	30	897
67	6	5656	6594	gi1466613	nikB (Escherichia coli)	56	32	939
89	3	2364	1810	gi1482322	protein with homology to pail repressor of B. subtilis (Lactobacillus elbrueckii)	56	39	555
96	1	203	913	gi1145594	cAMP receptor protein (crp) (Escherichia coli)	56	35	711
109	12	18250	17846	gi11204367	hypothetical protein (GB-U14003_278) (Haemophilus influenzae)	56	27	405
112	8	5611	6678	gi1155588	glucose-fructose oxidoreductase (Symononas mobilis) pfr A42289 A42289 glucose-fructose oxidoreductase (BC 1.1. -) recursor - Symononas mobilis	56	40	1068
131	3	6604	5100	gi1619724	MgtE (Bacillus firmus)	56	30	1305
138	2	65	232	gi1413948	ipa-24d gene product (Bacillus subtilis)	56	31	168
138	4	823	1521	gi1580868	ipa-22r gene product (Bacillus subtilis)	56	31	699
146	2	740	447	gi11046009	M. genitalium predicted coding region MG309 (Mycoplasma genitalium)	56	37	294
149	2	1639	1067	gi1945380	terminase small subunit (Bacteriophage L1-II)	56	35	573
163	1	2	223	gi1143947	glutamine synthetase (Bacteroides fragilis)	56	30	222
166	5	4745	6449	gi1405792	ORF154 (Pseudomonas putida)	56	26	297
187	1	31	393	gi1311237	H(+)-transporting ATP synthase (Zea mays)	56	30	363
190	1	2	373	gi11109686	ProX (Bacillus subtilis)	56	35	372
191	8	11538	9943	gi1581070	acyl coenzyme A synthetase (Escherichia coli)	56	35	1596
195	1	1291	647	gi11510242	collagenase (Methanococcus jannaschii)	56	34	645
230	3	2323	2072	gi140363	heat shock protein (Clostridium acetobutylicum)	56	39	252
238	5	3383	3775	gi11477533	sarA (Staphylococcus aureus)	56	31	393
270	2	813	1712	gi1765073	autolysin (Staphylococcus aureus)	56	41	900

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
290	1	3221	1632	gi 547513	orf3 (Haemophilus influenzae)	56	34	1590
297	5	1140	1373	gi 1511556	M. jannaschii predicted coding region M31561 (Methanococcus jannaschii)	56	40	234
321	2	2947	1799	gi 1001801	hypothetical protein (Synecocystis sp.)	56	31	1149
359	2	1279	641	gi 46336	mol1 gene product (Rhizobium meliloti)	56	26	639
371	2	360	1823	gi 145304	L-ribulokinase (Escherichia coli)	56	39	1464
391	4	1762	2409	gi 1001634	hypothetical protein (Synecocystis sp.)	56	34	648
402	1	380	192	gi 1438904	5-HT4L receptor (Homo sapiens)	56	48	189
416	4	2480	2109	gi 1408486	HS74A gene product (Bacillus subtilis)	56	31	372
424	3	1756	2334	gi 142471	acetolactate decarboxylase (Bacillus subtilis)	56	32	579
457	1	1907	1017	gi 1205194	formamidopyrimidine-DNA glycosylase (Haemophilus influenzae)	56	36	891
458	2	2423	1812	gi 15466	terminase (Bacteriophage SP1)	56	37	612
504	2	2152	1283	gi 1142681	lpp38 (Pseudomonas haemolytica)	56	38	870
611	1	1	1284	gi 217049	brnQ protein (Salmonella typhimurium)	56	37	1284
604	3	1099	1701	gi 467109	r1m: 30S ribosomal protein S18 alanine acetyltransferase: 229_CL170 (Mycobacterium leprae)	56	43	603
660	5	3547	3774	gi 1229106	ZK930.1 (Caenorhabditis elegans)	56	30	228
707	1	35	400	gi 153929	NADPH-sulfite reductase flavoprotein component (Salmonella typhimurium)	56	38	366
709	2	1385	1095	gi 1510801	hydrogenase accessory protein (Methanococcus jannaschii)	56	38	291
718	1	1	495	gi 413948	lpa-24d gene product (Bacillus subtilis)	56	35	495
744	1	87	677	gi 928836	repressor protein (Lactococcus lactis phage BK5-7)	56	35	591
790	1	776	399	gi 1511513	ABC transporter, probable ATP-binding subunit (Methanococcus jannaschii)	56	31	378
795	1	3	407	gi 1205382	cell division protein (Haemophilus influenzae)	56	34	405
813	1	19	930	gi 1222161	permease (Haemophilus influenzae)	56	28	912
855	1	3	515	gi 1256621	26.7% of identity in 165 aa to a Thermophilic bacterium hypothetical protein 6, putative (Bacillus subtilis)	56	33	513
968	1	2	466	gi 547513	orf3 (Haemophilus influenzae)	56	37	465
973	2	1049	732	gi 886022	HexR (Pseudomonas aeruginosa)	56	31	318
1203	1	5	223	gi 184251	HHG-1 (Homo sapiens)	56	34	219

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1976	1	452	237	gi 9806	lysine-rich aspartic acid-rich protein [Plasmodium chabaudi] r[S22183]S22183 lysine/aspartic acid-rich protein - Plasmodium baud	56	33	216
2161	1	2	400	gi 1237015	ORF4 [Bacillus subtilis]	56	27	399
2958	1	362	183	gi 466685	No definition line found [Escherichia coli]	56	26	180
2979	1	421	212	gi 1206354	spore germination and vegetative growth protein [Haemophilus influenzae]	56	40	210
2994	2	526	326	gi 836646	phosphoribosylformino-praic ketolase [Rhodobacter phaeoides]	56	29	201
3026	1	179	328	gi 143106	penicillin V amidase [Bacillus sphaericus]	56	30	150
3189	1	289	146	gi 1166604	Similar to aldehyde dehydrogenase [Caenorhabditis elegans]	56	37	144
3770	1	63	401	gi 1125145	acetyl-CoA C-acyltransferase [Mangifera indica]	56	43	339
4054	2	720	361	gi 1205355	Na+/H+ antiporter [Haemophilus influenzae]	56	31	360
4145	1	1	324	gi 726095	long-chain acyl-CoA dehydrogenase [Mus musculus]	56	36	324
4200	1	505	254	gi 155588	glucose-fructose oxidoreductase [Zymomonas mobilis] pir[A42289]A42289 glucose-fructose oxidoreductase [EC 1.1.1.-] recurzor - Zymomonas mobilis	56	40	252
4273	1	575	355	gi 308861	OTG start codon [Lactococcus lactis]	56	33	321
1	3	4095	3436	gi 5341	Putative orf YCLM8c, len:192 [Saccharomyces cerevisiae] r[S53591]S53591 hypothetical protein - yeast [Saccharomyces evisiae]	55	25	660
11	12	9377	8505	gi 216773	haloacetate dehalogenase H-1 [Moraxella sp.]	55	32	873
12	4	5133	4534	gi 467337	unknown [Bacillus subtilis]	55	26	600
19	5	5404	5844	gi 1001719	hypothetical protein [Synchocystis sp.]	55	25	441
23	13	14087	12339	gi 474190	lucA gene product [Escherichia coli]	55	30	1749
32	7	5368	6888	gi 1340086	unknown [Mycobacterium tuberculosis]	55	37	1521
34	3	2569	1808	gi 1303968	YqjQ [Bacillus subtilis]	55	39	762
34	5	3960	3412	gi 1303962	YqjK [Bacillus subtilis]	55	33	549
36	1	1291	647	gi 606045	ORF_0118 [Escherichia coli]	55	27	645
36	6	6220	5243	gi 1001341	hypothetical protein [Synchocystis sp.]	55	31	978
47	3	3054	3821	gi 1001819	hypothetical protein [Synchocystis sp.]	55	21	768
49	1	2065	1127	gi 403373	glycerophosphoryl diester phosphodiesterase [Bacillus subtilis] pir[SJ7251]SJ7251 glycerophosphoryl diester phosphodiesterase - acillus subtilis	55	36	939

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match	% sim	% ident	length (nt)
67	11	8966	9565	gi 151053	norA199 protein [Staphylococcus aureus]	55	23	600
75	3	881	1273	gi 1698	L-histidinol: NAD ⁺ oxidoreductase [EC 1.1.1.23] (aa 1-434) [Escherichia coli]	55	33	393
82	9	15387	14196	gi 136221	carboxypeptidase [Sulfolobus solfataricus]	55	35	1194
87	4	3517	4917	gi 1064812	function unknown [Bacillus subtilis]	55	26	1401
88	2	1172	1636	gi 882463	protein-[(p)]-phosphotransferase [Escherichia coli]	55	35	465
92	1	127	516	gi 1377832	unknown [Bacillus subtilis]	55	36	390
100	2	836	2035	gi 1170274	isoxanthin epoxidase [Nicotiana glauca]	55	36	1200
100	5	5137	4658	gi 396660	unknown open reading frame [Buchnera aphidicola]	55	29	480
108	3	4266	2986	gi 149866	[M. jannaschii] predicted coding region MJ1024 [Methanococcus jannaschii]	55	31	1381
114	3	2616	1834	gi 1511367	formate dehydrogenase, alpha subunit [Methanococcus jannaschii]	55	29	783
144	3	1805	1476	gi 1100787	unknown [Saccharomyces cerevisiae]	55	35	310
165	5	6212	5508	gi 1045884	[M. genitalium] predicted coding region MG199 [Mycoplasma genitalium]	55	27	705
189	5	2205	2576	gi 143569	ATP synthase a subunit [Bacillus firmus]	55	35	372
191	6	9136	6857	gi 559411	B0272.3 [Caenorhabditis elegans]	55	39	2280
194	2	364	636	gi 1145768	K7 kinase-like protein [Dictyostelium discoideum]	55	34	273
209	4	1335	1676	gi 1473357	thi4 gene product [Schizosaccharomyces pombe]	55	37	549
211	2	1693	1145	gi 410130	ORF6 [Bacillus subtilis]	55	28	729
213	2	844	1372	gi 633692	Tran [Yersinia enterocolitica]	55	35	342
214	7	4144	5481	gi 1001793	hypothetical protein [Synchocystis sp.]	55	30	1318
221	7	11473	9197	gi 1466520	pocR [Salmonella typhimurium]	55	32	2277
233	8	5908	4817	gi 1237063	unknown [Mycobacterium tuberculosis]	55	38	1092
236	4	1375	2340	gi 1146199	putative [Bacillus subtilis]	55	32	966
243	2	380	1885	gi 1459907	mercuric reductase [Plasmodium falciparum]	55	29	1506
258	1	786	394	gi 1455006	orf6 [Rhodococcus fascians]	55	36	393
281	1	126	938	gi 1408493	homologous to SwissProt:YDA_ECOLI hypothetical protein [Bacillus subtilis]	55	35	813
316	3	1323	2102	gi 1486447	[LuxA homologue [Rhizobium sp.]	55	30	780
326	5	2968	2744	gi 1296824	proline iminopeptidase [Lactobacillus helveticus]	55	36	225

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	mdtqh gene name	% sim	% ident	length (nt)
351	2	2322	1429	gi11204820	hydrogen peroxide-inducible activator (Haemophilus influenzae)	55	28	894
353	4	2197	2412	gi11272475	chitin synthase (Emicella nidulans)	55	50	216
380	1	14	379	gi1142554	ATP synthase 1 subunit (Bacillus megaterium)	55	37	366
383	1	462	232	gi1189272	ferrichrome-binding protein (Bacillus subtilis)	55	36	231
386	1	3	938	gi11510251	DNA helicase, putative (Methanococcus jannaschii)	55	30	936
410	2	1208	1891	gi11205144	multidrug resistance protein (Haemophilus influenzae)	55	27	684
483	2	411	833	gi1113934	ipa-10r gene product (Bacillus subtilis)	55	26	423
529	3	1777	1433	gi11606150	ORF_309 [Escherichia coli]	55	33	345
555	1	1088	585	gi1143407	para-aminobenzoic acid synthase, component 1 (pab) (Bacillus subtilis)	55	28	504
555	1	402	202	gi11223961	CDP-tylase epimerase (Yersinia pseudotuberculosis)	55	41	201
582	1	751	452	gi11256643	20.2% identity with NADH dehydrogenase of the Leishmania major mitochondrion; putative (Bacillus subtilis)	55	36	300
645	5	2260	2057	gi1210824	fusion protein F (Bovine respiratory syncytial virus) p1r-J01481 VQNZBA (fusion glycoprotein precursor - bovine respiratory syncytial virus (strain A51908))	55	25	204
672	2	957	2216	gi11511333	M. jannaschii predicted coding region M3122 (Methanococcus jannaschii)	55	36	1260
730	1	955	479	gi11537007	ORF_379 [Escherichia coli]	55	30	477
737	1	1859	945	gi11536963	CG Site No. 18166 [Escherichia coli]	55	30	915
742	2	228	572	gi1304160	product unknown (Bacillus subtilis)	55	38	345
817	2	1211	903	gi11136289	histidine kinase A (Dictyostelium discoideum)	55	29	309
819	1	582	355	gi11558073	polymorphic antigen (Plasmodium falciparum)	55	22	228
832	2	1152	724	gi140367	ORF [Clostridium acetobutylicum]	55	32	429
840	1	769	386	gi11205875	pseudouridylylase synthase 1 (Haemophilus influenzae)	55	39	384
1021	1	23	529	gi148563	beta-lactamase (Yersinia enterocolitica)	55	38	507
1026	1	60	335	gi147804	Opp C (AM-301) (Salmonella typhimurium)	55	26	276
1525	1	1	282	gi11477533	sarA (Staphylococcus aureus)	55	29	282
1814	2	224	985	gi11046078	M. genitalium predicted coding region M3169 (Mycoplasma genitalium)	55	38	762
3254	1	427	254	gi11413968	ipa-44d gene product (Bacillus subtilis)	55	30	174

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	length (nt)
3695	1	686	345	gi 216773	haloacetate dehalogenase H-1 [Moraxella sp.]	55	32	342
3721	1	1	312	gi 42029	ORF1 gene product [Escherichia coli]	55	31	312
3799	1	3	272	gi 42029	ORF1 gene product [Escherichia coli]	55	38	270
3889	1	22	423	gi 1129145	acetyl-CoA C-acyltransferase [Mangifera indica]	55	45	402
3916	1	2	385	gi 529754	apoc [Streptococcus pyogenes]	55	38	384
3945	1	4	198	gi 476252	phase 1 flagellin [Salmonella enterica]	55	36	195
4074	1	488	246	gi 42029	ORF1 gene product [Escherichia coli]	55	38	243
4184	1	2	343	gi 1524267	unknown [Mycobacterium tuberculosis]	55	28	342
4284	1	14	208	gi 1100774	ferredoxin-dependent glutamate synthase [Synechocystis sp.]	55	36	195
4457	2	644	378	gi 180189	cerebellar-degeneration-related antigen (CDR14) [Homo sapiens] gi 182737 cerebellar degeneration-associated protein [Homo sapiens] pir A29770 A29770 cerebellar degeneration-related protein - human	55	38	267
4514	1	2	244	gi 216773	haloacetate dehalogenase H-1 [Moraxella sp.]	55	32	243
4599	1	432	217	gi 1129145	acetyl-CoA C-acyltransferase [Mangifera indica]	55	42	216
4606	1	416	210	gi 386120	myosin alpha heavy chain (S2 subfragment) [rabbits, masseter, epitide Partial, 234 aa]	55	27	207
5	8	5348	4932	gi 536069	ORF VBL047c [Saccharomyces cerevisiae]	54	27	417
12	7	7166	6165	gi 1205504	homoserine acetyltransferase [Haemophilus influenzae]	54	30	1002
23	16	17086	15326	gi 474192	lucC gene product [Escherichia coli]	54	31	1761
35	1	2	979	gi 48034	small subunit of soluble hydrogenase (AA 1-384) [Synechococcus sp.] ir S06919 HQVCS soluble hydrogenase (BC 1.12.-.-) small chain - nechococcus sp. (PCC 6716)	54	36	978
37	11	9437	8667	gi 537207	ORF f277 [Escherichia coli]	54	38	771
37	12	8165	8132	gi 1160967	palmitoyl-protein thioesterase [Homo sapiens]	54	37	168
46	15	13025	11804	gi 438473	protein is hydrophobic, with homology to E. coli Prow, putative bacillus subtilis	54	28	780
56	2	203	736	gi 1256139	YbbJ [Bacillus subtilis]	54	34	534
57	13	11117	10179	gi 1151248	inosine-uridine preferring nucleoside hydrolase [Crithidia fasciculata]	54	32	939
66	2	516	1133	gi 1335781	Cap [Drosophila melanogaster]	54	29	618
70	10	8116	8646	gi 1399823	PhoE [Rhizobium meliloti]	54	31	531

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
70	15	12556	11801	[sp P02983 TCR_5	TETRACYCLINE RESISTANCE PROTEIN.	54	29	756
87	5	4915	5706	[gi 1064811	function unknown [Bacillus subtilis]	54	33	792
92	4	3005	2289	[gi 1205366	oligopeptide transport ATP-binding protein [Haemophilus influenzae]	54	31	717
103	2	2596	1556	[gi 710495	protein kinase [Bacillus brevis]	54	33	1041
105	2	3585	2095	[gi 143727	putative [Bacillus subtilis]	54	30	1491
112	4	2317	2712	[gi 153724	[HaC [Streptococcus pneumoniae]	54	41	396
127	2	1720	2493	[gi 144297	acetyl esterase [XyNC] [Caldocellum saccharolyticum] pir[B7202 B7202	54	34	774
					acetyl esterase (EC 3.1.1.6) [XyNC] - Caldocellum saccharolyticum			
138	5	1600	3306	[gi 42473	pyruvate oxidase [Escherichia coli]	54	36	1707
152	2	525	1172	[gi 1377834	unknown [Bacillus subtilis]	54	23	648
161	9	4831	5469	[gi 903305	[ORF73 [Bacillus subtilis]	54	28	639
161	13	6694	7251	[gi 1511039	phosphate transport system regulatory protein [Methanococcus jannaschii]	54	32	558
164	6	1263	4543	[gi 1204976	[prolyl-L-lysine synthetase [Haemophilus influenzae]	54	34	1281
164	120	21602	22243	[gi 143582	[spolIIEA protein [Bacillus subtilis]	54	32	642
171	6	5683	4250	[gi 436965	[malA] gene products [Bacillus stearothermophilus] pir[S43914 S43914	54	37	1434
					hypothetical protein 1 - Bacillus stearothermophilus			
206	18	19208	19720	[gi 1240016	R09E10.3 [Caenorhabditis elegans]	54	38	533
218	2	1090	1905	[gi 467378	unknown [Bacillus subtilis]	54	26	816
220	1	1322	663	[gi 1353761	myosin II heavy chain [Naegleria fowleri]	54	22	660
220	13	12655	13059	[pir S00485 S004	gene 11-1 protein precursor - Plasmodium falciparum (fragments)	54	35	405
221	3	2030	3709	[gi 1303813	[yqew [Bacillus subtilis]	54	34	1680
272	7	5055	4219	[gi 62964	arylamine N-acetyltransferase (AA 1-290) [Gallus gallus] ir[S06652 YVCH23	54	33	837
					arylamine N-acetyltransferase (EC 2.3.1.5) (clone NAT-3) - chicken			
316	7	4141	4701	[gi 682769	[mccE gene product [Escherichia coli]	54	31	561
316	10	6994	8742	[gi 413951	[ipa-27d gene product [Bacillus subtilis]	54	28	1749
338	3	3377	2214	[gi 490328	[LORF F [unidentified]	54	28	1164
341	4	3201	3614	[gi 171959	[myosin-like protein [Saccharomyces cerevisiae]	54	25	416

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
146	1	1820	912	gi1396400	similar to eukaryotic Na ⁺ /H ⁺ exchangers [Escherichia coli] sp P32703 YJCE_ECOLI_HYPOTHETICAL 60.5 KD PROTEIN IN SOYB-ACS HYPERGENIC REGION (0549)	54	34	909
348	2	623	1351	gi1537109	ORF_343a [Escherichia coli]	54	34	729
378	2	1007	1942	sp P02983 TCR_S	TETRACYCLINE RESISTANCE PROTEIN	54	31	936
408	6	4351	5301	gi1474190	lucA gene product [Escherichia coli]	54	29	951
444	9	7934	8854	gi1216267	ORF2 [Bacillus megaterium]	54	32	921
463	2	2717	2229	gi104160	product unknown [Bacillus subtilis]	54	50	489
502	2	1696	1133	gi1205015	hypothetical protein (SP.P10120) [Haemophilus influenzae]	54	38	564
505	6	6262	5357	gi1500558	12-hydroxyhepta-2,4-diene-1,7-dioate isomerase [Methanococcus jannaschii]	54	41	906
550	1	2736	1522	gi140100	rodC (tag3) polypeptide (AA 1-746) [Bacillus subtilis] tr S06049 S06049 rodC protein - Bacillus subtilis p P13485 TAGP_BACSU TECHOIC ACID BIOSYNTHESIS PROTEIN F	54	35	1215
551	5	3305	4279	gi1950197	unknown [Corynebacterium glutamicum]	54	34	975
558	2	1356	958	gi1485090	No definition line found [Caenorhabditis elegans]	54	32	399
580	1	91	936	gi1311906	fused envelope glycoprotein precursor [Friend spleen focus-forming virus]	54	45	846
603	3	554	757	gi1323423	ORF YCR234w [Saccharomyces cerevisiae]	54	36	204
617	1	25	249	gi1219959	ornithine transcarbamylase [Homo sapiens]	54	40	225
622	3	1097	1480	gi1303873	YqoZ [Bacillus subtilis]	54	25	384
623	1	3	404	gi1063250	low homology to P20 protein of Bacillus licheniformis and bleomycin acetyltransferase of Streptomyces verticillius [Bacillus subtilis]	54	45	402
689	1	1547	1011	gi1552446	NADH dehydrogenase subunit 4 [Apis mellifera ligustica] pir S52968 S52968 NADH dehydrogenase chain 4 - honeybee mitochondrion (SCC4)	54	30	537
725	2	686	1441	gi1987096	sensory protein kinase [Streptomyces hygroscopicus]	54	26	756
956	1	1	249	pir S30782 S307	Integrin homolog - yeast [Saccharomyces cerevisiae]	54	24	249
978	2	1137	859	gi1301994	ORF YML091w [Saccharomyces cerevisiae]	54	33	279
1314	1	3	281	gi1001108	hypothetical protein [Synecocystis sp.]	54	33	279
2450	1	1	228	gi1045057	ch-700 [Homo sapiens]	54	32	228
2934	1	1	387	gi1580870	ipa-37d qosa gene product [Bacillus subtilis]	54	36	387
2970	1	499	251	sp P3734P YECE_	HYPOTHETICAL PROTEIN IN ASP5 5' REGION (FRAGMENT)	54	42	249

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3002	1	1	309	gi 44027	Tna protein [Lactococcus lactis]	54	33	309
3561	1	9	464	gi 151259	HMG-CoA reductase (EC 1.1.1.86) [Pseudomonas mevalonii] pir A44756 A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.86) Pseudomonas sp.	54	35	456
3572	1	72	401	gi 450688	hadM gene of Ecoprr1 gene product [Escherichia coli] pir S38437 S38437 hadM protein - Escherichia coli pir S09629 S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	54	36	330
3829	1	798	400	gi 1322245	mevalonate pyrophosphate decarboxylase [Rattus norvegicus]	54	29	399
3809	1	1	273	gi 29865	CENP-E (Homo sapiens)	54	30	273
3921	1	3	209	pir S24325 S243	glucan 1,4-beta-glucosidase (EC 3.2.1.74) - Pseudomonas fluorescens subsp. cellulosa	54	34	207
4438	1	566	285	gi 1196657	unknown protein [Mycoplasma pneumoniae]	54	30	282
4459	1	3	272	gi 1046081	hypothetical protein (CB:D26185_10) [Mycoplasma genitalium]	54	38	270
4564	1	3	221	gi 216267	ORF2 [Bacillus megaterium]	54	38	219
23	12	12538	10685	gi 474192	lucC gene product [Escherichia coli]	53	35	1854
23	14	14841	13579	gi 42029	ORF1 gene product [Escherichia coli]	53	32	1263
24	3	4440	3940	gi 1369947	ic2 gene product [Bacteriophage 81]	53	36	501
26	4	3818	4618	gi 1486247	unknown [Bacillus subtilis]	53	37	801
38	6	2856	3998	gi 405880	lye1 [Escherichia coli]	53	40	1143
38	10	9380	7806	gi 1399954	thyroid sodium/iodide symporter NIS [Rattus norvegicus]	53	29	1575
56	10	12324	12100	pir A54592 A545	110K actin filam. associated protein - chicken	53	32	225
57	6	5047	4583	pir A00341 DE2P	alcohol dehydrogenase (EC 1.1.1.1) - fission yeast (Schizosaccharomyces pombe)	53	39	465
57	12	10515	8932	gi 480429	putative transcriptional regulator [Bacillus stearothermophilus]	53	30	1584
67	12	9496	10218	gi 1511555	quinolone resistance norA protein protein [Methanococcus jamaehilli]	53	31	723
69	3	3125	2382	gi 1687017	arabinogalactan-protein, AGP [Nicotiana glauca, cell-suspension culture filtrate, Peptide, 461 aa]	53	30	744
79	1	3	1031	gi 1523802	glucanase [Anabaena variabilis]	53	32	1029
80	1	673	338	gi 452428	ATPase 3 [Plasmodium falciparum]	53	36	336
88	4	1910	2524	gi 137034	ORF_0488 [Escherichia coli]	53	25	615
88	5	2467	3282	gi 537034	ORF_0488 [Escherichia coli]	53	29	816

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match	Accession	Match gene name	% sim	% ident	Length (nt)
92	8	5870	5505	gi 399598	amphotropic murine retrovirus receptor [Rattus norvegicus]		53	33	366
94	5	4417	3239	gi 173038	tropomyosin (TPM) [Saccharomyces cerevisiae]		53	25	1179
99	5	4207	5433	sp P28246 BCR_E	BICYCLOMYCIN RESISTANCE PROTEIN (SULFONAMIDE RESISTANCE PROTEIN)		53	30	1227
120	3	1639	2262	gi 576655	ORF1 [Vibrio anguillarum]		53	35	624
120	11	7257	8897	gi 1524397	glycine betaine transporter Opd [Bacillus subtilis]		53	33	1641
127	6	6893	5685	gi 1256630	putative [Bacillus subtilis]		53	32	1209
147	2	255	557	gi 581648	epia gene product [Staphylococcus epidermidis]		53	34	303
158	4	4705	4256	gi 151004	musoidy regulatory protein Alor [Pseudomonas aeruginosa] pIr[A32802 A32802 regulatory protein alor - Pseudomonas aeruginosa sp P26275 ALCR_PSEAE POSITIVE ALGINATE BIOSYNTHESIS REGULATORY PROTEIN		53	32	450
171	7	5717	5421	gi 1510669	hypothetical protein (GP-D64044_18) [Methanococcus jannaschii]		53	34	297
191	9	13087	11483	gi 298085	acetoacetate decarboxylase [Clostridium acetobutylicum] pIr[B49346 B49346 butyrate-acetoacetate CoA-transferase (EC 8.3.9) small chain - Clostridium acetobutylicum sp P33752 CTFA_CLOAB BUTYRATE-ACETOACETATE COA-TRANSFERASE SUBUNIT (EC 2.8.3.9) (COAT A)		53	31	1605
203	5	3763	4326	gi 143456	ipoB protein (ctg start codon) [Bacillus subtilis]		53	29	564
206	17	18204	18971	gi 304136	acetylglutamate kinase [Bacillus stearothermophilus] sp Q07905 ARGB_BACST ACETYLGLUTAMATE KINASE (EC 2.7.2.8) (NAG INASE) (AGK) [N-ACETYL-L-GLUTAMATE 5-PHOSPHOTRANSFERASE]		53	36	768
212	10	4021	4221	gi 9478	protein kinase [Plasmodium falciparum]		53	28	201
231	2	1580	1350	gi 537506	paramyosin [Dirofilaria immitis]		53	34	231
272	6	2719	3249	pIr A33141 A331	hypothetical protein (gcfD 3' region) - Streptococcus mutans		53	34	531
308	3	927	2576	gi 606232	ORF_0696 [Escherichia coli]		53	33	1650
320	7	5645	5884	gi 160596	RNA polymerase III largest subunit [Plasmodium falciparum] sp P27625 RPC1_PLAFA DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT (EC 2.7.7.6)		53	33	240
327	1	218	901	gi 854601	unknown [Schizosaccharomyces pombe]		53	31	684
341	2	212	2500	gi 1633732	ORF1 [Campylobacter jejuni]		53	31	2289
351	1	763	383	sp P31675 VABM	HYPOTHETICAL 42.7 KD PROTEIN IN TBPA-LEUD INTERGENIC REGION (ORF104)		53	32	381
433	7	5087	4731	gi 1001561	MHC class II analog [Staphylococcus aureus]		53	30	357
454	2	1240	980	pIr A60328 A603	40K cell wall protein precursor (sr 5' region) - Streptococcus mutans (strain ONZ175, serotype f)		53	27	261

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S. aureus - Putative coding regions of novel proteins similar to known proteins

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470	4	1123	1761	gi 516826	rat GCP360 (Rattus rattus)	53	30	639
483	1	432	217	gi 1480429	putative transcriptional regulator (Bacillus stearothermophilus)	53	33	216
544	1	516	1259	gi 46587	ORF 1 (AA 1 - 121) (1 is 2nd base in codon) (Staphylococcus aureus) ir S15765 S15765 hypothetical protein 1 (hib 5' region) - apylococcus aureus (fragment)	53	38	744
558	10	3957	3754	gi 15140	res gene (Bacteriophage P1)	53	32	200
603	2	339	620	gi 507738	Hmp (Vibrio parahaemolyticus)	53	26	282
693	1	1669	941	gi 153123	toxic shock syndrome toxin-1 precursor (Staphylococcus aureus) pir A24606 XCSAS1 toxic shock syndrome toxin-1 precursor - taphylococcus aureus	53	38	729
766	1	2	673	gi 687600	orfA2: orfA2 forms an operon with orfA1 (Listeria monocytogenes)	53	43	672
781	1	667	335	gi 1204551	pillin biogenesis protein (Haemophilus influenzae)	53	26	333
801	1	3	545	gi 1279400	SapA protein (Escherichia coli)	53	25	543
803	1	2	910	gi 695278	lipase-like enzyme (Alcaligenes eutrophus)	53	30	909
872	1	1177	590	gi 298032	EP (Streptococcus suis)	53	30	588
910	1	2	184	gi 1044936	unknown (Schizosaccharomyces pombe)	53	29	183
943	1	794	399	gi 390508	similar to unidentified ORF near 47 minutes (Escherichia coli) sp P31436 YICK_ECOLI HYPOTHETICAL 43.5 KD PROTEIN IN SELC-HLPA HYPERGENIC REGION	53	30	396
988	1	1004	504	gi 142441	ORF 3; putative (Bacillus subtilis)	53	28	501
1064	1	3	434	gi 305080	myosin heavy chain (Entamoeba histolytica)	53	26	432
1366	1	3	452	gi 308852	transmembrane protein (Lactococcus lactis)	53	33	450
1758	1	792	397	gi 1001774	hypothetical protein (Synecocystis sp.)	53	30	396
1897	1	1	447	gi 1303949	YqjX (Bacillus subtilis)	53	27	447
2381	1	798	400	gi 1146243	22.4% identity with Escherichia coli DNA-damage inducible protein ... putative (Bacillus subtilis)	53	37	399
3537	1	1	327	gi 450688	hscdm gene of Ecoprt gene product (Escherichia coli) pir S18437 S18437 hscdm protein - Escherichia coli pir S09623 S09623 hypothetical protein A - Escherichia coli (S08 40-520)	53	35	327
3747	2	137	397	gi 1477486	transposase (Burkholderia cepacia)	53	53	261
11	5	3049	3441	gi 868224	No definition line found (Caenorhabditis elegans)	52	33	393

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
15	5	2205	2369	gi 215966	G41 protein (gag start codon) [Bacteriophage T4]	52	34	165
19	3	2429	3808	gi 1205379	UDP-murac-pentapeptide synthetase [Haemophilus influenzae]	52	31	1380
24	1	6920	3462	gi 579124	predicted 86.4kd protein; 52kd observed [Mycobacteriophage L5] p1r[530971]530971 gene 26 protein - Mycobacterium phage L5 sp Q05233 Q05233 BPML5 MINOR TAIL PROTEIN GP26. (SUB 2-837)	52	32	3459
37	5	3015	3935	gi 1500543	P115 protein [Methanococcus jannaschii]	52	25	921
38	13	8795	9703	gi 46851	glucose kinase [Streptomyces coelicolor]	52	29	909
44	16	10617	11066	gi 42012	moaE gene product [Escherichia coli]	52	36	450
46	1	3	521	gi 1040957	NADH dehydrogenase subunit 6 [Anopheles trinkae]	52	25	519
51	110	5531	6280	gi 388269	traC [Pseudomonas]	52	32	750
56	5	3968	2826	gi 181949	endothelial differentiation protein (edg-1) [Homo sapiens] p1r[A35300]A35300 G protein-coupled receptor edg-1 human sp P21453 P21453 HUMAN PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.	52	23	1143
57	5	4850	4173	gi 304153	sorbitol dehydrogenase [Bacillus subtilis]	52	27	678
62	5	3364	2870	gi 1072399	phaE gene product [Rhizobium meliloti]	52	25	495
62	6	4445	3651	gi 46485	NADH dehydrogenase [Synecococcus PCC7942]	52	27	795
67	14	11355	12962	gi 1511365	glutamate synthase (NADPH), subunit alpha [Methanococcus jannaschii]	52	30	1608
67	21	16935	18158	gi 1204393	hypothetical protein (SP:P1122) [Haemophilus influenzae]	52	25	1224
70	4	2185	1997	gi 7227	cytoplasmic dynein heavy chain [Dictyostellium discoideum] r[A44357]A44357 dynein heavy chain, cytosolic - slime mold cytoskeleton [dictyostellium]	52	36	189
96	10	10005	10664	gi 1408485	B650 gene product [Bacillus subtilis]	52	26	660
103	5	3986	3351	gi 1009368	respiratory nitrate reductase [Bacillus subtilis]	52	42	636
109	3	4102	3350	gi 699274	lmbE gene product [Mycobacterium leprae]	52	39	753
109	19	15732	17300	gi 1526981	amino acid permease YeeP like protein [Salmonella typhimurium]	52	30	1569
121	3	1412	981	gi 72931	unknown [Saccharomyces cerevisiae]	52	32	432
125	3	865	1680	gi 1296975	puT gene product [Porphyromonas gingivalis]	52	38	816
130	2	659	1807	gi 1256634	25.8% identity over 120 aa with the Synecococcus sp. HpeV protein; putative [Bacillus subtilis]	52	36	1149
149	1	1164	583	gi 1225943	P86X terminase [Bacillus subtilis]	52	33	582
149	14	4687	4415	gi 1510368	M. jannaschii predicted coding region M2072 [Methanococcus jannaschii]	52	35	273

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
167	1	216	1001	gi 146025	cell division protein [Escherichia coli]	52	43	786
188	1	120	1256	gi 474915	orf 337; translated orf similarity to SM: BCR-ECOLI bicyclomycin resistance protein of Escherichia coli [Coxiella burnetii] pir S44207 S44207 hypothetical protein 337 - Coxiella burnetii (SUB-338)	52	26	1137
195	9	9161	8760	gi 1028	mitochondrial outer membrane 72K protein [Neurospora crassa] r A36882 A36882 72K mitochondrial outer membrane protein - Neurospora crassa	52	25	402
200	3	2065	2607	gi 142439	ATP-dependent nuclease [Bacillus subtilis]	52	35	543
203	4	2776	3684	gi 1303698	BitD [Bacillus subtilis]	52	25	909
227	8	5250	5651	gi 305080	myosin heavy chain [Entamoeba histolytica]	52	24	402
242	1	21	1424	gi 1060877	[BcrV] [Escherichia coli]	52	32	1404
249	5	4526	4753	pir C37222 C372	cytochrome P450 1A1, hepatic - dog (fragment)	52	21	228
255	1	2107	1055	gi 143290	penicillin-binding protein [Bacillus subtilis]	52	28	1053
276	7	3963	3664	gi 1001610	hypothetical protein [Synchocystis sp.]	52	30	300
276	8	4456	4055	gi 416235	orf L3 [Mycoplasma capricolum]	52	26	402
289	2	1856	1449	gi 150900	OTF phosphohydrolase [Proteus vulgaris]	52	34	408
325	1	1	279	gi 1204874	polypeptide deformylase (formylmethionine deformylase) [Haemophilus influenzae]	52	33	279
340	1	2017	1010	gi 1215695	peptide transport system protein SapF homolog; SapF homolog [Mycoplasma pneumoniae]	52	33	1008
375	3	340	1878	gi 467446	similar to SpoVB [Bacillus subtilis]	52	28	1539
424	4	4104	3262	gi 1878239	unknown [Mycobacterium tuberculosis]	52	34	843
430	1	3	575	pir A42606 A426	orfA 5' to orf405 - Saccharopolyspora erythraea (fragment)	52	28	573
444	4	4728	3712	gi 1408494	homologous to penicillin acylase [Bacillus subtilis]	52	31	1017
465	1	1802	903	gi 143331	alkaline phosphatase regulatory protein [Bacillus subtilis] pir A27650 A27650 regulatory protein phoR - Bacillus subtilis sp P23545 PHO_R_BACSU ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN PHO (BC 2.7.3.3)	52	36	900
469	5	4705	4169	gi 755152	highly hydrophobic integral membrane protein [Bacillus subtilis] sp P42953 TAGC_BACSU TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN AGO	52	32	537
495	1	1262	633	gi 1204607	transcription activator [Haemophilus influenzae]	52	25	630
505	7	6004	5762	gi 142440	ATP-dependent nuclease [Bacillus subtilis]	52	28	243

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
517	2	1162	1614	gi 166162	Bacteriophage phi-11 int gene activator [Staphylococcus acteriophage phi 11]	52	35	453
543	2	444	1295	gi 1215693	putative orf; G9_orf434 [Mycoplasma pneumoniae]	52	25	852
586	1	1	316	gi 581648	lepiB gene product [Staphylococcus epidermidis]	52	36	336
773	1	848	426	gi 1279769	[FdhC [Methanobacterium thermoformicum]	52	30	423
1120	2	100	330	gi 142439	ATP-dependent nuclease [Bacillus subtilis]	52	35	231
1614	1	691	347	gi 289262	[comE ORF] [Bacillus subtilis]	52	28	345
2495	1	1	324	gi 216151	DNA polymerase (gene L; ttg start codon) [Bacteriophage SP02] gi 579197 SP02 DNA polymerase (aa 1-648) [Bacteriophage SP02] p1r[A21498] [DUBP52 DNA-directed DNA polymerase (EC 2.7.7.1) - phage P02]	52	34	324
2931	1	566	285	gi 1256136	YbbG [Bacillus subtilis]	52	30	282
2943	1	577	320	gi 11713	[h18A ORF (AA 1-245) [Escherichia coli]	52	35	258
2993	1	588	295	gi 298032	EF [Streptococcus suis]	52	34	294
3667	1	612	307	gi 849025	hypothetical 64.7-kDa protein [Bacillus subtilis]	52	36	306
3944	1	478	260	gi 1218040	BAA [Bacillus licheniformis]	52	36	219
3954	2	613	347	gi 854064	[087 Human herpesvirus 6]	52	50	267
3986	1	90	401	gi 1205919	[Na+ and Cl- dependent gamma-aminobutyric acid transporter [Haemophilus influenzae]	52	33	312
4002	1	3	389	gi 40003	[oxoglutarate dehydrogenase (NADP+)] [Bacillus subtilis] p[P23129] [ODO1_BACSU 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE)]	52	42	387
4020	1	1	249	gi 159388	[ornithine decarboxylase [Leishmania donovani]	52	47	249
4098	1	438	220	gi 409795	[No definition line found [Escherichia coli]	52	32	219
4248	1	3	212	gi 965077	[AdpP [Saccharomyces cerevisiae]	52	40	210
7	1	3	575	gi 895747	[putative cel operon regulator [Bacillus subtilis]	51	28	573
21	4	2479	3276	gi 1510962	[indole-3-glycerol phosphate synthase [Methanococcus jannaschii]	51	32	798
22	9	5301	5966	gi 1303933	[VqIN [Bacillus subtilis]	51	25	666
43	3	1516	1283	gi 1519460	[Srpl [Schizosaccharomyces pombe]	51	31	234
44	17	11042	11305	gi 42011	[moaD gene product [Escherichia coli]	51	35	264
51	11	6453	6731	gi 495471	[vacuolating toxin [Helicobacter pylori]	51	37	279

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52	4	2537	2995	gi1256652	25% identity to the E.coli regulatory protein MprA; putative [Bacillus subtilis]	51	32	459
57	10	7331	6843	gi1508173	81% domain of PPS-dependent GAT transport and phosphorylation Escherichia coli	51	32	489
59	1	29	1111	gi1299163	alanine dehydrogenase [Bacillus subtilis]	51	33	1083
67	20	15791	16576	gi1510977	M. jannaschii predicted coding region M0938 [Methanococcus jannaschii]	51	24	786
69	2	1559	1218	gi1467359	unknown [Bacillus subtilis]	51	34	342
71	1	3	1196	gi1298032	EF [Streptococcus suis]	51	32	1194
78	2	149	176	gi1161242	proliferating cell nuclear antigen [Styela clava]	51	28	174
99	4	3357	4040	gi1642795	TFIID subunit TAF155 [Homo sapiens]	51	25	684
109	1	2852	1428	gi1580920	rodD (gtaA) polypeptide (AA 1-673) [Bacillus subtilis] pir[S06048/S06048] probable rod protein - Bacillus subtilis sp[11484/TAGE_BACSU PROB3802 POLYGLYCEROL-PHOSPHATE] LPGA-GLUCOSYLTRANSFERASE (EC 2.4.1.53) (TECHNOIC ACID BIOSYNTHESIS PROTEIN E).	51	27	1425
109	9	6007	6693	gi1204815	hypothetical protein (SP:P32662) [Haemophilus influenzae]	51	23	687
112	3	1066	2352	pir[S05330/S053]	maltose-binding protein precursor - Enterobacter aerogenes	51	42	1287
112	13	14432	12855	gi1405857	yehU [Escherichia coli]	51	29	1578
114	9	9725	8967	gi1435098	orf1 [Mycoplasma capricolum]	51	30	759
115	1	1	912	gi1431110	ORF Y010R/w [Saccharomycus curvialis]	51	28	912
127	10	9647	10477	gi1204314	H. influenzae predicted coding region H10056 [Haemophilus influenzae]	51	37	831
152	9	6814	7356	gi1431929	MunI regulatory protein [Mycoplasma sp.]	51	38	543
154	2	575	1153	gi1237044	unknown [Mycobacterium tuberculosis]	51	36	579
154	7	6587	5634	gi1409286	barU [Bacillus subtilis]	51	27	954
171	8	6943	6236	gi1205484	hypothetical protein (SP:P33918) [Haemophilus influenzae]	51	32	708
184	1	1	291	gi1466886	BL496_C_206 [Mycobacterium lepreae]	51	33	291
212	5	1501	2139	pir/A45605/A456	mature-parasite-infected erythrocyte surface antigen MESA - Plasmodium falciparum	51	23	639
228	2	707	1378	gi18204	nuclear protein [Drosophila melanogaster]	51	27	672
236	8	8137	7481	gi149272	Asparaginase [Bacillus licheniformis]	51	31	657
243	4	4637	3546	gi1511102	melvalonate kinase [Methanococcus jannaschii]	51	29	1092

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257	4	3540	3373	gi 204579	H. influenzae predicted coding region HI0326 [Haemophilus influenzae]	51	22	168
258	3	2397	1609	gi 160299	glutamic acid-rich protein (Plasmodium falciparum) pfr A54514 A54514 glutamic acid-rich protein precursor - Plasmodium aliciparum	51	34	789
265	5	2419	3591	gi 580841	fl [Bacillus subtilis]	51	32	1173
298	2	518	748	gi 1336162	SCP8 (Streptococcus agalactiae)	51	34	231
316	9	5817	7049	gi 413953	ipa-29d gene product [Bacillus subtilis]	51	39	1233
332	2	3775	2057	gi 1209012	murs [Thermus aquaticus thermophilus]	51	26	1719
364	4	3816	4991	gi 528991	unknown [Bacillus subtilis]	51	32	1176
440	2	448	684	gi 2819	transferase (GAL10) (AA 1 - 687) [Kluyveromyces fragilis] pfr S01407 KUNYG UDP-glucose 4-epimerase (EC 5.1.3.2) - yeast uyveromyces marxianus var. lactis	51	32	237
495	2	1353	1177	gi 297861	protease G [Erwinia chrysanthemi]	51	41	177
495	3	2287	1718	gi 1513317	serine rich protein [Encarnoba histolytica]	51	25	570
506	1	840	421	gi 455320	cII protein [Bacteriophage P4]	51	33	420
500	1	1474	983	gi 587532	orf. len. 201. CAI: 0.16 [Saccharomyces cerevisiae] pfr S48818 S48818 hypothetical protein - yeast [Saccharomyces erevisiae]	51	30	492
607	3	479	934	gi 1511524	hypothetical protein (SP-P7002) [Methanococcus jannaschii]	51	40	456
686	2	127	600	gi 493017	endocarditis specific antigen [Enterococcus faecalis]	51	30	474
726	1	31	230	gi 11351851	unknown [Prochlorococcus marinus]	51	45	198
861	1	176	652	gi 410145	dehydroquinase dehydratase [Bacillus subtilis]	51	34	477
869	1	782	393	gi 40100	rodC (tag3) polypeptide (AA 1-746) [Bacillus subtilis] ir S06049 S06049 rodC protein - Bacillus subtilis p P13485 TAGC_BACSU TECHNIC ACID BIOSYNTHESIS PROTEIN F.	51	23	390
1003	1	642	322	gi 1279707	hypothetical phosphoglycerate mutase [Saccharomyces cerevisiae]	51	39	321
1046	2	866	624	gi 510257	glycosyltransferase [Escherichia coli]	51	29	243
1467	1	702	352	gi 1511175	M. jannaschii predicted coding region MJ1177 [Methanococcus jannaschii]	51	32	351
2558	1	457	230	sp P10582 DPOM	DNA POLYMERASE (EC 2.7.7.7) (S-1 DNA ORF 3).	51	26	228
3003	1	779	399	gi 809543	CbrC protein [Erwinia chrysanthemi]	51	27	381
3604	1	1	399	gi 364210 JC42	[3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) - mouse	51	37	399
3732	1	2	316	gi 145906	acyl-CoA synthetase [Escherichia coli]	51	33	315

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3791	1	2	274	gi1061351	semaphorin III family homolog (Homo sapiens)	51	37	273
3995	1	46	336	gi216346	surfactin synthetase (Bacillus subtilis)	51	38	291
4193	1	612	307	gi42749	ribosomal protein L12 (AA 1-179) [Escherichia coli] tr[S04776]XNECPL peptide N-acetyltransferase rimM (EC 2.3.1.-) - cherichia coli	51	25	306
4539	1	367	185	gi1408494	homologous to penicillin acylase (Bacillus subtilis)	51	40	183
4562	1	442	239	gi1458280	coded for by C. elegans cDNA cm0167; Similar to hydromethylglutaryl-CoA synthase [Caenorhabditis elegans]	51	35	204
1	4	3576	4859	gi559160	GRAIL score: null; cap site and late promoter motifs present petream; putative (Autographa californica nuclear polyhedrosis virus)	50	44	1284
11	7	4044	5165	gi1146207	putative (Bacillus subtilis)	50	35	1122
11	13	10509	9496	gi1208451	hypothetical protein [Synecocystis sp.]	50	39	1014
19	3	2034	1018	gi413966	ipa-42d gene product (Bacillus subtilis)	50	29	1017
20	11	8586	8407	gi1321159	ORF YGR103W [Saccharomyces cerevisiae]	50	28	180
24	5	5408	4824	gi1496280	structural protein [Bacteriophage Tuc2009]	50	29	585
34	4	1926	2759	gi1303966	Yqj0 [Bacillus subtilis]	50	36	814
38	30	22865	23440	gi1072179	Similar to dihydroflavonol-4-reductase (maize, petunia, tomato) [Caenorhabditis elegans]	50	32	576
47	2	1705	2976	gi153015	FemA protein [Staphylococcus aureus]	50	29	1272
56	13	15290	15841	gi1606096	ONF_1167; end overlaps end of o100 by 14 bases; start overlaps t174, thar starts possible [Escherichia coli]	50	30	552
57	1	2135	1077	gi1640922	xylool dehydrogenase (unidentified hemiascomycete)	50	29	1059
58	2	628	1761	gi143725	putative (Bacillus subtilis)	50	29	1134
88	6	4393	3884	gi1072179	Similar to dihydroflavonol-4-reductase (maize, petunia, tomato) [Caenorhabditis elegans]	50	32	510
89	5	3700	3356	gi1276658	ONF174 gene product (Porphyra purpurea)	50	25	345
141	1	3	239	gi1476024	carbamoyl phosphate synthetase II (Plasmodium falciparum)	50	33	237
151	1	186	626	gi1403441	unknown [Mycobacterium tuberculosis]	50	35	441
166	7	11065	9623	gi1895747	putative col operon regulator (Bacillus subtilis)	50	32	1443
201	6	5284	5096	gi160229	circumsporozoite protein (Plasmodium reichenowi)	50	42	189
206	22	30784	29555	gi11052754	LarP integral membrane protein [Lactococcus lactis]	50	24	1230

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
211	4	1523	1927	gi 410131	ORF7 (Bacillus subtilis)	50	29	405
214	4	2411	3295	sp P37348 YECE	HYPOTHETICAL PROTEIN IN ASP5 5' REGION (FRAGMENT)	50	37	885
228	7	5068	4406	gi 313580	envelope protein (Human immunodeficiency virus type 1) p1r[S35835]S35835 envelope protein - human immunodeficiency virus type 1 (fragment) (SUB 1-77)	50	35	663
272	2	3048	1723	gi 1408485	B65G gene product (Bacillus subtilis)	50	22	1326
273	2	1616	984	gi 184186	phosphoglycerate mutase (Saccharomyces cerevisiae)	50	28	613
328	2	2507	1605	gi 148896	lipoprotein (Haemophilus influenzae)	50	26	903
332	4	5469	3802	gi 1526347	DNA polymerase family X (Thermus aquaticus)	50	27	1668
342	5	3473	1931	gi 456562	G-box binding factor (Dictyostelium discoideum)	50	35	459
352	1	1478	741	gi 288301	ORF2 gene product (Bacillus megaterium)	50	29	738
408	7	5299	5523	gi 11665	ORF2116 (Marchantia polymorpha)	50	27	225
420	3	650	1825	gi 1757842	UDP-sugar hydrolase (Escherichia coli)	50	30	1176
464	1	1	591	gi 487282	[Na ⁺ -ATPase subunit J (Enterococcus hirae)	50	29	591
472	2	1418	864	gi 551875	BglR (Lactococcus lactis)	50	23	555
520	1	23	541	gi 567036	CapB (Staphylococcus aureus)	50	27	519
529	1	6	410	gi 1256652	25% identity to the E. coli regulatory protein MprA, putative (Bacillus subtilis)	50	34	405
534	5	7726	6059	gi 295671	selected as a weak suppressor of a mutant of the subunit AC10 of DNA dependent RNA polymerase I and III (Saccharomyces cerevisiae)	50	18	1668
647	1	2990	1497	gi 405568	TraI protein shares sequence similarity with a family of topoisomerases [Plasmid pSR41]	50	31	1494
664	3	1133	711	gi 410007	Leukocidin P component (Staphylococcus aureus, MRSA No. 4, Peptide, 23 aa)	50	32	423
678	1	1	627	gi 238032	EF (Streptococcus suis)	50	29	627
755	3	947	1171	gi 150572	cytochrome c1 precursor (EC 1.10.2.2) (Paracoccus denitrificans) gi 45465 cytochrome c1 (AA 1-450) (Paracoccus denitrificans) p1r[C29413]C29413 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor - Paracoccus denitrificans sp P13627 CY1	50	37	225
827	1	1363	683	gi 142020	heterocyst differentiation protein (Azobacter sp.)	50	21	681
892	1	3	752	gi 458485	B65G gene product (Bacillus subtilis)	50	27	750
910	2	438	887	gi 104727	tyrosine-specific transport protein (Haemophilus influenzae)	50	25	450

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
933	1	524	760	gi11203451	cell division inhibitor [Haemophilus influenzae]	50	32	237
973	1	424	236	gi1886947	orf3 gene product [Saccharomyces cerevisiae]	50	40	189
1009	1	653	429	gi1153727	M protein [group C streptococcus]	50	28	225
1027	1	511	257	gi1410914	[ipa-10r gene product [Bacillus subtilis]	50	25	255
1153	2	556	326	gi1773676	ncxa [Alcaligenes xylosoxydans]	50	36	231
1222	1	798	400	gi11408485	B65G gene product [Bacillus subtilis]	50	21	399
1350	1	692	399	gi1289272	ferrichrome-binding protein [Bacillus subtilis]	50	32	294
2945	1	366	184	gi1171704	hexaprenyl pyrophosphate synthetase (COQ1) [Saccharomyces erevisiae]	50	34	183
2968	2	1604	804	gi1397526	clumping factor [Staphylococcus aureus]	50	33	801
2998	2	657	394	gi1495696	F54E7.3 gene product [Caenorhabditis elegans]	50	40	264
3046	2	506	306	gi1318191318	acyl carrier protein - Arabidopsis thaliana (fragment)	50	32	201
3063	1	547	275	gi1174190	lucA gene product [Escherichia coli]	50	29	273
3174	1	3	146	gi1151900	alcohol dehydrogenase [Rhodospirillum rubrum]	50	31	144
3792	1	625	314	gi11001423	hypothetical protein [Synecococcus sp.]	50	35	312
3800	1	2	262	gi1144713	NAD-dependent beta-hydroxybutyryl coenzyme A dehydrogenase Clostridium acetobutylicum	50	28	261
3946	1	373	188	gi1576765	cytochrome b [Myrmecia pilosula]	50	38	186
3984	1	578	291	gi1373481984	HYPOTHETICAL PROTEIN IN ASP5 5' REGION (FRAGMENT)	50	37	288
37	10	8250	7885	gi1204367	hypothetical protein [GB-U14003.278] [Haemophilus influenzae]	49	30	366
46	16	13802	14848	gi1466860	lact: B1308_F1_34 [Mycobacterium leprae]	49	24	1047
59	5	2267	3601	gi1606304	ORF_0462 [Escherichia coli]	49	27	1335
112	18	17884	18615	gi1559502	ND4 protein (AA 1 - 405) [Caenorhabditis elegans]	49	25	732
138	9	6973	7902	gi1303953	esterase [Acinetobacter calcoaceticus]	49	29	930
217	6	4401	5138	gi1496254	fibronectin/fibrinogen-binding protein [Streptococcus pyogenes]	49	31	738
220	12	11803	12657	gi1397526	clumping factor [Staphylococcus aureus]	49	31	855
228	4	1842	2492	gi15216921828	hypothetical protein 9 - Plasmodium falciparum	49	28	651
268	1	5016	2614	gi1143047	ORF8 [Bacillus subtilis]	49	26	2403

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
271	2	1164	1373	gi 1001257	hypothetical protein [Synecocystis sp.]	49	38	210
300	3	4340	3180	gi 1510796	hypothetical protein [GP.X91006.2] [Methanococcus jannaschii]	49	26	1161
381	1	2281	1142	gi 396301	matcha PS0041: bacterial regulatory proteins, araC family signature [Escherichia coli]	49	29	1140
466	1	3	947	gi 303863	Yagp [Bacillus subtilis]	49	26	945
666	1	379	191	gi 633112	ORF1 [Streptococcus sobrinus]	49	29	189
670	2	403	1014	gi 1122758	unknown [Bacillus subtilis]	49	32	612
709	1	1433	795	gi 144830	xpAC [Bacillus subtilis]	49	29	639
831	1	943	473	gi 401786	phosphonamutase [Mycoplasma pirum]	49	29	471
1052	1	422	213	gi 1303799	Yqen [Bacillus subtilis]	49	21	210
1800	1	342	172	gi 216300	peptidoglycan synthesis enzyme [Bacillus subtilis] sp P37585 HURG_BACSU HURG PROTEIN UPD-N-ACETYLGLUCOSAMINE-N-ACETYLURAMYL-PENTAPEPTIDE PYROPHOSPHORYL-UNDECAPHENOL N-ACETYLGLUCOSAMINE RANSFERASE)	49	28	171
2430	1	2	376	sp P27434 YFCA_	HYPOTHETICAL 36.2 KD PROTEIN IN NDK-OEPE INTERGENIC REGION.	49	26	375
3096	1	542	273	gi 516360	surfactin synthetase [Bacillus subtilis]	49	25	270
32	4	3771	3100	gi 1217963	hepatocyte nuclear factor 4 gamma (HNF4gamma) [Homo sapiens]	48	36	672
38	1	1	609	gi 1205790	H. influenzae predicted coding region H1555 [Haemophilus influenzae]	48	28	609
45	6	5021	6427	gi 1534267	unknown [Mycobacterium tuberculosis]	48	20	1407
59	14	16346	31096	gi 1197336	ImpJ protein [Mycoplasma hominis]	48	28	14751
61	1	3	608	gi 1511555	quinolone resistance nra protein [Methanococcus jannaschii]	48	30	606
61	3	3311	3646	gi 1303893	Yqph [Bacillus subtilis]	48	29	336
114	1	98	415	gi 671708	[sus] homolog; similar to Drosophila melanogaster suppressor of able [su(s)] protein, Swiss-Prot Accession Number P22293 [Drosophila virilis]	48	25	318
121	1	1131	610	gi 1314584	unknown [Sphingomonas 588]	48	29	522
136	1	2014	1280	gi 1205968	H. influenzae predicted coding region H1738 [Haemophilus influenzae]	48	23	735
171	10	8220	9557	gi 1208454	hypothetical protein [Synecocystis sp.]	48	34	1338
175	1	3625	1814	gi 396400	similar to eukaryotic Na+/H+ exchangers [Escherichia coli] sp P32703 XUCE_ECOLI_HYPOTHETICAL 60.5 KD PROTEIN IN SOUR-ACS HYPERGENIC REGION 10549)	48	29	1812
194	1	2	385	gi 1510493	M. jannaschii predicted coding region M20419 [Methanococcus jannaschii]	48	25	384

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
197	1	901	452	gi 1045714	sporidial/putrescine transport ATP-binding protein [Mycoplasma genitalium]	48	25	450
203	1	1	396	gi 940288	protein localized in the nucleoli of pea nuclei; ORF, putative Pisum sativum	48	29	396
204	1	1363	698	gi 529202	No definition line found [Caenorhabditis elegans]	48	25	666
206	20	14815	27760	gi 5111490	Gramicidin S synthetase 2 [Bacillus brevis]	48	27	7056
212	1	2	166	gi 295899	nucleolin [Xenopus laevis]	48	34	165
220	10	12652	11426	gi 44073	SecY protein [Lactococcus lactis]	48	23	1227
243	6	6450	5491	gi 1184118	mevalonate kinase [Methanobacterium thermoautotrophicum]	48	30	960
264	4	5434	3308	gi 1015903	ORF YJRI51c [Saccharomyces cerevisiae]	48	26	2127
441	1	1532	768	gi 142863	replication initiation protein [Bacillus subtilis] pir B36580 B36580 replication initiation protein - Bacillus subtilis	48	23	765
444	5	3898	5298	gi 145836	putative [Escherichia coli]	48	24	1401
484	2	388	1110	gi 146551	transmembrane protein (kdpD) [Escherichia coli]	48	18	723
542	3	1425	2000	pir 528365 5289	N-carbamoyl-L-asparagine amidohydrolase (EC 3.5.1.59) - Arthrobacter sp.	48	27	576
566	1	3	1019	gi 153490	tetracycline C resistance and export protein [Streptomyces laueaeensis]	48	24	1017
611	1	2	730	gi 1103507	unknown [Schizosaccharomyces pombe]	48	38	729
624	1	1255	665	gi 144859	ORF B [Clostridium perfringens]	48	26	591
846	1	1014	508	gi 537506	paraoxyan [Drofilaria imitica]	48	27	507
1020	1	66	950	gi 1499876	magnesium and cobalt transport protein [Methanococcus jannaschii]	48	30	885
1227	1	1	174	gi 493730	lipoxigenase [Pisum sativum]	48	35	174
1266	1	1	405	gi 682452	ORF f211, alternate name yppA; orf5 of X14236 [Escherichia coli] gi 41425 ORF5 (AA 3-197) [Escherichia coli] (SUB 15-211)	48	24	405
2071	1	707	381	gi 1408486	HST4A gene product [Bacillus subtilis]	48	25	327
2198	1	463	233	gi 1500401	reverse gyrase [Methanococcus jannaschii]	48	40	231
2425	1	476	246	pir H48563 H485	G1 protein - fowlpox virus (strain HP444) (fragment)	48	40	231
2432	1	446	225	gi 1353703	Trlo [Homo sapiens]	48	33	222
2453	1	794	399	gi 142850	division initiation protein [Bacillus subtilis]	48	29	396
2998	1	469	236	gi 577569	PepV [Lactobacillus delbrueckii]	48	31	234

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3042	1	14	280	gi 945219	mucin (Homo sapiens)	48	35	267
3686	1	1	405	gi 145836	putative [Escherichia coli]	48	25	405
4027	2	492	301	pir-S51177[S511]	trans-activator protein - Equine infectious anemia virus	48	32	192
4	2	1641	2232	gi 1303989	YgkI [Bacillus subtilis]	47	24	1410
24	2	599	1084	gi 1540083	PC4-1 gene product [Bradyzia hygida]	47	28	486
16	10	7524	6925	gi 1209223	esterase [Acinetobacter lwoffii]	47	26	500
43	2	196	1884	gi 1603455	unknown [Mycobacterium tuberculosis]	47	27	1689
44	122	16118	15108	gi 1511555	quinolone resistance nraA protein [Methanococcus jannaschii]	47	31	1011
69	7	7141	6710	gi 438466	Possible operon with orfG. Hydrophilic, no homologue in the database; putative [Bacillus subtilis]	47	29	432
81	4	5022	4279	gi 466882	pps1; B1496.C2.189 [Mycobacterium leprae]	47	24	744
120	12	9135	8863	gi 927340	D9509.27p; CA1; 0.12 [Saccharomyces cerevisiae]	47	38	273
142	1	2022	1174	gi 486143	ORF YKL094w [Saccharomyces cerevisiae]	47	32	849
168	1	2178	1093	gi 1177234	hypothetical EcsB protein [Bacillus subtilis]	47	29	1086
263	1	1884	943	gi 142822	D-alanine racemase cds [Bacillus subtilis]	47	34	942
279	1	1109	561	gi 516608	2 predicted membrane helices, homology with B. subtilis men Orf3 Rowland et. al. unpublished accession number M74883, approximately 1 minutes on updated Radd map; putative [Escherichia coli] sp P37355 YF88_ECOLI HYPOTHETICAL 26.7 KD PROTEIN IN MEND-MENB	47	31	549
345	2	2620	1676	gi 1204835	hippuricase [Haemophilus influenzae]	47	28	945
389	2	152	400	gi 456562	G-box binding factor [Dictyostellium discoideum]	47	32	249
391	1	1	831	gi 1420856	myo-inositol transporter [Schizosaccharomyces pombe]	47	19	831
404	3	2072	2773	gi 1255425	C3JG8.2 gene product [Caenorhabditis elegans]	47	17	702
529	5	2145	3107	gi 1303973	YgJv [Bacillus subtilis]	47	29	963
565	2	2321	1257	gi 142824	processing protease [Bacillus subtilis]	47	28	1065
654	1	962	483	gi 243353	ORF 5' of ECRF3 [herpesvirus saimiri] HSV, host-squirrel monkey, optide, 407 aa	47	23	480
692	1	115	633	gi 150756	40 kDa protein (Plasmid pJH1)	47	25	519
765	1	1634	819	gi 1256621	26.7% of identity in 165 aa to a Thermophilic bacterium hypothetical protein 6, putative [Bacillus subtilis]	47	28	816

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
825	2	211	1023	gi 397526	clumping factor (Staphylococcus aureus)	47	32	813
914	1	1	615	gi 558073	polymorphic antigen (Plasmodium falciparum)	47	29	615
1076	1	1	753	gi 1147557	aspartate aminotransferase (Bacillus circulans)	47	33	753
1351	1	793	398	gi 755153	ATP-binding protein (Bacillus subtilis)	47	20	396
4192	1	3	293	gi 145836	putative (Escherichia coli)	47	24	291
5	6	4708	4361	gi 305080	myosin heavy chain (Entamoeba histolytica)	46	30	348
11	4	2777	3058	gi 601639	Yel040p (Saccharomyces cerevisiae)	46	28	282
46	11	10518	10100	gi 1246901	ATP-dependent DNA ligase (Candida albicans)	46	28	219
61	4	3941	7930	gi 1298032	EF (Streptococcus suis)	46	35	3990
132	4	5028	4093	gi 1511057	hypothetical protein SP:R45869 (Methanococcus jannaschii)	46	25	936
170	4	4719	3652	gi 851910 8519	IG4 protein - Sauroleishmania tarentolae	46	26	1068
191	7	9543	8284	gi 1041334	F5405.7 (Caenorhabditis elegans)	46	25	1260
253	1	1	396	gi 1204449	dihydroliipoamide acetyltransferase (Haemophilus influenzae)	46	35	396
264	3	437	973	gi 180189	cerebellar-degeneration-related antigen (CDR34) (Homo sapiens) cerebellar degeneration-associated protein (Homo sapiens) pir A29770 A29770 cerebellar degeneration-related protein - human	46	29	537
273	1	485	285	gi 1607573	envelope glycoprotein C2V3 region (Human immunodeficiency virus type 1)	46	35	201
350	1	1	563	gi 517052	ORF_286 (Escherichia coli)	46	35	561
384	1	2	862	gi 1121884	(lurea?) amidolyase (Haemophilus influenzae)	46	31	861
410	4	1876	2490	gi 1110518	proton antiporter efflux pump (Mycobacterium smegmatis)	46	24	615
432	1	2663	1455	gi 1197634	orf4; putative transporter; Method: conceptual translation supplied by author (Mycobacterium smegmatis)	46	27	1209
458	1	2419	1211	gi 115470	portal protein (Bacteriophage SPPI)	46	30	1209
517	5	2477	4192	gi 11523812	orf5 (Bacteriophage A2)	46	21	1716
540	3	1512	1285	gi 215635	pacA (Bacteriophage P1)	46	30	228
587	2	649	1242	gi 537148	ORF_181 (Escherichia coli)	46	29	594
1218	1	747	391	gi 1205656	single-stranded-DNA-specific exonuclease (Haemophilus influenzae)	46	30	357

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3695	1	1	402	g1 450688	hadM gene of Ecoprr1 gene product [Escherichia coli] pir S38437 S38437 hadM protein - Escherichia coli pir S09629 S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	46	33	402
4176	1	673	338	g1 51460	PIM-C.1 gene product [Xenopus laevis]	46	31	336
37	7	4813	5922	g1 606064	ORF_408 [Escherichia coli]	45	24	1110
38	16	11699	12004	g1 452192	protein tyrosine phosphatase (PTP-BAS, type 2) [Homo sapiens]	45	24	306
87	2	1748	2407	g1 1064813	homologous to sp:PHOR_BACSU [Bacillus subtilis]	45	23	660
103	12	14182	13385	g1 1001307	hypothetical protein [Synchocystis sp.]	45	22	798
112	14	14791	13811	g1 204389	H. influenzae predicted coding region H10131 [Haemophilus influenzae]	45	23	981
145	4	4483	3461	g1 220578	open reading frame [Mus musculus]	45	20	1023
170	6	6329	4965	g1 238657	AppC-cytochrome d oxidase, subunit I homolog [Escherichia coli, K12, eptide, 514 aa]	45	27	1365
206	2	5230	4346	g1 1222056	aminotransferase [Haemophilus influenzae]	45	27	885
228	1	60	716	g1 160299	glutamic acid-rich protein [Plasmodium falciparum] pir A54514 A54514 glutamic acid-rich protein precursor - Plasmodium falciparum	45	23	657
288	1	2	1015	g1 1255425	C3JCR.2 gene product [Caenorhabditis elegans]	45	23	1014
313	3	4339	3128	g1 581140	NADH dehydrogenase [Escherichia coli]	45	30	1212
332	1	914	459	g1 870966	F47A4.2 [Caenorhabditis elegans]	45	20	456
344	1	3	221	g1 171225	kinesin-related protein [Saccharomyces cerevisiae]	45	26	219
441	2	1501	1073	g1 142863	replication initiation protein [Bacillus subtilis] pir B26580 B26580 replication initiation protein - Bacillus ubtilis	45	27	429
672	1	2	982	g1 1511334	M. jannaschii predicted coding region MJ1323 [Methanococcus jannaschii]	45	22	981
763	3	1345	851	g1 606180	ORF_5310 [Escherichia coli]	45	24	495
886	3	379	846	g1 726426	similar to protein kinases and C. elegans proteins F37C12.8 and 37C12.5 [Caenorhabditis elegans]	45	30	468
948	1	3	473	g1 156400	myosin heavy chain (isozyme unc-54) [Caenorhabditis elegans] pir A33958 HMW myosin heavy chain B - Caenorhabditis elegans sp P02566 MYSB_CAEEL MYOSIN HEAVY CHAIN B (MHC B)	45	35	471
1158	1	2	376	g1 441155	transmission-blocking target antigen [Plasmodium falciparum]	45	35	375
2551	1	4	285	g1 1276705	ORF287 gene product [Porphyra purpurea]	45	28	282
3967	1	42	374	g1 976025	HraA [Escherichia coli]	45	28	333

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match accession	Match gene name	% sim	% ident	Length (nt)
52	7	6931	5846	gi 467378	unknown [Bacillus subtilis]	44	22	1086
138	8	6475	6849	gi 173028	Choreodxin II [Saccharomyces cerevisiae]	44	28	375
221	5	7032	5617	gi 151490	tetracycline C resistance and export protein [Streptomyces laevis]	44	21	1416
252	2	1331	1122	gi 1204989	hypothetical protein [GB-U00022.9] [Haemophilus influenzae]	44	30	210
263	2	3265	2093	gi 1136221	carboxypeptidase [Sulfolobus solfataricus]	44	26	1173
365	4	4963	3524	gi 1296822	orf1 gene product [Lactobacillus helveticus]	44	31	1440
543	3	1315	1833	gi 063250	low homology to P20 protein of bacillus licheniformis and bleomycin acetyltransferase of Streptomyces verticillius [Bacillus subtilis]	44	24	519
544	4	3942	4892	gi 951460	FM-C-1 gene product [Xenopus laevis]	44	32	951
792	1	1224	613	gi 205680	high molecular weight neurofilament [Rattus norvegicus]	44	28	612
46	18	11303	11911	gi 1511614	polyphosphatase-guanine dinucleotide biosynthesis protein A [Methanococcus jamaehilli]	43	27	609
59	8	3665	5128	gi 153490	tetracycline C resistance and export protein [Streptomyces laevis]	43	21	1464
59	10	5536	7527	gi 153022	lipase [Staphylococcus epidermidis]	43	22	1992
99	1	1346	681	gi 1413051	unknown [Mycobacterium tuberculosis]	43	21	666
310	8	9402	12134	gi 397526	clumping factor [Staphylococcus aureus]	43	21	2733
432	3	2782	2303	pir A60540 A605	sporozoite surface protein 2 - Plasmodium yoelii (fragment)	43	29	480
519	3	2547	3122	sp Q06530 DMSU	SULFIDE DEHYDROGENASE (FLAVOCYTOCHROME C) FLAVOPROTEIN CHAIN PRECURSOR (EC 1.8.2.-) (FC) (FCS)	43	23	576
4	13	12053	13321	gi 255671	selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependent RNA polymerase I and III [Saccharomyces cerevisiae]	42	18	1269
94	2	1768	1091	gi 501027	ORF2 [Trypanosoma brucei]	42	31	678
127	4	5791	4550	gi 42029	ORF1 gene product [Escherichia coli]	42	21	1242
297	3	1515	1036	gi 142790	ORF1, putative [Bacillus firmus]	42	25	480
344	6	4097	3525	gi 40320	ORF 2 [AA 1-203] [Bacillus thuringiensis]	42	30	573
512	1	2167	1115	gi 405957	yefE [Escherichia coli]	42	23	1053
631	1	2434	1223	gi 580920	rodD (gtaA) polypeptide (AA 1-673) [Bacillus subtilis] pir S05048 S06048 probable rod protein - Bacillus subtilis sp P13484 TAGE.BACSU PROBABLE POLY (GLYCEROL-PHOSPHATE) LPHN-GLUCOSYLTRANSFERASE (EC 2.4.1.52) (TECHOIC ACID BIOSYNTHESIS PROTEIN E)	42	24	1212

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
685	3	2359	1739	gi 1303784	Yqad [Bacillus subtilis]	42	19	621
4132	1	787	395	gi 1022910	protein tyrosine phosphatase [Dictyostelium discoideum]	42	25	393
86	2	1375	884	gi 309506	spermidine/spermine N1-acetyltransferase [Mus saxicola] pir S430[S430] spermidine/spermine N1-acetyltransferase - spiny ouse [Mus saxicola]	41	30	492
191	12	14797	14075	gi 124957	orf4 gene product [Methanosarcina barkeri]	41	22	723
212	6	2150	3127	gi 15873	observed 35.2kd protein [Mycobacteriophage 15]	41	26	978
213	3	1263	2000	gi 633692	Trsa [Yersinia enterocolitica]	41	18	738
408	4	2625	3386	gi 1197634	orf4; putative transporter; Method: conceptual translation supplied by author [Mycobacterium smegmatis]	41	24	762
542	1	3	1103	gi 457146	rhostry protein [Plasmodium yoelii]	41	21	1101
924	1	2	475	pir JH0148 JH01	nucleolin - rat	41	30	474
1562	1	1	402	gi 552184	asparagine-rich antigen Pf35-2 [Plasmodium falciparum] pir S27826[S27826] asparagine-rich antigen Pf35-2 - Plasmodium falciparum (fragment)	40	20	402
2395	1	518	261	pir S42251 S422	hypothetical protein 5 - fowlpox virus	40	18	258
4077	1	3	305	gi 1055055	coded for by C. elegans cDNA YK379.5; coded for by C. elegans cDNA YK39.5; coded for by C. elegans cDNA yk189.5; alternatively spliced form of F32C9.8b [Caenorhabditis elegans]	39	21	303
918	1	1003	503	gi 1255425	C33G8.2 gene product [Caenorhabditis elegans]	37	25	501
59	12	8294	10636	gi 535260	STARP antigen [Plasmodium reichenowi]	36	24	2343
63	5	3550	8079	gi 298032	EF [Streptococcus suis]	36	19	4530
544	3	2507	3601	gi 1015903	OMF YJR15c [Saccharomyces cerevisiae]	35	22	1095
63	4	1949	3574	gi 552195	circumsporozoite protein [Plasmodium falciparum] sp P05691 CSP_PLAFL CIRCUMSPOROZOITE PROTEIN (CS) (FRAGMENT)	32	27	1626

TABLE 2

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
4	1	1234	692
4	3	1712	2278
4	4	3703	3032
4	14	113073	12585
5	2	2539	1601
5	3	1532	1771
5	7	4741	4550
5	9	7939	6422
5	12	8711	8547
6	4	2359	1982
8	1	349	176
11	8	5144	5983
11	9	5568	6498
11	10	6472	6284
11	16	10954	11271
12	5	5352	4942
12	6	4596	4862
15	3	1895	1650
16	10	11263	10835
18	2	1093	917
20	9	9125	7764
20	10	8571	8330
20	12	9201	8803
20	13	12158	10470
21	1	674	339
23	6	6138	5485
23	8	6376	5942

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
23	9	7651	6881
23	15	12618	12830
24	4	4556	4185
24	6	5642	5241
25	2	1824	2402
31	2	505	849
31	3	1177	1524
31	4	2454	3005
32	2	765	1388
32	9	7952	8575
32	10	8591	8728
32	11	9738	9379
32	12	10797	10087
34	2	1315	1049
36	7	5226	5801
36	11	7575	7261
36	12	7424	7621
37	4	3158	2964
38	2	1585	980
38	11	6425	6868
38	20	16982	16371
38	26	20253	20804
38	27	20722	21264
39	1	1	627
40	1	805	404
43	1	796	428
44	4	2674	2324

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
44	5	2484	3263
44	14	10587	10129
44	20	11724	13536
44	21	13596	13994
45	7	6575	6297
46	8	6165	6520
46	12	10449	10976
46	17	15032	15424
47	1	288	1079
48	9	7620	7778
50	1	1612	962
50	2	1621	1316
51	1	738	370
51	5	2520	2245
53	1	442	287
53	7	6705	6319
54	7	9014	8709
55	1	592	326
55	3	1052	786
56	1	1	261
56	3	1551	1228
56	4	1970	1560
56	17	19092	18712
57	4	3694	3521
57	8	5436	5822
58	9	8885	8553
59	3	1366	1509

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
59	6	3026	2802
59	7	3770	3570
59	9	4946	4563
59	11	7518	8378
59	13	10401	116403
62	2	2696	1521
62	11	5440	5757
63	1	1	336
67	1	900	1781
67	2	1774	2610
67	3	2591	3904
67	8	7110	6955
68	1	78	326
70	6	6761	5199
70	11	8935	8645
77	3	1590	1192
79	2	1509	1228
79	3	1411	1791
83	1	2	403
85	9	8300	8653
85	10	8969	8781
86	3	1426	1232
87	8	9187	9366
88	3	1620	1922
89	1	3	161
89	7	5042	4878
91	1	1098	550

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
91	3	3938	3141
92	2	449	928
92	3	1958	1467
92	9	5638	6024
94	1	661	312
94	3	2445	1813
94	4	2583	2197
96	11	10601	11050
99	6	4672	4523
99	7	5014	4784
100	8	7658	7287
102	7	4697	4368
103	3	2496	2035
104	1	2	694
104	2	699	1277
105	1	1235	693
105	3	3233	2655
105	1	3	221
106	3	1209	1355
107	1	1081	542
109	4	4025	3651
109	13	11625	11996
109	14	11981	12268
109	20	17401	17688
110	1	2	760
114	10	8764	9384
116	1	1	309

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig No	ORF ID	Start (nt)	Stop (nt)
116	3	6273	4462
116	8	11049	9976
116	9	10313	10158
120	5	3703	3320
120	6	4270	3869
120	13	9290	9844
121	2	417	569
126	3	1090	818
127	3	2648	3196
127	5	4084	4395
131	6	6773	6438
132	2	715	1695
134	1	2	667
135	2	512	258
135	3	1124	729
138	1	3	152
138	7	6008	6463
140	1	2060	1032
140	2	2019	1513
140	5	2387	2743
142	2	1360	2388
142	7	8830	7586
143	7	7290	6502
144	1	1227	640
146	1	2	511
146	3	502	1350
146	4	3673	2540

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
146	5	2874	3071
147	1	1	339
149	11	3956	3615
149	12	4036	3785
149	13	4507	4145
149	15	4807	4610
149	16	5495	5049
149	18	5739	5491
149	21	7416	7054
149	23	9216	8521
149	24	9681	9106
149	25	10679	9897
150	2	2303	1587
154	3	1795	1508
154	8	6586	6398
154	14	12704	12147
154	15	13531	12803
156	1	315	593
157	3	1183	2237
158	2	1471	1064
159	3	452	808
161	2	876	1808
161	6	4653	4279
161	7	4803	4340
161	8	4896	4717
161	11	5817	5638
163	2	1606	840

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
163	5	2796	2344
163	7	2952	2647
163	9	4905	5132
164	3	1338	1147
166	3	5213	4854
168	4	2500	2868
168	5	3595	4158
170	3	2517	2777
171	2	2277	1450
171	11	12576	11125
172	1	3	278
172	2	1940	1149
173	1	1289	708
173	5	7001	6114
174	2	593	1105
175	3	2552	2890
175	5	3820	3335
175	7	4342	4506
182	4	5477	4986
184	5	6043	5702
188	2	1210	1755
188	4	2647	2994
189	6	2614	3039
190	3	1998	2564
191	1	1	153
191	2	950	669
191	10	11786	13039

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
191	11	12902	12163
192	1	91	426
195	3	2106	1932
195	5	2899	2606
198	2	1016	1591
201	1	170	625
203	2	783	1466
206	6	8930	7815
206	12	11947	13636
206	21	28208	27960
212	2	170	817
212	3	796	1167
212	7	3128	3436
212	9	3749	4075
213	1	1	705
214	2	1076	570
214	6	4084	3738
214	9	6600	6995
214	10	7884	7469
217	1	1927	965
218	1	178	657
218	3	1776	2156
220	2	1851	1369
220	3	1251	2262
220	7	8275	7208
220	8	10244	8661
220	9	11796	10216

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
221	4	3095	2613
221	9	11428	10757
226	1	3	659
226	2	2196	1459
226	3	1476	1961
227	1	2	487
227	2	460	975
227	4	1855	2121
227	5	2052	2345
227	6	4760	3768
227	9	5591	6367
228	5	2503	2877
228	6	2846	3526
233	7	3944	3762
236	2	809	579
238	2	1975	1391
239	2	1417	905
241	5	4495	4334
242	2	1677	1363
243	1	127	576
246	1	1291	847
246	2	3035	1962
245	2	1614	1258
246	1	69	215
246	4	738	1733
249	3	3906	3712
250	1	494	249

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
254	1	1	156
256	2	956	1144
257	3	3700	3227
260	4	4906	4580
261	4	2196	2606
261	6	3214	3681
264	2	155	439
264	5	5252	4533
264	6	4739	5107
267	2	1323	931
268	4	5140	4700
272	1	862	446
272	3	1200	1439
272	9	4691	4909
272	10	6469	6035
276	4	1746	1901
278	1	224	553
278	5	3299	3448
278	7	4849	5127
285	2	551	736
288	3	1756	1950
288	5	2055	2276
289	1	2107	1055
290	2	2214	1932
291	2	332	622
291	5	1545	2051
295	3	1606	1149

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
295	4	2728	2141
295	5	2220	2762
297	2	788	465
298	1	2	205
300	2	2380	1928
301	7	2794	2624
304	1	3	194
306	1	109	654
306	5	4036	4257
307	1	674	339
307	8	3645	3995
308	1	1	654
308	2	1120	599
308	4	2643	2332
313	2	2316	1919
314	1	10	702
316	2	982	1341
316	6	2758	3165
317	1	2	1114
317	3	4570	3458
321	6	5645	5217
321	7	6319	6140
321	8	7450	6794
322	2	827	543
326	2	165	1112
326	3	1117	1467
328	1	936	469

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig	ORF	Start	Stop
id	id	(nt)	(nt)
328	5	3452	3276
329	1	3	719
329	2	781	1212
329	3	1471	1833
330	1	576	289
330	3	1447	1623
332	3	2353	2204
332	7	4971	5138
333	2	3295	3128
335	1	864	433
337	2	95	526
340	2	1658	1356
341	1	3	281
341	3	2476	3192
341	5	3618	3944
341	6	3929	4558
344	5	3197	2889
345	1	1532	768
346	2	221	592
350	3	1410	1598
352	2	2178	1765
352	3	7316	4596
352	7	7967	8404
352	8	8906	9247
352	9	10171	9854
359	1	1	546
362	1	3	656

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
364	2	2158	1808
364	8	10974	10714
365	2	1612	1313
365	5	4680	4090
365	7	4980	6239
366	3	520	1719
367	3	906	1085
368	1	748	494
375	1	2	136
380	3	1351	1097
389	1	1	276
390	1	2	877
390	2	1373	1549
391	2	751	560
395	1	391	197
396	1	2132	1068
398	3	1344	1141
399	1	176	569
401	3	566	847
402	2	100	465
404	8	5561	5370
408	2	3507	2269
408	3	2875	2672
408	5	3524	4423
410	3	2111	1890
413	1	880	488
416	1	607	320

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
416	2	578	847
416	3	2195	1590
417	1	3	179
417	2	161	616
420	2	788	513
422	2	357	677
431	2	856	1407
432	2	446	1084
433	1	1	417
433	3	2311	2033
434	1	942	535
434	2	1089	1235
440	1	1	450
442	2	1269	3320
443	3	1873	1520
444	1	1	696
444	7	6761	6366
451	1	940	614
453	2	896	636
453	8	3833	4786
453	9	4718	4512
453	10	4937	4731
455	1	434	219
455	2	472	930
459	1	265	687
462	1	2	247
466	2	1494	907

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
467	1	634	349
468	1	2	250
469	1	1488	925
469	3	2386	3372
469	4	3464	3706
470	1	77	538
470	6	4098	3694
470	7	6330	5686
470	9	7351	8181
470	10	8175	9773
471	1	940	500
471	2	1562	1017
476	1	70	267
477	1	2	760
477	3	1764	2081
477	4	2086	2332
480	5	4016	4261
481	2	956	480
486	3	613	774
487	6	1795	2112
488	1	715	359
492	1	127	675
493	1	2	520
493	2	496	1242
502	3	1149	1571
504	1	690	346
505	5	4566	4150

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
511	2	1741	1232
512	2	583	747
515	1	609	812
517	4	2179	2511
520	4	2097	2360
520	6	1908	1669
527	1	1	498
528	1	637	335
529	2	1679	1704
530	7	5298	5534
536	1	308	156
538	1	1362	736
538	3	2203	2880
538	5	3531	3121
538	6	4348	3721
540	1	996	664
540	2	1495	1011
541	1	89	433
541	2	719	432
542	2	1048	1272
545	2	1012	734
551	1	2145	1129
555	2	892	704
558	3	1357	1154
558	4	1760	1458
558	5	2105	1821
558	6	2166	2020

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
558	7	2636	2322
558	8	3053	2802
558	9	3986	3453
560	1	475	921
565	3	1706	1485
571	1	308	156
571	3	994	1206
577	1	2	199
577	2	163	453
579	1	1	477
579	2	1784	1200
583	1	1988	996
585	1	946	539
587	1	22	573
588	2	1896	1372
588	3	1742	1554
590	1	47	334
592	2	1455	1141
593	1	2	775
593	2	817	1122
595	1	87	890
596	3	1593	1435
602	1	8	169
603	5	1071	1469
606	1	312	768
607	5	1444	1226
610	1	1029	541

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
612	1	3	900
616	1	991	650
617	2	726	491
622	1	36	347
625	4	2046	2549
627	1	67	210
628	1	901	452
631	3	4789	4004
634	1	1448	759
636	1	189	368
636	2	1929	1063
637	2	2323	1994
638	1	227	1081
639	1	518	261
639	2	1377	811
641	1	118	444
642	3	1615	1331
642	4	2260	1847
643	1	3	608
645	4	1534	1758
645	6	2025	2321
645	7	2940	2488
648	1	2	1045
660	1	77	601
660	2	576	872
661	1	1725	961
664	2	89	304

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
667	1	3	413
668	1	1	330
671	2	612	516
673	1	3	338
674	2	865	584
679	1	1	237
679	3	1589	1906
688	1	1236	835
688	2	1352	1077
694	1	3	143
696	2	818	432
706	1	36	224
709	3	1183	1449
711	1	3	908
715	1	3	167
716	1	2	637
721	1	133	570
722	1	763	383
723	1	1656	829
723	2	1498	1112
727	1	2	472
729	1	268	441
731	1	130	828
735	1	2	214
736	1	3	782
738	1	2	298
742	1	3	230

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
745	3	1148	780
748	2	282	464
749	1	685	344
751	1	501	452
755	1	37	522
755	2	520	918
756	2	663	400
764	2	1033	746
767	1	1	405
768	1	2	373
771	1	1058	534
778	1	1735	902
785	1	1790	1023
787	1	1260	631
791	1	3	224
799	1	15	260
804	1	304	711
805	1	3	680
808	1	219	842
810	1	2221	1112
810	2	1774	1442
812	1	38	979
817	1	714	358
818	2	487	1104
819	2	1529	1032
819	3	1748	1419
820	1	195	1064

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
828	1	506	255
829	1	48	800
830	1	578	291
832	1	594	298
835	1	320	796
840	3	491	709
845	1	912	457
850	2	303	449
853	1	715	359
860	1	2	256
864	1	18	410
864	2	383	715
864	6	1676	1428
870	1	1	588
873	1	906	454
875	1	584	294
877	1	1661	1010
878	1	981	544
879	1	1567	785
881	1	1	243
882	1	389	604
890	1	2	508
905	1	793	398
906	1	852	544
912	1	373	188
913	1	3	290
913	2	1092	547

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
915	1	6	161
915	2	169	402
921	1	126	386
927	1	1578	808
928	1	2	385
929	1	2	400
932	1	2	400
934	1	1	384
936	1	1052	528
937	1	2	616
945	1	220	645
945	2	649	1242
946	1	1702	950
949	1	1	270
951	1	3	362
955	1	3	143
960	1	723	400
963	1	1	162
965	1	690	346
966	1	1079	606
969	1	3	302
971	1	12	170
974	1	319	161
976	1	692	348
977	1	2	211
982	1	1926	982
984	1	589	296

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig	ORF	Start	Stop
.ip	ID	(nt)	(nt)
987	1	3	467
993	1	1	525
994	1	920	549
1006	1	557	318
1014	1	624	313
1015	1	2	463
1016	1	288	145
1019	1	1205	660
1022	1	839	474
1024	1	595	299
1024	2	276	431
1030	1	673	338
1032	1	355	179
1040	1	794	399
1043	1	3	289
1044	2	115	399
1047	1	1	159
1051	1	704	354
1051	2	1233	733
1063	1	2	400
1069	1	2	148
1069	2	769	533
1075	1	707	399
1077	1	97	405
1081	1	58	438
1086	1	1	384
1087	2	246	431

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1088	1	3	374
1096	1	474	238
1098	1	1015	509
1100	1	1020	511
1100	2	1520	1158
1101	1	703	353
1102	1	385	194
1107	1	2	580
1114	1	3	422
1115	1	2	268
1119	1	22	267
1129	1	40	342
1112	1	360	181
1133	1	609	376
1144	1	446	225
1147	1	556	280
1153	1	1	153
1154	1	3	818
1159	1	1	330
1161	1	341	186
1164	1	427	254
1171	1	19	240
1171	2	108	299
1183	1	2	379
1195	1	355	179
1196	1	1	189
1200	1	33	197

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1203	2	129	464
1222	2	105	401
1232	1	1	387
1240	1	2	175
1247	1	320	311
1271	1	412	221
1286	1	2	595
1295	1	1	165
1306	1	367	185
1314	2	158	631
1316	1	58	570
1359	1	384	193
1370	1	1	402
1371	1	1	345
1374	1	710	357
1378	1	2	400
1392	1	3	413
1411	1	202	432
1433	1	311	167
1450	1	2	256
1453	1	255	149
1471	1	721	398
1477	1	869	639
1502	1	794	399
1518	1	126	449
1534	1	283	143
1546	1	3	401

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1547	1	506	285
1583	1	3	350
1587	1	3	563
1602	2	170	679
1629	1	1	402
1665	1	468	235
1760	1	625	314
1762	1	3	200
1876	2	119	286
1895	1	2	379
1931	1	758	400
1976	2	715	383
2055	2	252	401
2056	1	331	167
2150	1	523	263
2157	1	794	399
2164	1	564	283
2175	1	218	400
2212	1	452	331
2338	1	732	367
2342	1	3	167
2352	1	330	166
2352	2	622	398
2355	1	47	352
2356	1	679	341
2359	1	301	352
2421	1	296	350

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
3046	1	367	185
3049	1	553	278
3050	1	3	314
3052	1	504	253
3065	1	2	157
3070	1	357	190
3075	1	440	222
3080	1	1	285
3092	1	320	162
3093	1	411	250
3100	1	52	237
3103	1	47	298
3118	1	344	174
3123	1	2	145
3127	1	1	147
3138	1	336	169
3142	1	388	203
3144	1	664	386
3151	1	337	170
3155	2	202	384
3168	1	12	176
3205	1	288	145
3282	1	1	150
3303	2	239	400
3371	2	211	399
3356	1	2	148
3358	2	36	401

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
3046	1	367	185
3049	1	553	278
3050	1	3	314
3052	1	504	253
3065	1	2	157
3070	1	357	190
3075	1	440	222
3080	1	1	285
3092	1	320	162
3093	1	411	250
3100	1	52	237
3103	1	47	298
3118	1	344	174
3123	1	2	145
3127	1	1	147
3138	1	336	169
3142	1	188	203
3144	1	664	386
3151	1	337	170
3155	2	202	384
3168	1	12	176
3205	1	288	145
3282	1	1	150
3303	2	239	400
3371	2	211	399
3558	1	2	148
3558	2	36	401

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
3568	1	751	377
3595	1	757	380
3618	1	2	238
3618	2	130	402
3622	1	86	358
3622	2	654	398
3642	1	876	439
3649	1	781	398
3651	1	625	314
3664	1	467	637
3674	1	55	402
3677	1	619	311
3704	1	1	402
3726	1	535	269
3765	1	510	256
3779	1	554	357
3794	1	266	135
3794	2	667	377
3796	2	638	375
3801	1	474	262
3806	1	453	298
3807	1	42	389
3815	1	798	400
3827	1	3	320
3842	1	781	392
3853	1	671	399
3855	1	1	324

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
3857	1	2	235
3861	1	590	297
3865	1	695	399
3897	1	3	173
3897	2	143	400
3898	2	225	401
3921	2	103	342
3927	1	70	375
3930	1	76	234
3946	2	651	382
3951	2	105	377
3965	1	646	344
3973	1	795	400
3981	1	3	311
3996	1	3	356
4001	1	481	296
4003	1	90	335
4018	1	2	259
4018	2	186	401
4021	1	1	345
4043	1	3	344
4054	1	3	344
4066	1	1	150
4070	1	1	324
4072	2	187	390
4073	1	1	285
4077	2	127	372

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
4083	1	3	359
4090	1	27	368
4101	1	103	297
4105	1	1	306
4107	1	570	286
4119	1	629	339
4121	1	740	372
4123	1	3	230
4127	1	3	341
4128	1	2	331
4130	1	768	415
4146	1	97	381
4157	1	3	206
4186	1	505	254
4224	1	510	256
4239	1	1	348
4242	1	709	356
4252	1	589	296
4253	1	1	174
4256	1	568	323
4258	2	498	334
4267	1	284	144
4271	1	2	304
4287	1	303	163
4289	1	471	319
4302	1	153	305
4304	1	1	186

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
4304	2	96	314
4306	1	2	151
4318	1	576	289
4322	1	5	146
4331	1	439	221
4331	2	528	364
4338	1	728	399
4346	1	471	277
4367	2	117	311
4375	1	2	268
4381	1	574	326
4384	1	614	309
4397	1	9	311
4402	1	1	249
4403	1	606	328
4406	1	3	317
4411	1	2	280
4411	2	697	398
4412	1	2	364
4418	1	3	230
4424	1	601	398
4443	1	437	215
4471	1	643	323
4478	1	540	271
4482	1	50	289
4489	1	601	302
4491	1	12	206

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
4495	1	3	179
4496	1	500	252
4500	1	130	306
4511	1	493	248
4518	1	1	246
4526	1	480	241
4527	1	2	163
4532	1	3	239
4542	1	11	175
4567	1	36	200
4573	1	1	231
4578	1	642	322
4619	1	1	180
4620	1	349	176
4662	1	1	246
4669	1	2	157
4680	1	28	183
4690	1	344	174

Table 4

ORF	SEQ ID NO	BLAST	Antigenic Regions			
		HOMOLOG	Region 1	Region 2	Region 3	Region 4
168_6	5192	lipoprotein	36-45	84-103	152-161	176-185
238_1	5193	chrA	21-39	48-58	84-95	232-249
51_2	5194	OppB gene product (B. sub	20-36	70-79	100-112	121-131
278_3	5195	lipoprotein 1	20-29	59-73	85-97	162-171
276_2	5196	lipoprotein	21-33	65-74	177-186	211-220
45_4	5197	ProX	28-37	59-69	85-100	120-129
315_8	5198	hypothetical protein	45-54	88-97	182-192	243-253
154_15	5199	unknown	31-40	48-58	79-88	95-104
228_3	5200	unknown	25-38	40-52	64-74	80-89
228_6	5201	unknown	29-41	89-101	128-143	173-184
50_1	5202	unknown	21-33	52-61	168-182	197-206
112_7	5203	iron-binding periplasmic	21-31	58-67	92-101	111-120
442_1	5204	unknown	30-39	91-100	122-137	182-192
66_2	5205	unknown	50-59	104-116	127-136	167-182
304_2	5206	Q-binding periplasmic	19-28	48-57	75-84	103-116
44_1	5207	hypothetical protein	27-36	86-95	129-138	192-201
161_4	5208	SphX	27-44	149-161	166-175	201-210
46_5	5209	cmpC (permease)	21-33	61-70	83-92	100-109
942_1	5210	traH [Plasmid pSK41]	83-92	109-118	127-142	
5_4	5211	ORF (S. aureus)	12-22	87-96	111-120	151-160
20_4	5212	peptidoglycan hydrolase (S.	24-34	129-138	141-150	161-171
328_2	5213	lipoprotein (H. flu)	81-90	123-133	290-299	
520_2	5214	fibronectin binding protein	44-54	63-79	81-90	95-110
771_1	5215	emm1 gene product (S. pyx	30-39	65-82	96-106	112-121
999_1	5216	predicted trithorax prot. (D	7-16	120-129	157-166	
853_1	5217	ORF2136 (Marchantia polyr	43-52	88-97	102-111	
287_1	5218	psaA homolog	13-22	28-44	72-82	114-124
288_2	5219	cell wall enzyme	14-23	89-98		
596_2	5220	penicillin binding protein 2b	40-49	59-68	76-87	106-115
217_5	5221	fibronectin/fibrinogen bindi	28-37	40-49	62-71	93-111
217_6	5222	fibronectin/fibrinogen bp	10-19	31-40	54-62	73-92
528_3	5223	myosin cross reactive prote	4-13	29-47	60-73	90-99
171_11	5224	EF	20-31	91-110		
63_4	5225	penicillin binding protein 2b	12-21	59-68	95-104	
353_2	5226		46-55	62-71		
743_1	5227	29 kDa protein in fimA regi	23-32	68-79	94-103	175-184
342_4	5228	Twitching motility	10-19	48-60	83-92	111-121
69_3	5229	arabinogalactan protein	97-106	132-141	158-167	180-189
70_6	5230	nodulin	36-45	48-57	137-160	179-188
129_2	5231	glycerol diester phosphodie	8-17	41-50	55-74	97-106
58_5	5232	PBP (S. aureus)	26-35	70-79	117-126	152-161
188_3	5233	MHC class II analog (S. aure	72-81	94-103	115-124	136-145
236_6	5234	histidine kinase domain (Dic	24-33	52-67	81-94	106-121
310_8	5235	clumping factor (S. aureus)	59-71	77-86	93-102	118-127
601_1	5236	novel antigen/ORF2 (S. aur	45-54	91-104	108-117	186-195
544_3	5237	ORF YJR151c (S. cerevisae	76-90	101-111	131-140	154-164
662_1	5238	MHC class II analog (S. aure	22-32	71-80	89-98	114-122
87_7	5239	5' nucleotidase precursor ('	29-45	62-71	105-114	125-137
120_1	5240	B65G gene product (B. sub	102-111			

Table 4

ORF	Antigenic		Regions (c nt)			
	Region 5	Region 6	Region 7	Region 8	Region 9	Region 10
168_6	244-272	303-315				
238_1	260-269	291-301	308-317			
51_2	140-152	188-208	211-220	256-266	273-283	
278_3	198-209					
276_2	255-268					
45_4	177-199	221-230	234-243	268-279	284-293	304-313
316_8						
154_15	148-157	177-187	202-211			
228_3	101-119	139-154	166-181			
228_6						
50_1						
112_7	136-149	197-211	218-229	253-273		
442_1	199-210	247-257	264-277	287-309		
66_2						
304_2	178-187	250-259				
44_1						
161_4						
46_5	131-141	162-176	206-215	243-252	264-273	285-294
942_1						
5_4	189-205	230-239	246-264	301-318	340-354	378-387
20_4	202-212	217-234	260-275	314-336	366-373	380-391
328_2						
520_2						
771_1	145-154					
999_1						
853_1						
287_1	154-164					
288_2						
596_2	121-130					
217_5	244-253	259-268	288-297	302-311		
217_6	144-158	174-183	188-197	207-216	226-242	
528_3						
171_11						
63_4						
353_2						
743_1	197-207					
342_4						
69_3	195-211					
70_6	206-215	263-272	291-301	331-340	358-371	390-414
129_2	117-127	141-157	168-183	202-211	222-231	261-270
58_5	184-203	260-269	275-299	330-344	372-381	424-433
188_3						
236_6	138-147	163-172	187-198	244-261	268-278	308-317
310_8	131-140	144-153	177-186	190-199	204-213	216-227
601_1	208-218					
544_3	170-179	184-193	224-235	274-287	327-336	352-361
662_1						
87_7						
120_1						

Table 4

5	ORF	Antigenic		Regions		(cont)	
		Region 11	Region 12	Region 13	Region 14	Region 15	Region 16
	168_6						
	238_1						
	51_2						
10	278_3						
	276_2						
	45_4						
	316_8						
	154_15						
15	228_3						
	228_6						
	50_1						
	112_7						
	442_1						
20	66_2						
	304_2						
	44_1						
	161_4						
	46_5	306-315					
25	942_1						
	5_4	393-407	416-426	456-465			
	20_4	396-405	410-419	461-481			
	328_2						
	520_2						
30	771_1						
	999_1						
	853_1						
	287_1						
	288_2						
35	596_2						
	217_5						
	217_6						
	528_3						
	171_11						
40	63_4						
	353_2						
	743_1						
	342_4						
	69_3						
45	70_6	453-471	506-515				
	129_2	296-315					
	58_5						
	188_3						
50	236_6	358-377	410-423	428-439	442-457	467-476	480-493
	310_8	238-251	256-275	281-290	296-310	314-333	338-347
	601_1						
	544_3						
	662_1						
55	87_7						
	120_1						

Table 4

5	ORF	Antigenic Regions (cont)				
		Region 17	Region 18	Region 19	Region 20	Region 21
	168_6					
	238_1					
	51_2					
10	278_3					
	276_2					
	45_4					
	316_8					
	154_15					
15	228_3					
	228_6					
	50_1					
	112_7					
	442_1					
20	66_2					
	304_2					
	44_1					
	161_4					
	46_5					
25	942_1					
	5_4					
	20_4					
	328_2					
	520_2					
30	771_1					
	999_1					
	853_1					
	287_1					
	288_2					
35	596_2					
	217_5					
	217_6					
	528_3					
	171_11					
40	63_4					
	353_2					
	743_1					
	342_4					
	69_3					
45	70_6					
	129_2					
	58_5					
	188_3					
	236_6					
50	310_8	357-366	370-379	429-438	443-452	478-487
	601_1					
	544_3					
	662_1					
55	87_7					
	120_1					

Table 4

5	ORF	Antigenic Regions (cont)				Region 27	Region 28
		Region 23	Region 24	Region 25	Region 26		
	168_6						
	238_1						
	51_2						
10	278_3						
	276_2						
	45_4						
	316_8						
	154_15						
15	228_3						
	228_6						
	50_1						
	112_7						
	442_1						
20	66_2						
	304_2						
	44_1						
	161_4						
	46_5						
25	942_1						
	5_1						
	20_4						
	328_2						
	520_2						
30	771_1						
	999_1						
	853_1						
	287_1						
	288_2						
35	596_2						
	217_5						
	217_6						
	528_3						
	171_11						
40	63_4						
	353_2						
	743_1						
	342_4						
	69_3						
45	70_6						
	129_2						
	58_5						
	188_3						
	236_6						
50	310_8	622-632	670-685	708-718	823-836	858-867	877-886
	601_1						
	544_3						
	662_1						
	87_7						
55	120_1						

Table 4

5

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ORF	Antigenic Region 29	Regions Region 30	(cont)
168_6			
238_1			
51_2			
278_3			
276_2			
45_4			
316_8			
154_15			
228_3			
228_6			
50_1			
112_7			
442_1			
66_2			
304_2			
44_1			
161_4			
46_5			
942_1			
5_4			
20_4			
328_2			
520_2			
771_1			
999_1			
853_1			
287_1			
288_2			
596_2			
217_5			
217_6			
528_3			
171_11			
63_4			
353_2			
743_1			
342_4			
69_3			
70_6			
129_2			
58_5			
188_3			
236_6			
310_8			
601_1			
544_3			
662_1			
87_7			
120_1			

Table 4

ORF	BLAST		Antigenic Regions			
	HOMOLOG		Region 1	Region 2	Region 3	Region 4
46_1	5241	aldehyde dehydrogenase	8-17	36-52	83-96	112-121
63_4	5242	glycerol ester hydrolase (P.	9-26	57-73	93-107	123-133
174_6	5243	ketopantoate hydroxymeth	71-80	203-212	242-254	265-274
206_16	5244	ornithine acetyltransferase	1-10	34-43	54-63	194-210
267_1	5245	NaH-antiporter protein (E. f	120-129	332-347	398-408	
322_1	5246	acriflavin resistance protein	58-75	153-164	203-231	264-284
415_2	5247	transport ATP-binding prot	108-126	218-227	298-308	315-334
214_3	5248	2-nitropropane dioxygenase	123-136	216-233	283-292	297-306
587_3	5249	clumping factor	5-14	43-54	59-68	76-95
685_1	5250	signal peptidase	59-68	72-81	86-95	99-108
54_3	5251	fibronectin binding protein I	23-32	37-46	50-59	89-98
54_4	5252	fibronectin binding protein I	43-52	66-75	95-104	147-156
54_5	5253	fibronectin binding protein I	49-60	81-90		
54_6	5254	fibronectin binding protein I	55-71	82-97	139-158	175-186
328_1	5255	lipoprotein (H. flu)	11-20	61-70	96-105	

Table 4

ORF	Antigenic Regions (cont)					
	Region 5	Region 6	Region 7	Region 8	Region 9	Region 10
46_1	215-242	333-352	376-385	416-432	471-487	
63_4	145-154	191-202	212-223	245-265	274-283	291-300
174_6						
206_16	239-259	275-284				
267_1						
322_1	298-319	350-359				
415_2	344-353	371-380	395-404	456-465	486-495	518-527
214_3	318-337	365-375				
587_3	106-115	142-151	156-166	173-182	186-198	204-213
685_1	113-122	130-145				
54_3	128-138	185-194	217-226	251-260	268-277	295-305
54_4	175-188	191-200	203-212	220-229		
54_5						
54_6	220-230	287-304	317-326	344-353	364-373	378-387
328_1						

Table 4

ORF	Antigenic Regions			(cont)		
	Region 11	Region 12	Region 13	Region 14	Region 15	Region 17
46_1						
63_4	306-315	319-328	366-376	395-420	453-462	467-476
174_6						
206_16						
267_1						
322_1						
415_2	539-555					
214_3						
587_3	217-226	278-287	318-327	332-342	351-360	377-386
685_1						
54_3	316-325	329-345	355-372	387-396	416-425	438-448
54_4						
54_5						
54_6	396-407	427-436	514-531	541-550	569-578	612-622
328_1						

Table 4

ORF	Antigenic Regions (cont)					
	Region 18	Region 19	Region 20	Region 21	Region 22	Region 23
46_1						
63_4	485-500	513-525				
174_6						
206_16						
267_1						
322_1						
415_2						
214_3						
587_3	396-405	426-442	459-470	485-494	505-514	531-562
685_1						
54_3	455-462	472-491	517-536			
54_4						
54_5						
54_6	639-648	673-681	703-715	723-732	749-760	772-788
328_1						

Table 4

ORF	Antigenic Regions (cont)					
	Region 24	Region 25	Region 26	Region 27	Region 28	Region 29
46_1						
63_4						
174_6						
206_16						
267_1						
322_1						
415_2						
214_3						
587_3	567-578	584-601	607-840	844-854	858-870	877-886
685_1						
54_3						
54_4						
54_5						
54_6	793-802	811-826	834-848	866-876	893-903	907-918
328_1						

Table 4

ORF	Antigenic Regions (cont)	
	Region 30	Region 31
46_1		
63_4		
174_6		
206_16		
267_1		
322_1		
415_2		
214_3		
587_3	889-911	927-936
685_1		
54_3		
54_4		
54_5		
54_6	925-944	951-997
328_1		

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANT:

10 (A) NAME: Human Genome Sciences, Inc.
(B) STREET: 9410 Key West Avenue
(C) CITY: Rockville
(D) STATE: Maryland
15 (E) COUNTRY: US
(F) POSTAL CODE: 20850

(ii) TITLE OF INVENTION: Staphylococcus aureus Poly-
nucleotides and Sequences

20 (iii) NUMBER OF SEQUENCES: 5255

(v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
(B) COMPUTER: HP Vectra 486/33
(C) OPERATING SYSTEM: MSDOS version 6.2
30 (D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
35 (B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/009,861
40 (B) FILING DATE: 05-JAN-1996

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5895 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

10 TCCATTATGA AGTCACAAGT ACTATAAGCT GCGATGTTAC CAATGTTTTT TAAATCCCA 60
 GTAATAAAAT CAAAAAATAA GTTAAATAAT GTATTCATTT TAAGTCCTCC TTAATAAAGa 120
 15 aaataGGTAA TAATGTAATA GCTTCTATTA TGATGCCTAA TTGAATGAAT TGGGCAAATG 180
 GCTCTTTGAT GATAAGTGTG ATAATGAAAA GGGTTAAACT AACATAATC GCATAATATT 240
 TTTTTCGTTT AATAAGTCGC ACAGGAATGG GCTTCTTTTT AGTTGCTGCA GGAGCATATA 300
 20 CTGAGATTAC ACCTAAAGAA ATAAGTGTGA AAATAATCAT AATTAAAAAG TTAATATGAA 360
 AATTTACTAT TACTAAAGGT AAAAGTATAA ATAGTATAAT ACTTTCTACA TAACACCAAAA 420
 AAGAAGAAGG TGCATGTGCa CCATGTGCAT GtCTTCTTAT TAAATAAAAT GTTAAATTCG 480
 25 TAATTAACGT AAACAGAAAA ATGTTTAAAA TATAGGCAAT AGTATACATA ACAATTAATT 540
 TACCTATATT TTTAGCTAAG ACCTGCATCC CTAATCGTAC TTGCAAAAAT TGAATATGAT 600
 30 CTAAGTTATT TCTCTTTTGA AGATACGTGG CAAACTGGTC AATTTTATTA TCAAAATAAT 660
 TCAATTTTAC ACCACTCTCC TCACTGTCAT TATACGATTT AGTACAATCT TTTATCATTa 720
 TATTGCCTAA CTGTAGGAAA TAAATACTTA ACTGTTAAAT GTAATTTGTA TTTAATATTT 780
 35 TAACATAAAA AAATTTACAG TTAAGAATAA AAAACGACTA GTTAAGAAAA ATTGGAAAAT 840
 AAATGCTTTT AGCATGTTTT AATATAACTA GATCACAGAG ATGTGATGGA AAATAGTTGA 900
 TGAGFTGTTT AATTTTAAGA ATTTTATCT TAATTAAGGA AGGAGTGATT TCAATGGCAC 960
 40 AAGATATCAT TTCAACAATC GGTGACTTAG TAAATGGAT TATCGACACA GTGAACAAAT 1020
 TCACTAAAAA ATAAGATGAA TAATTAATTA CTTTCATTGT AAATTGTGTA TCTTCGTATA 1080
 45 GTACTAAAAG TATGAGTTAT TAAGCCATCC CAACTTAATA ACCATGTAAA ATTAGCAAGT 1140
 GAGTAACATT TGCTAGTAGA GTTAGTTTCC TTGGACTCAG TGCTATGTAT TTTTCTTAAT 1200
 TATCATTACA GATAATTATT TCTAGCATGT AAGCTATCGT AAACAACATC GATTTATCAT 1260
 50 TATTTGATAA ATAAAATTTT TTTCATAATT AATAACATCC CCAAAAATAG ATTGAAAAAA 1320
 TAACTGTAAA ACATTCCCTT AATAATAAGT ATGGTCGTGA GCCCTCCCA AGCTCGCGGC 1380
 CTTTTTTGTA ATGAAGAAGG GATGAGTTAA TCATCATTAT GAGACCCGCC GTTAAATAT 1440

	TCATTTGCAA	AGGGCGAAAT	GGGTTCTTAC	TGAGTTATCT	ATTATAAAAA	AATAAACATA	1560
	GACTTATGAA	AAATCTCTCA	TAAATCTATG	TTTAGTCATG	aCATGTGTTA	AATATTATTT	1620
5	CGGGCGCTTC	TTATTTATAC	AAATCTAATT	TAATACTTTT	AAATACAGGT	ATATTTTCgC	1680
	GTTGCTGTTT	TACTTCATTT	AAGTTTAAAT	CTACAGTCAA	AATATCTGCG	GATTCAATTTA	1740
10	ATTCTCCAAC	TAAATCTCCA	TTTGGGTTTA	TAACTATCGA	ATGACCAGCA	TATTCTGTGT	1800
	TACCATCGAA	TCCAGTGCTA	TTAGTTCCAA	TGACAAACAT	ATTATTTTCA	ATTGCACGTG	1860
	CCTTTAGTAA	TGAATGCCAA	TGTTGAAGAC	GTGACATAGG	CCATTGCGCC	ACATAAAATG	1920
15	CAATTTTAGC	ACCACTACGA	GCAGGATATC	TTAATAATTC	TGGAAAACGT	AAATCATAAC	1980
	AGATAAGTTG	GGTCACATAA	GTACCGTCAG	ACAATTGAAA	GGGTTTCAGCT	ACGTATTTCGC	2040
	CAGCGGTAA	AAATTCATGC	TCTCTTAACA	TAGGAACTAA	ATGAACTTTG	TCGTATTCaT	2100
20	TAATCAGCTG	GCCACTTTTA	TTCACACTAA	AAGCTGTATT	AAATATTTGA	TTGTTTCTAA	2160
	TGTTAGAAAC	TGACCCAGCT	ACGATATCGA	CTTTATATTT	TTCAGCTAAA	TGTTTAATAA	2220
25	ATGAAAAACT	TTGTCCTAGA	TTATTATCTG	CTTTTTCATT	TAAATGCTCT	AAATCATAGC	2280
	CATTATTCCA	CATTTCAGGT	AAAACGACTA	CATCTACTTC	AGCATTCTATA	TTTTTTTCGA	2340
	ACCATTGCGT	TATTTGAGTT	TCATTTTTAG	AACTATCTCC	AAAAACAATC	GGTAATTGAT	2400
30	AAATTTGGAC	TTTCATAACA	TCACATCCTT	GATAGATCTT	ATATATAACT	TACTAAAAGT	2460
	TATGTTGAAA	CGCAAAAAAC	GAGCACAAGA	CATAAAATCA	AAGTCCTAGG	CTCTACAAAG	2520
	TTATATTGAC	AGTAGTTGAT	GGGGCCCCAA	CATAGAGAAA	TTGGAACACC	AATTTCTACA	2580
35	GACAATGCAA	GTTGGGGTGG	GCTCTAACAT	AAAGAAATAC	TTTTTCTTTA	GAAATTAGTA	2640
	TTTCTTATAC	ATGAGTTTTA	CTCATGTATT	CCTATTCTTA	AGTGCACATT	AGCAGCGGCT	2700
	AATGTGTAAG	AACTACTACA	TAATGAATAA	CTAATGATTC	TTTATCATTT	CTGTCCCATT	2760
40	CCTAACAATA	TATTGATTAT	TTTTTTTATTA	CGAAACGATC	TTCCACTGGA	TTAAATGTTT	2820
	TTTCGCCAGC	AGCTTCACGA	ATATCACCAA	ATGGCATTG	AGCAATAAGT	TTCCAACTTT	2880
45	TAGGAATATT	AAATTCATTT	GAAGTCATCT	CATCAACAAG	TGGATTATAG	TGTTGTAATG	2940
	AAGCACCTAT	GCCTTTAGTA	GCTAATGCAG	TCCAAATTGC	AAATTGATGC	ATGGCATTG	3000
	TTTGAGTTGA	CCATATTGCA	AAATTATCAT	AGTAGTTTGG	CATTTGTTCT	TGTAAACCAC	3060
50	TTACAACATC	TTGATCTTCA	TAAAACAAAA	TTGTACCGTA	TGAATGTTTG	AAGTTATCAA	3120
	TTTTTTGTTC	AGTTGGCTCG	AAATCACGAT	TCTCTCCCAT	GACTTCTTTT	AAAATTGCTT	3180
55	TTGTGTTATC	CCAAAATTTA	TTATTGTTGT	CATTTAACAA	GAGAACAATT	CTAGTTGATT	3240

	CATCGCTAAT TGATATCGAA TCTTTCAAAT TATATATTGA ACGTCTTTCT TCCATTGCAT	3360
	TGTCAAAAGT CATTGCTTTT TTATCTTTTT TAAATAAGCC CATAATTATT GTCCTTCTT	3420
5	TAGTAAAGAA TACTTAATAG ACTAAGTATA AAATTTATAC TCGTACTTGT AAAGCAATAT	3480
	TTACGAAAAT TTCAAGAATA TTAATATTCA TTTTCAAATT CCAAATATAA ATGCATTTTC	3540
10	AACGCATATT TATTATACTT AGATTAATAC TTACATGAAA AAGGGAGGTG TCTCGTGAAA	3600
	TGTCATATCA TTGGTTTAAG AAAATGTTAC TTTCAACAAG TATTTTAATT TTAAGTAGTA	3660
	GTAGTTTAGG GCTTGCAACG CACACAGTTG AAGCAAAGGA TAACTTAAAT GGAGAAAAAC	3720
15	CAACTACTAA TTTGAATCAT AATATAACTT CACCATCAGT AAATAGTGAA ATGAATAATA	3780
	ATGAGACTGG GACACCTCAC GAATCAAATC AAACGGGTAA TGAAGGAACA GGTTCGAATA	3840
	GTCGTGATGC TAATCCTGAT TCGAATAATG TGAAGCCAGA CTCAAACAAC CAAAACCCAA	3900
20	GTACAGATTC AAAACCAGAC CCAAATAACC AAAACTCAAG TCCGAATCCT AAACCAGATC	3960
	CAGATAACCC GAAACCAAAA CCGGATCCAA AACCAGACCC AGATAAACCA AAGCCAAATC	4020
25	CGGATCCAAA ACCAGATCCA GATAACCCGA AACCAAATCC AGATCCAAAA CCAGACCCAG	4080
	ATAAACCAAA GCCAAATCCG GATCCAAAAC CAGATCCAGA TAAACCAAAG CCAAATCCGA	4140
	ATCCAAAACC AGACCCTAAT AAGCCAAATC CTAACCCGTC ACCAGATCCC GATCAACCTG	4200
30	GGGATTCCAA TCATTCTGGT GGCTCGAAAA ATGGGGGGAC ATGGAACCCA AATGCTTCAG	4260
	ATGGATCTAA TCAAGGTCAA TGGCAACCAA ATGGGAATCA AGGAAACTCA CAAAATCCTA	4320
	CTGGTAATGA TTTTGTATCC CAACGATTTT TAGCCTTGGC AAATGGGGCT TACAAGTATA	4380
35	ATCCGTATAT TTAAATCAA ATTAATAAGT TGGGCAAAGA TTATGGAGAA GTTACTGATG	4440
	AAGACATTTA TAATATTATT CGAAAACAAa ATTTCAGCGG AAATGCATAT TTAAATGGAT	4500
	TACAACAGCA ATCGAATTAC TTTAGATTCC aATATTTCAA TCCATTGAAA TCAGAAAGGT	4560
40	ACTATCGTAA TTTAGATGAA CAAGTACTCG CATTAATTAC TGGTGAAATT GGATCAATGC	4620
	CAGATTTGAA AAAGCCCGAA GATAAGCCGG ATTCAAACA ACGCTCATTT GAACCGCATG	4680
45	AAAAAGACGA TTTTACAGTA GTTAAAAAAC AAGAAGATAA TAAGAAAAGT GCGTCAACTG	4740
	CATATAGTAA AAGTTGGCTA GCAATTGTAT GTTCTATGAT GGTGGTATTT TCAATCATGC	4800
	TATTCTTATT TGTAAAGCGA AATAAAAAGA AAAATAAAAA CGAATCACAG CGACGATAAT	4860
50	CCGTGTGTGA TTCGTTTTTT TTATTATGGA ATAAAAATGT GATATATAAA ATTCGCTTGT	4920
	TCCGTGGCTT TTTTCAAAGC CTCAGGATTA AGTAATTGGA ATATAACGAC AAATCCGTTT	4980
55	TGTAACATAT GGATAATAAT TGGAACAGCA AGCCGTTTTG TCCAAACATA TGCTAATGAA	5040

AATATTAATG AACTTACTGT TGTAGCAATA ATAAATGCCA CGATACGATT ACCTTTAATC 5160
 GCATTAAATA ATTCTCCAAA GATTACTTTT CTGAATACAT ATTCTTCTAA TAAAGGACCA 5220
 5 ATAATAGATA CAAAGAAGAT AAATATAGGT ATTTTTCGAG CAATAATAAT TAGCTTTTCT 5280
 GTATTAGGAC TTAATTGTTG TCCACCATAA ATTTGCGTTA ATACAATGCT CACTACCATT 5340
 10 TGATAAATCA TTACCAATGC AAATCCAAGC AATGCCCATG GAATGATATA TTTTTTAGGT 5400
 TCTTTAACTT CTAATTCTAA TTTTGTGGA TTTTAAATTT TTAAATTAAT TAAAATAATC 5460
 GTCGTGGCGG CGATTAAAAA TAGAACAAGT TGTATGTAAA TGACTGCTTT AGTCAGTTCT 5520
 15 ATGCCACTAT ATTGTACAAA TGGTAATTTT TTTACAATGA GAAGCGGTAA AAATTGAGAC 5580
 AATATATAAA TAATAACAGT TAGCAATGAT GCCCATAATC tTGTCATAAT TTTCTCCAA 5640
 ATATTGTTT ATAATTTATT TTATCGTAAA TAACTTGAAG TTACAAAAC TAATTAAAAG 5700
 20 GTTATGACTT GAAATTTTGA CCAATTTGA TTATTATAAA TGTATGTTAG CACTCTTTAA 5760
 TGTTAAGTGC TAACTTTAG GTTTTTTAAG GAGGAACAAT CATGCTAAAA CCAATTGGAA 5820
 25 ATCGTGTGAT TATTGAGAAA AAAGAACAAG AACAAACAAC TAAAAGTGGn ATTGTTTAAC 5880
 TGATAGTGCT AAAGA 5895

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6796 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TTTGAAAAAA CAAGGTACGA TTGGTTTAAT AACATATATG AGAACCGATT CTACACGTAT 60
 40 TTCaGATACT GCCAAAGTTG AAGCAAAACA GTATATAACT GATAAATACG GTGAATCTTA 120
 CACTTCTAAA CGTAAAGCAT CAGGGAAACA AGGTGACCaa GATGCCCATG AGGCTATTAG 180
 45 ACCTTCAAGT ACTATGCGTA CGCCAGATGA TATGAAGTCA TTTTGTACGA AAGACCAATA 240
 CCGATTATAC AAATTAATTT GGAACGATT TGTGCTAGT CAAATGGCTC CAGCAATACT 300
 TGATACAGTC TCATTAGACA TAACACAAGG TGACATTAAA TTTAGAGCGA ATGGTCAAAC 360
 50 AATCAAGTTT AAAGGATTTA TGACACTTTA TGTAGAAACT AAAGATGATA GTGATAGCGA 420
 AAAGGAAAAT AAAGTGCCTA AATTAGAGCA AGGTGATAAA GTCACAGCAA CTCAAATTGA 480
 55 ACCAGCTCAA CACTATACAC AACCACCTCC AAGATATACT GAGGCGAGAT TAGTAAAAAC 540

	AAAGCGTAAC TATGTCAAAT TAGAAAGTAA GCGTTTTGTT CCTACTGAGT TGGGAGAAAT	660
	AGTTCATGAA CAAGTGAAAG AATACTTCCC AGAGATTATT GATGTGGAAT TCACAGTGAA	720
5	TATGGAAACG TTAAGTGATA AGATTGCAGA AGGCGACATT ACATGGAGGA AAGTAATCGA	780
	CGGTTTCTTT AGTAGCTTTA AACAAAGATGT TGAACGTGCT GAAGAAGAGA TGGAAAAGAT	840
10	TGAAATCAAA GATGAGCCAG CCGGTGAAGA CTGTGAAATT TGTGGTTCTC CTATGGTTAT	900
	AAAAATGGGA CGCTATGGTA AGTTCATGGC TTGCTCAAAC TTCCCGGATT GTCGTAATAC	960
	AAAAGCGATA GTTAAGTCTA TTGGTGTTAA ATGTCCAAAA TGTAATGaTG GTGACGTCGT	1020
15	AGAAAGAAAA TCTAAAAAGA ATCGTGTCTT TTATGGATGT TCGAAATATC CTGAATGCGA	1080
	CTTTATCTCT TGGGATAAGC CGATTGGAAG AGATTGTCCA AAATGTAACC AATATCTTGT	1140
	TGAAAATAAA AAAGGCAAGA CAACACAAGT AATATGTTCA AATTGCGATT ATAAAGAGGC	1200
20	AGCGCAGAAA TAATATTTTT ATTTCTAGA TACATTTTAA GATTGTAAA TAGAATCATT	1260
	AGTGAATCTT ATTTTAAAGA TAGTAAAGGA TTAATCTAAA TAAGTCCGGA TAATATAAAC	1320
25	ATAACAACAT AATTAAmAGA CATAAATGAC aATAAAAGGA GTATAGAAAT GACTCAAAC	1380
	GTAATGTAA TAGGTGCTGG TCTTGCCGGT TCAGAAGCGG CATATCAATT AGCTGAAAGA	1440
	GGAATTAAAG TTAATCTAAT AGAGATGAGA CCTGTAAAC AACACCAGC GCACCATACT	1500
30	GATAAATTTG CGGAACCTGT ATGTTCCAAT TCATTACGCG GAAATGCTTT AACTAATGGT	1560
	GTGGGTGTTT TAAAAGAAGA AATGAGAAGA TTGAATTCTA TAATTATTGA AGCGGCTGAT	1620
	AAGGCACGAG TTCCAGCTGG TGGTGCTTA GCAGTTGATA GACACGATT TTCAGGTTAT	1680
35	ATTACTGAAA CACTTAAAA TCATGAAAAT ATCACAGTTA TTAATGAAGA AATTAATGCC	1740
	ATTCCAGATG GATACACAAT TATCGCAACA GGACCACTTA CTACAGAAAC CCTTGCGCAA	1800
	GAAATAGTGG ACATTACTGG TAAAGATCAA CTTTATTTCT ATGATGCGGC TGCTCCAATT	1860
40	ATTGAAAAAG AATCTATTGA TATGGATAAA GTTTACTTAA AGTCCCGTTA TGATAAAGGT	1920
	GAAGCTGCAT ATTTAAACTG TCCTATGACT GAGGATGAAT TTAATCGCTT TTATGATGCA	1980
45	GTATTAGAAG CTGAAGTTGC GCCTGTAAAT TCATTTGAAA AAGAAAAATA TTTCGAGGGT	2040
	TGTATGCCTT TTGAAGTAAT GGCAGAACGC GGACGCAAGA CATTACTATT TGGACCAATG	2100
	AAACCAGTAG GATTAGAAGA TCCAAAGACT GGGAAACGTC CTTATGCGGT GGTTCATTA	2160
50	AGACAAGATG ACGCTGCTGG TACACTCTAC AATATTGTTG GCTTCCAAAC GCATTTAAAA	2220
	TGGGGAGCTC AAAAAGAAGT CATTAAATTA ATTCCAGGCT TAGAAAATGT TGATATTGTT	2280
55	AGATATGGTG TGATGCATAG AAATACCTTC ATTAATTCAC CGGACGTATT AAACGAGAAA	2340

	TATGTAGAAA	GCGCagctAG	CGGCTTAGTT	GCAGGTATCA	ATCTTGCGCA	TAAAATATTA	2460
5	GGCAAGGGTG	AGGTAGTATT	TCCGAGAGAA	ACAATGATTG	GAAGTATGGC	TTACTATATT	2520
	TCTCATGCTA	AAAACAATAA	GAATTTCCAA	CCTATGAATG	CTAACTTCGG	GTTATTACCA	2580
	TCTTTAGAAA	CTAGAATTAA	AGATAAAAAA	GAACGCTATG	AAGCACAAGC	TAATAGAGCT	2640
10	TTGGATTACT	TAGAAAATTT	CAAAAAAACT	TTATAAAATA	GTTAGAAAGA	CTAGATATGC	2700
	TATTCATTCT	TAAGTCATCA	ACGAGTAAGT	AATGACTTTC	TAAATGGAAA	ATACTTATCC	2760
	TAGTCTTTTT	AATTTTGGAA	TTGTTACGTA	TTTCTGACAA	TTTAGAATTC	GCATTCAAAA	2820
15	AATATCTAAA	TAAATAACAC	GCAATAAGTT	GATTGATGTA	ACATGTAAGA	GAATGTTTTA	2880
	AATAAACTTT	ATTTAAAAGG	CAATGAAATA	ATAAATGGCA	AGGCTATTAA	TAAAGACTTT	2940
	TAGTAATTAA	TTTAAAAAAG	AGGTATTCTA	ATTAAACAGGT	TTTCCGATTA	GTTACAATTA	3000
20	TTTAATTCTC	AAAAGATTTA	GAATTGATTA	TCAAATTACT	GTAAGCCCTT	TGCTGTATAT	3060
	GCTACAATTC	TTATTGATGG	AGGGTAAATG	TATTGAATCA	TATTCAAGAT	GCGTTTTTAA	3120
25	ATACATTGAA	AGTTGAACGG	AATTTTTTCGG	AACACACATT	GAAATCATAT	CAAGATGACT	3180
	TAATTCAGTT	TAATCAATTT	TTAGAACAAG	AACATTTAGA	GTTGAATACT	TTTGAATACA	3240
	GAGATGCTAG	AAATTATTTG	AGCTATTTAT	ATTCAAATCA	TTTGAAAAGA	ACATCTGTTT	3300
30	CTCGTAAAT	CTCAACGTTA	AGAACTTTCT	ATGAATATTG	GATGACGCTT	GATGAGAACA	3360
	TTATTAATCC	ATTTGTTCAA	TTAGTACATC	CGAAAAAAGA	AAAATATCTT	CCGCAATTCT	3420
	TTTACGAAGA	AGAAATGGAA	GCGTTATTCA	AAACTGTAGA	AGAGGACACT	TCAAAAAATT	3480
35	TACGGGATCG	AGTTATTCTT	GAATTGTTGT	ATGCTACAGG	CATCCGTGTT	TCGGAATTAG	3540
	TAAATATTAA	AAAACAAGAT	ATAGATTTTT	ACGCGAATGG	TGTTACCGTA	TTAGGAAAAG	3600
	GGAGCAAAGA	GCGCTTTGTA	CCGTTTGGTG	CTTATTGTAG	ACAAAGCATC	GAAAATTATT	3660
40	TAGAACATTT	CAAACCAATT	CAGTCATGCA	ATCATGATTT	TCTTATTGTA	AATATGAAGG	3720
	GTGAAGCAAT	CACTGAACGC	GGTGACGAT	ATGTTTTTAA	TGATATTGTT	AAACGAACAG	3780
45	CAGGCGTAAG	TGAGATTTCAT	CCCCACAAGC	TCAGACATAC	ATTGCAACG	CATTTATTGA	3840
	ATCAAGGTGC	AGACCTAAGA	ACAGTACAAT	CGTTATTAGG	TCATGTTAAT	TTGTCAACAA	3900
	CTGGTAAATA	TACACACGTA	TCTAACCAAC	AATTAAGAAA	AGTGTATCTA	AATGCACATC	3960
50	CTCGAGCGAA	AAAGGAGAAT	GAAACATGAG	TAATACAACA	TTACATGCAA	CAACAATTTA	4020
	TGCTGTAAGA	CATAATGGGA	AAGCAGCTAT	GGCTGGAGAT	GGGCAAGTAA	CGCTTGGTCA	4080
55	ACAAGTCATC	ATGAAACAAA	CGGCAAGAAA	AGTGCGACGT	TTATATGAAG	GTAAAGTGTT	4140

	ATTACAACAG TTTAGTGGTA ACTTAGAAAAG AGCTGCTGTT GAATTGGCAC AAGAATGGCG	4260
	AGGCGATAAA CAATTACGTC AATTAGAAGC TATGCTAATT GTAATGGATA AAGATGCTAT	4320
5	TTTAGTTGTC AGTGGAAC TGCGAAGTTAT TGCTCCAGAT GATGACCTTA TCGCTATTGG	4380
	ATCAGGAGGC AACTACGCAT TAAGCGCAGG ACGTGCATTG AAACGCCATG CATCGCATT	4440
10	GTCTGCTGAA GAAATGGCAT ATGAGAGCTT GAAAGTAGCG GCTGATATTT GTGTCTTTAC	4500
	CAACGATAAT ATTGTTGTCTG AAACACTATA ATAATCAGAG CACGATAAAT AATTACGAGC	4560
	AATTAATTTT AGTTAAAAGA CGGAGGAATG AAATTAATGG ATACAGCTGG AATAAGATTA	4620
15	ACTCCAAAAG AAATCGTATC TAAATTAAAT GAATACATCG TTGGACAAAA TGATGCTAAA	4680
	CGTAAAGTGG CAATTGCCCT ACGTAATCGA TACAGAAGAA GTTTATTAGA TGAGGAATCA	4740
	AAGCAAGAAA TTTCACCTAA AAATATTTTG ATGATTGGAC CAACCGGCGT TGGTAAAAC	4800
20	GAAATTGCAA GAAGAATGGC CAAAGTTGTC GCGCGCCCAT TTATAAAAGT AGAAGCTACT	4860
	AAATTTACTG AGGTAGGTTA TGTAGGACGA GATGTTGAAA GTATGGTTAG AGATCTTGTT	4920
25	GATGTTTCAG TAAGATTAGT CAAGGCGCAG AAAAAATCAT TGGTACAAGA TGAAGCAACA	4980
	GCTAAGGCCA ATGAAAAACT TGTTAAGTTA TTAGTTCCAA GTATGAAAA GAAAGCGTCT	5040
	CAAACGAATA ATCCTTTAGA GTCACTTTTC GGAGGTGCAA TTCCAAATTT CGGACAAAAT	5100
30	AACGAAGATG AAGAAGAACC ACCTACTGAG GAAATTAAAA CAAAACGTTT TGAAATTAAG	5160
	AGACAGCTAG AAGAAGGCAA ACTTGAAAA GAAAGGTAA GAATTAAAGT CGAACAAGAT	5220
	CCTGGTGCTT TAGGTATGCT AGGTACAAAT CAAATCAGC AAATGCAAGA GATGATGAAT	5280
35	CAATTAATGC CTAAAAAGAA AGTTGAGCGA GAAGTTGCTG TTGAGACGGC AAGGAAAATC	5340
	TTAGCTGATA GTTATGCGGA TGAAC TAATT GATCAAGAAA GCGCTAACCA AGAAGCGCTT	5400
	GAATTAGCAG AACAAATGGG TATCATCTTT ATAGATGAAA TCGACAAAGT TCGACGAAT	5460
40	AATCATAATA GTGGTCAAGA TGTCTCAAGA CAAGGTGTTT AAAGAGATAT TTTACCTATA	5520
	CTTGAAGGTA GCGTTATTCA AACCAAATAT GGTACTGTGA ATACTGAACA TATGCTGTTT	5580
45	ATAGGTGCTG GAGCTTTCCA TGTATCTAAG CCGAGTGAAT TGATACCAGA ATTGCAAGGT	5640
	CGTTTTCCGA TTAGAGTTGA ACTTGATAGT TTATCGGTAG AAGATTTTGT AAGAATTTTG	5700
	ACAGAACCAA AATTGTCATT AATTAAACAA TATGAAGCAT TGCTTCAAAC AGAAGAAGTT	5760
50	ACTGTAAACT TTACCGATGA AGCAATTACT CGCTTAGCTG AGATTGCTTA TCAAGTAAAT	5820
	CAAGATACAG ACAACATTGG TGCACGTCGA CTTCATACAA TTTTAGAAAA GATGCTAGAA	5880
55	GATTTATCAT TCGAAGCACC AAGTATGCCG AATGCAGTTG TAGATATTAC CCCACAATAT	5940

AAATATACAA AAGGAGAAAA ATTCATGAGC TTATTATCTA AAACGAGAGA GTTAAACACG 6060
 TTACTTCAAA AACACAAAGG TATTGCGGTT GATTTTAAAG ATGTAGCACA AACGATTAGT 6120
 5 AGCGTAACTG TAACAAATGT ATTTATTGTA TCGCGTCGAG GTAAAATTTT AGGATCGAGT 6180
 CTAAATGAAT TATTAAAAAG TCAAAGAATT ATTCAAATGT TGGAAGAAAG ACATATTCCA 6240
 10 AGTGAATATA CAGAACGATT AATGGAAGTT AAACAAACAG AATCAAATAT TGATATCGAC 6300
 AATGTATTAA CAGTATTCCC ACCTGAAAAC AGAGAATTAT TCATAGATAG TCGTACAACT 6360
 ATCTTCCCAA TTTTAGGTGG AGGGGAAAGA TTAGGTACAT TAGTACTTGG TCAAGTACAT 6420
 15 GATGATTTTA ATGAaAAATGA TTTGGTACTA GGTGAATATG CTGCTACAGT TATTGGTATG 6480
 GAAaTCTTAC GTGAGAAGCA TAGTGAAGTA GAAaAAGAAG CGCGCGATAA AGCTGCTATT 6540
 ACAATGGCAA TTAATTCATT ATCTTATTCT GAAAAAGAAG CGATTGAACA TATCTTTGAA 6600
 20 GAACTTGGCG GTACGGAAGG CCTATTAATC GCATCAAAAG TTGCAGATAG AGTTGGTATT 6660
 ACTAGATCTG TAATTGTAAA TGCACCTACG AAATTAGAAA GTGCTGGTGT AATTGAATCA 6720
 25 CGTTCTTTAG GAATGAAAGG TACTTTTATT AAAGTTAAAA AAGAAAAATT CTTAGATGAA 6780
 TTAGAAAAAA GTAAAT 6796

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2073 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATCTTAAAAT TnAAAATTAT CACGCCTTTT GaACAGCTTT GTAACCaTct GGACGATCAT 60
 40 KAAATTCCaA TGTAATCCT GGTTTAAaGT TGATCTTTAA CCTTATTTAA AyCACCAATT 120
 GTACGTATAT TATGTTGTTT AGCAAAATCA CGTTTTACAG CTAAAGCATA CGTATTGTTA 180
 45 TACTTCATTG GTTTTAACAT AGTCATTTGA TATTTCTTTT CAAGACTTTG CTTAGCTTGT 240
 TCATAAACTT TTTTCTCTTC TTTTGACTTC AATGGTTCTT TTGTTAATTC ACCTAAAACT 300
 GTTCCAGTAA ATTCTAAATA CCCATCTATA TCGTCAGATT TTAAAGCATT AAATAAAAAAT 360
 50 GCTGTTTTGC CCATACCATC TTTCACCTCT ACAGTATTTT TGGTCTCTTC TTCTATTAAA 420
 ATTTTATACA TATTTGTAAT AATCGATGGC TCGGAGCCAA GCTTTCCAGC TAACGTAATT 480
 55 TTATCACCTT TTTGTGCAAA CATAGGAATA GCGATAGCCA GTATAATAAT CATCACTATA 540

	TCAAATATAA TTGCCAATAA GGCTGCTGGA ATTGCACCTA ATAATATCAA CGATGCATTG	660
	TTACGGTCTA TACCTAATAA AATTAAATCT CCTAGTCCGC CTGCACCAAT TAATGCTGCT	720
5	AGTGTGCTG TACCTATAAT TAATACCATA GCCGTTCTTA CACCAGCCAT TATAACAGGC	780
	ATTGCTATCG GAAGTTCGAC TTTAGTTAAA CGTCTAAATG GTTTCATACC TATACCTTTA	840
10	GCCGCTTCAA TGAGTGATGG ATCAACTTCT TTAATTCCAG TATACGTATT CCTTAAAATT	900
	GGTAACAACG CATACTACT AAGTGCAATA ATTGCTGGCA CACGACCGAT ACCAAATAAA	960
	GGAATCATT AACTAATAA TGCCAACGAT GGTATGGTTT GAAGAATTGC CGCAATATTC	1020
15	ATTACGATTT CAGATATCGT TTTAGTCTTC GTTAATAAAA TACCTAATGG TACCGCAATA	1080
	GCAGTTGCAA TCAATAATGC GATAAATGAT ATTTGAATAT GTTCTATCAT TGTCGAAAAG	1140
	AGTTGCCCT TACGTTCACT CAATATGTCg AAAAAGTTAG TCATGTTGAG CTACCTCCTT	1200
20	TTTCTGGGAC AAATATTTGA AGATATCTTT CCTATCAATA ACATATTGAC CTACGCTATC	1260
	TTCTTGCATG ACAATGACAC GCTCGCTCTC TGATAAAAGT TGATACAATA CTTCAATTGG	1320
	TTGATTGTCA TAAACAATTG GATAAGCGCT CATAGATGTA ACCTCATCGA TTGGTTTCAT	1380
25	AATATCCAAG TCACGGATAA TTGCGTTCTC TTCAACACAT GGCGCATCAT CTTCTAAATG	1440
	ACTACCCATA AATTGTTTAA CAAATTCATC TTGAGGATTA TTTTAAATC CTTCTGGTGT	1500
30	GTCAATTTGT TCAATATGCC CTTCAATCAA AAGACAAATC TTATCACCAA GTTTCATCGC	1560
	CTCTGAATA TCATGTGTAA CAAATATGAT TGTCTTCTTA ATTTTAGTTT GTAATTCAAT	1620
	TAAATCATCT TGAAGTTTTT CTCGGCTGAT TGGGTCTAAT GCACTAAACG GTTCATCCAT	1680
35	TAAAATAACT GGTGGATCAG CTGCTAACGC ACGTATAACT CCTACACGTT GTCGTTGCCC	1740
	CCCTGACAAT TCATCAGGTT TTCTGTTTTT ATATTTTTCA GGTTCTAATC CAACCATTC	1800
	AAGTAATTCA TCTACTCTTT TATCTATATC TTTTCTTTC CACTTTTTCA TTTGTGGCAC	1860
40	TTGTGCAAtA TTTTCTTTGa wGTcAtATG TGGGAATAAT GCAATCTGCT GcAATACGTA	1920
	TCCAATATCC CAACKCATTT CGTATACTGG ATAATCACTT ATTGGTTTAT CTTTAAAATA	1980
45	AATATAACCT TCACTTAAGT GAATGAGTCG ATTAATCATT TTTAATGTCG TAGTTTTTCC	2040
	ACAACCTGAA GGTCCAATTA GCACAAAAA TTC	2073

(2) INFORMATION FOR SEQ ID NO: 4:

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

	ACTATTCTAG CTTCATCAGT TATCATATAT TCTTTGAAAC ACTTGTAAGA AAATATAATG	60
5	AGTATTTACT ACATAATGAT ATTTCAAATT AGAAAAAAGG AAGTTATGAT TTAATGGCCT	120
	TGAGCCTATC ATAACCTCCT TTTATCATTT TATTGTTGTG TTGATGTTTC GATAACGTGG	180
10	TACATCTTAT CAAACATCAA TTCGAAACCA TGCACCATGG CATCATGATA TTCTTTTTTC	240
	TTTTGCTTGT ATTCTAAATT AGTAAATCGT CTTTCTTTTT CAACTAATGA ACGATAATAA	300
	AATAGCATT TGGTGCCACC TGTTTCACGT TCAAAAAATT CTACCTCAAT GACATCTTGC	360
15	GTTTCACTTA GTCCAGGCAT ACCGATAGTC ATCTTAACGT ATTCATCCAT AACTAAAGAT	420
	TCATAAATGC CTTCAATCAC ATTTACTTTG CCATTACGTT GTTGATCTAC AATACGATAT	480
	TTACCGCCTT CTTTAACGTC CGCTTCAATC TCTTTATTCTG TTCTGGCTGA TGTCATAAAC	540
20	CATTGTTTCA ACAAATCTTT CTTTGTCCTAA GCTTCGTATA CTAACCTCTGG AGAAAATTTA	600
	TAAAGCTTTT CAATTTCAAC TTCGACATGT TCATTCTCTA CATTAAATTT TGCCACTGTT	660
	GTCCACCCAC TTTGCTCTT ACTTTTATTT TAACGTATTT TTGCTCAGTT CCAAACATAG	720
25	ATGATCATCA TTTTAAAG ATTAGCGTTA TACGGTGAGT ACAACATGAT CTGTTAATAT	780
	AACAAGCCAC CTTACTTGGC TACATCGATA TATTGTTAAG CATTAAATGTT TCATTTCTTG	840
30	ACTAGTGTTT TTTTITAGCT TTGGAAAATT AAATAAAATC GCAATAAGTC CGCATACACC	900
	TAATAATATA GGATAAATGC TGTATGGGAA TAACATTAAAC GGTGAAATAC CAGCTACACC	960
	AGCCGCTGaa ATGACTTGCG GGCTATATGG TAATAAACCT TGGAAGCAGC CTCCAAATAT	1020
35	ATCAAGAATA CTTGCTGATT TCCTTGAATC TACATCATAT TCATCTGCAA TATTTTTAGC	1080
	TAAAGGACCT GACATAATAA TAGAGATGGT GTTGTTTGCC GTGGCAATAT CTGCGACACT	1140
	TACCAAACTA GCAATTCCTA ATTCTGCGCC ACGCTTTGAT TTCACTTTAG AGCGAACAAA	1200
40	TTGCAACAAC CATTCAATAC CACCATTGTG TTGAATAATA CCGACTAAAC CACCAATTAG	1260
	CAACGCAATC ATAGCAATAT CTTCCATGCT TATAATACCT TTGGACACTG CATCTAGTAG	1320
45	CCCCATCCAA CCGAATGAAC CATCTATGAG ACCAATGATT CCGGCTAATA ATGTTCCGCC	1380
	AATCAATACG ATAATGACAT TTACACCTAA TAATGCTAAT ACCAATACTA AGATATACGG	1440
	TACAACTTTA ATTAGATTAT AATCATAGTt TTTAGCATGA TTTAAAGAAA TGCCATTTCGT	1500
50	TAAGAAATAC AGAATAATAA TCGTTAAAAT AGCACCTGGC AATACAATTT TAAAGTTTAC	1560
	TCTGAATTTA TCTTTCATTT TCGTATGTTG TGTTCTAACC GCAGCAATTG TTGTATCTGA	1620
55	AATCATTGAT AGATTATCGC CGAACATTGC ACCTCCAACA ACTGTAGCCa tTGctAGCGC	1680

	TCCTACAGAC	GTCCCCATAG	ATATAGAAAC	AAACATACAA	ATCACAAACA	ATCCTACAAT	1800
5	AATTAAATTT	TCTGGGATTA	ATGATAGTCC	TAAATTAAC	GTCGACTTTA	CGCCACCCAT	1860
	TTTTTCAGCT	GTATTTGAAA	ATGCACCTGC	TAAAATAAAA	ATCAACATCA	TTAAAACAAT	1920
	GTTTGAATGG	CCTGCACCTT	TCGTGAAGAC	CTCAACTTTT	TTAGCAAATG	ATTCTTTTCG	1980
10	ATTCATTAAT	AACGCCACAA	TTACCGTTAT	CGTAATTGCA	ACATTTAATG	GCATTGAAGT	2040
	AAAATCACCT	GTGATAATAC	CTACGCCTAA	AAACAACGCC	ACAAATAATA	ACAAGGGGAA	2100
	TAATGCCCAA	GCATTGCTCT	TTTTATGTAC	TTCCATCCTT	TTTACCTGCT	TTCCAATTAA	2160
15	AAATACCTCT	TTCTCACAAA	CGATGAAGAA	AGAGGTTTTT	ATGTGCTTTA	CCTGCTTATC	2220
	TTCAAACCAT	TACGGTTACT	GGAATTGGCA	CATTGAGAT	GTTGCCGAGG	CTTCATAGGG	2280
	CCAGTCCCTC	CACCTCTCTA	GATAAGTGAT	GCTTATTTAC	GTTTACGTTA	CAAGATAATC	2340
20	CTTAGTACGT	CAATCATAAA	TTAATCAGGA	GTCGTATAAT	ATTTTTCATA	AACAATCATT	2400
	GCTACTGTAA	TAATAATCAA	AACAATAATG	CTAATAACAA	GTAAAAGCCA	CCATTTAAGC	2460
25	ATTAATGCAA	TAAAAATGAA	CACGATAGAC	ACACTTACTA	ATATTAATGA	TATGACTTTA	2520
	AATTGCTGAA	CACGTTGCTT	GGAGATGACT	TTCAACTGTT	TGTTTGATAG	ACGCGTATTT	2580
	TTTATACTGA	TTCCAGTAT	ATTTTCTAAT	ATTTGAACCA	ATACGATACT	TATTGCAAAT	2640
30	ATAATAATTG	GTAAACATC	ATAGCTCCCT	ATAGTTAATG	TATAAATTAC	AAATCCAATG	2700
	TAAAGTAACC	CTGAGACAAA	GGATAAAAAG	TATGCGACGT	ATTTGTTAAA	CTTAATGATA	2760
	TGCTTTTTAA	CGTTTTGATG	TGTAAACCAT	ACATTCGAAA	CGATCGCAAC	TGCTACAAAT	2820
35	AATGTGAATA	CTATATATAA	TGGTAATTTT	TGTTTCAGGAA	AAACAGTCGC	TATTCCAAAA	2880
	GCTAATGCTA	AAATCAAAAA	TAATATAGCT	CTAGATACTA	TTAATGCCAT	AATAACAACC	2940
40	CCTTTGTTTA	ATATCGAGTT	TGCAAATTTA	CGTTTATCAG	CGTTTCTATG	ATCAGTACTT	3000
	CTACGGGTAG	CGTTTCTATG	TAATTTACAT	CATCTTAACA	TATAAATACT	TCGCTATTTA	3060
	ATTGAAAACA	TATCCTATTA	TTCTTTGTCC	GTTCTGACGT	TTAATATCTA	GCCTTAGGCA	3120
45	TTTCACTTGT	TAATGAATTT	AACTTTCTTC	CACTAACCGT	CCCTAAACCC	AATCCCGCAA	3180
	CAGTTTTTAA	CTTTTTTCGTT	GTTGTCCTGA	CATCCTCATT	AAGAAAGTTT	ATTCTGCTTA	3240
	AAACTTATAA	TCCACACCTT	GAGCAAACGC	TCCTTATGAC	AGAGTATTAA	AATAAGCCGA	3300
50	TAAAGATACA	CACCTTTACC	GACTATTTAA	AATACACTTC	ACCAATTCAT	TTTAATTTAA	3360
	TGGATTGAAG	TAATAAATTT	AATATTATGT	TGTTCAATTA	AAAGCTTCAT	ACAAACCTAA	3420
55	TCTATTTGCA	CTCCACCGCT	AACACCGAAC	ACTTGTCGGG	TTGTATAACT	TGATTCTTCT	3480

	GTTTTTTGAC	CAAATGTTGG	GATTTTACTT	TGAGGTTGTC	CACCAGAAAT	TTGTAATGGT	3600
	GACCAGAATG	GACCAGGCGC	TACACAGTTC	ACTCTAATTC	CTTTTGGTCC	TAATTCCTCT	3660
5	GAAAAACTTT	TAGTTAATGA	AATAATTGCT	GCTTTTGAAG	CGGCATAATC	ATGAAGAATA	3720
	GGACTAGGAT	TATAACCTTG	TACAGATGAT	GTCGTTGTAA	TTGACGCACC	CGGTTTTAAA	3780
	TATTCCAATG	CTTTTGAAC	TGTCCAAAAT	AGCGGATAGA	CATTCGTTTC	AAATGTTTCT	3840
10	GTAAATGCCT	CAGTTGTAAA	TCCATGAATA	TCATCATGAT	ACTGTTGATG	TCCAGCAACT	3900
	AAAGTAACAT	TATCTAAGCC	ACCTAATTGT	TGATATGCTT	GTTCAACAAG	GTCATAGTTG	3960
15	AACTGTTTCT	CTCTTATATC	ACCAGGAATT	AACACTGCCT	TTTGACCACT	TTCTTCAATC	4020
	ACTTGGCGTA	CTTCTTGTC	ATCTTGTTCT	TCACTCGGAA	GATAGTTAAT	CGCTACATCT	4080
	GCACCTTCTT	TAGCATACGC	AATTGCTGCT	GCACGCCCTA	TTGCTGAGTC	ACCACCTGTG	4140
20	ACTAATATTT	TATAGCCTTG	TAAGCGTTGA	TGACCTGGT	AAGACGTTTC	GCCACAATCG	4200
	GGTGCTGGCG	TCATTTTCTA	TTGTAAACCC	GGTACCTCTT	GTTCTTGTTT	TTTATAATCC	4260
	GTTGTTTTAA	ATTTTGTCT	AGGATCTTGA	GCTGCCATTT	TTTTACATCT	CCTTATTCGC	4320
25	TTAATGGTTA	TTATTTACCC	AATCTTCCTA	GGAACCTAAT	CATGATTACA	CTAAAAATTA	4380
	CTTCTCTCTT	TATAAAAAACA	AGCTCGAATT	ATTCATGCAA	TAGTCTCTTT	ACAAATTCAA	4440
30	CAAAATACTC	AGGTACTTTT	TCCAGAATCC	TTTCATCCGG	TTTATATTGA	GGATGATGTA	4500
	AATCATATTC	ACTATGAGAA	CCAATTAACG	CAAATACACT	TGGAAAATGT	TGACTATAAC	4560
	CTGAAAAATC	TTCTCCAATC	GTAAGCGGCT	GTTCCATCAT	TCCCACCTTA	TATCCAACAT	4620
35	GTTGGGCTAC	TGCAATTGCT	TTATGCGTCA	ATGCCTCATC	ATTCATCACA	GCGCCAGGTA	4680
	AATGCGTATA	ATTTAAATTA	ATTTTCATAT	TATATGCTTG	AGCCAATCCG	TCCGCAATAT	4740
	CTTGTAATCG	TGTTTCTACA	AGCTTTCGTA	CCACAGGATC	AAAACCTACG	ACTGTGCCTT	4800
40	GTACATACGC	ATGATCAGCA	ATGACATTCC	AAGTATTACC	ACATGATATT	TGTCCAATTG	4860
	TTACTACCGC	TTTCATCAAAC	GCAGATAGAT	TTCTACTAAC	TATGGATTGA	ATACTATTAA	4920
45	TCAATTGCGC	CAACACAATA	ACTGGATCGT	TGCATTGTTT	TGGCTTTGCA	GCATGACCAC	4980
	CCACGCCTTT	AATATGAAAC	TCAAAACGAT	CTACTGCTGA	TGTAATTGCC	CCTGTTTTGA	5040
	TTGCAAATGT	ACCTACCGAA	CGCGATGGGT	CATTATGAAA	ACCCAATACT	GCTTGTACAT	5100
50	CTTTTAATGC	ATGTGTTTCA	ATAATTTTAA	AAGCGCCATG	TCCTAGTTCT	TCTGCTGATT	5160
	GAAAAATGAA	TTTAACACGC	CCAGTAAGAG	TGCCCTCAAT	TTCTTTTAAT	TTTACAGCTG	5220
55	TAGCCAAAAT	ACTAGCCATG	TGAATATCAT	GACCACACGC	ATGCATAACA	CCTTCATTTT	5280

	CAGCTATACA ACTCAGACCT TGTCCCACTT CAGCAACAAG CCCAGTCGCA AGTGGTAAGT	5400
	CTAATATTCT AATATGATGT TCTGTTAAAA TATCTTTAAT TTTTGTGTA GTCTTAAATT	5460
5	CTTTATCGGA TAGTTCGGA AATIGATGAA AATACCTTCT CCAGGTAACA GCTTGATCTT	5520
	TTAATCCCAT CGGTCATTCC CCTTCCTTAA GTCAATGATA TGTGTCTAC CCTACGATGA	5580
10	TCATCTTTGA CTATTAAACG ATGATTTTAC AACAAATGTAC TCTTGTTAAT TGCTTTCGTT	5640
	AATGATAGAC AGTTGTTTAA TAATATCGTA ACACTGTTGT CAAACTATTG TAACTTTTAT	5700
	AATTGAGACT CTATACAAAA ACGTGTCTC GAATATACTT GTTTTTACAA ACCACAAAAA	5760
15	GCTCTAAACA TTAGTTTAAA CCAATGCTTA GAGCTTTCTA ATTATTTTAT GCTTTAAAAG	5820
	ATACTGTGTT ATCTACGATG ACCTTACCGT CTTTAATAAC TTTTCTGCG TGATTGATAC	5880
	CAAAATGATA TGGAATATAT TCATGATTTG GTGCATCCCA AATTACTAAA TTAGCCTTAT	5940
20	CACCTGTGTT AATTGTACCC GCGTTAATGT CTATTGCTTT AGCAGCATTG ACCGTAACAG	6000
	CATTCCAAAC TTCATTAGGT GATAGCTTTA ATTTCAAGGC TGCAATCGCC ATAACAAGTT	6060
25	GTAAGTTGTT TGTGACACTA CTACCAGGGT TATAATCAGT TGCTAATGCA ATCGCACCGT	6120
	TATTGTCAAG CATGCCTCTT GCATCTGCAT AATCTTCTTT ACCTAAATAG AACGTCGTTG	6180
	CAGGTAAGAG GACAGCTACA GTATCACTAT TTCGCAACTT TTCTTTTCCT TTATCACTAG	6240
30	AAGCTACTAA GTGGTCTGCT GATATTGCTT GTTCATCAAT TGCTAATTCC AGTCCGCCTA	6300
	ACGGATCAAT TTCATCCGCA TGTATTTTCA CTTTAAAACC TGCTTCTTTG GCTTTTGTGA	6360
	TATAATGTTG CGATTGTTCT ATTGTAAATA CACCTGTTTC ACAGAAAATA TCCGCAAAGT	6420
35	CTGCATATTG TTTTACTTCC GGAAGTAACG CAATCATTTT TTCTAAAAAT GCCTCATTG	6480
	AACTTGCCCTC TTTAGGTACA GCATGAGGCC CTAGGAAAGT ATGTTTCATG TCTAAATCAT	6540
	ATTTCTCAGC TAAACGATTA GACACTTTCA ATTGCTTCAG TTCATTTTCT CTATCTAATC	6600
40	CATAACCACT CTTACTTTCA ACTGCAAGCA CGCCGTGTTT AATCATAGTA AGCAAATCAT	6660
	GCTCTGCTTT TTAAACAAG TCATCTTCGG ATGTTTCTCT AGTAGCATTG ACGGTAGATA	6720
45	ATATGCCACC ACCCATTTCT AATATTTCAA GGTAAGACTT ACCTTGACGT TTTAATGACA	6780
	TCTCATGTTT TCGAGATCCA CCAAATGTTA AATGGGTATG TGCATCTACT AATGCTGGGG	6840
	AACTACCTT CCCACTAGCA TCAATCGTCT CAGTCGCATC GTAGTCATCT GTATGTGTTT	6900
50	CAGCATATAC AATTTTGCCA TCTTTAATGA CAACTGTACC ATTTTTCACA ACATTTAATT	6960
	CATCTAATTC CTTACCCTTC AAAGGTTTAT CTGTTGATCT CGGTAAAATT AATCTGCTA	7020
55	TATGATTAAT TATTAAATCA TTCATTACTT ATCACCTGCT TTATCAATCA TTGGAATATG	7080

	AACACCCATA	CCTGGGTCAG	TCGTCAATAC	ACGTTCCAAT	CTTCTTTCAG	CACGCTCTGA	7200
	TCCATCTGCT	ACAACAACCA	TACCCGCATG	AAGTGAATAT	CCCATGCCAA	CACCGCCACC	7260
5	GTGATGGAAT	GAAATCCATG	AACCACCTGC	AGCTGTGTTA	ATGAGTGCAT	TCAATACAGC	7320
	CCAATCACCA	ACCGCGTCAC	TACCATCTTT	CATACTTTCT	GTTTCACGGT	TAGGACTAGC	7380
	AACTGAACCA	GCATCTAAAT	GGTCTCGTCC	AATAACAATT	GGTGTGAAA	TTTCACCGTC	7440
10	ACGTACAAGA	CGATTTAAAG	CTAAGCCCAT	TTTCGCTCTT	TCTCCATAGC	CTAACCAAGC	7500
	AATACGTGAT	GGTAGTCCTT	GATATGAAAT	TTTTTCTTCA	GCTAAATCAA	GCCATCTTAA	7560
15	TAAC TTTTCA	TTTTCTGGGA	AAAGTTTGCG	CATTTCTTCA	TCCGCACGCT	CGATATCTTT	7620
	TGGATCACCA	CTCAACGCAG	CAAAGCGGAA	TGGCCCTTTA	CCTTCACAGA	ATAATGGTCT	7680
	AATGTAAGCT	GGTACAAAGC	CTGGGAAGTC	AAAAGCATTT	TTCACTCCGT	TATTGAAGGC	7740
20	TACTTGACGA	ATATTGTTAC	CATAATCAAA	TGCTACAGCG	CCACGTTTTT	GGAATTCAAG	7800
	CATTAATTCA	ACATGCTTTG	CCATTGAAGC	TTGTGACAGT	TCAACATATT	TTTTCGGATC	7860
	TTTTTCACGC	AATACTTTTG	CTTCTTCTAC	AGAGTATCCT	TGTGGCACAT	ATCCATTTAG	7920
25	CGGATCATGT	GCACTTGTTT	GGTCAGTAAT	AATGTCAATT	TTAAATCCTT	TTTCTAGAAT	7980
	CGCTTGATGG	ATGTCTACAG	CATTTCCAAC	TAACCCGATT	GATAATCCTT	CTCCACGTTT	8040
30	TTTCGCCTCT	TCTGCTAATT	TTAATGCTTC	ATCTAAATCA	GCTGTTTTAA	CATCACAGTA	8100
	TTTCGTATCA	ATTCGCTTAT	CAACACGTGT	TTCATCAACA	TCCACGCAA	TGCTACCCC	8160
	ATGATTCATA	GTAATTGCTA	ACGGTTGCGC	ACCACCCATA	CCACCTAAAC	CTGCTGTCAG	8220
35	TGTAACAGTG	CCTGCTAAAT	CTCCATTAAA	GTGTTGATTA	CCTAGCTCGG	CAAATGTCTC	8280
	ATAAGTACCT	TGCACAATAC	CTTGAGAACC	AATATATATC	CAACTACCGG	CTGTCATCTG	8340
	TCCATACATG	ATTAAACCTT	TTTTATCTAA	TTCATTAAAA	TGATCCCACT	TTGCCCATTC	8400
40	AGGCACTAAT	ACTGAATTTG	AAATTAATAC	ACGTGGCGCT	TCTTCATGTG	TTTTAAATAC	8460
	AGCAACTGGC	TTTCCTGATT	GTACTAACAT	TGTCTCATCT	GATTCTAATT	CTCGTAACGT	8520
45	TTTCTCTATT	GCTTCAAAAG	CTTCCCAATT	ACGTGCTGCT	TTTCCAATAC	CACCATAAAC	8580
	AACTAAATCT	TCTGGTCTTT	CAGCAACTTC	TGGGTCTAAA	TTGTTGTATA	ACATTCTAAG	8640
	TACTGCTTCT	TGTTCCCAAC	CTTTACACTC	AATACTCAAA	CCTTTTTTTTG	CTTGAATTTT	8700
50	TCTCATAAAA	TTGCTCCTG	TTCTTTTAAAG	AAGTTAATTC	CACTAAATTT	AAAACGCTTA	8760
	CATTATTATC	TTCAATATTC	ATTATAGTAT	GTTAAATAT	AGCCAACAAA	TATAAATAAA	8820
55	CTAATTATCC	ATAGCTTGAA	TCTATAAATA	AAAGGAGCAA	AACACATGAA	AATTATTTCAG	8880

	CATATTAGCC	AGCCATCTTT	AACTGCTACG	ATTAAAAAAA	TGGAAGCAGA	TTTAGGTTAT	9000
5	GACTTATTTA	CACGTTCAAC	AAAAGACATC	AAGATTACCG	AAAAAGGAAT	ACAGTTTTAT	9060
	CGTTATGCGA	GCGAATTAGT	TCAACAATAT	CGATCCACGA	TGGAAAAAAT	GTATGATTTA	9120
	AGCGTTACAT	CAGAACCAAG	GATAAAAATT	GGGACTCTTG	AATCTACGAA	TCAATGGATT	9180
10	GCGAATTTAA	TTCGAAAGCA	CCATTCCGAC	TACCCTGAAC	AGCAATATCG	TTTATATGAA	9240
	ATACATGATA	AACATCAATC	TATAGAGCAA	TTACTGAATT	TTAATATTCA	TTTAGCTATA	9300
	ACAAATGAAA	AAATAACCCA	CGAAGATATA	AGATCCATTC	CTTTATATGA	GGAATCTTAC	9360
15	ATTTTATTAG	CACCCAAGGA	AACATTTAAA	AATCAAAATT	GGGTAGATGT	TGAAAATTTG	9420
	CCACTCATAT	TACCAAACAA	AAATTCTCAA	GTGCGCAAAC	ACTTAGATGA	CTATTTTAAT	9480
	AGAAGAAATA	TTCTGCCAAA	TGTCGTTGTA	GAAACAGATC	GATTCTGAATC	AGCAGTTGGA	9540
20	TTTGTTTCATC	TCGGCTTAGG	TTACGCTATC	ATTCCGAGAT	TTTATTACCA	ATCATTTCAC	9600
	ACGTCTAATT	TAGAATATAA	AAAAATTCGT	CCAAACTTAG	GCCGAAAAAT	TTATATCAAT	9660
25	TACCATAAAA	AACGCAAACA	CTCCGAACAA	GTACATACAT	TCGTACAACA	ATGCCAAGAT	9720
	TATTTATATG	GACTTTTAGA	GGCTCTTTAA	CTTAAGTTAT	TAGAGCCTCT	TATGCAGTTG	9780
	CTCAGTCAAC	TGTATACCTT	TTGCCTTTAA	CTTAAGTTAT	TAGAGCCTCT	TATGCAGTTG	9840
30	CTCAGTCAAC	TGTATACCTT	TTGCCTTTAA	CTTAAGTTAT	TAGAGCCTCT	TATGCAGTTG	9900
	CTCAGTCAAC	TGTATACCTT	TTTCCTTTAA	CTTAAGTTAT	TAGAGCCTCT	TATGCAGTTG	9960
	CTCAGTCAAC	TGTATACCTT	TTGCCTTTAA	CTTAAGTTAT	TAGTGCCTCT	TATGTAGTTG	10020
35	CGTAGTCAaC	TGTaTACCTT	TTGCCTTTAA	CTTAAGTTAT	TAGAGCCTCT	TATGCAGTTG	10080
	CGCAGATCAT	CGTATAAAAA	TTAATGACGT	CATTTCAAAA	ATCGATACAA	AAATAATTTA	10140
40	TTATAAAAAAT	TCTAAGAAAG	AAGTGAAGCA	GATGTTAAAA	TCTATTAATC	ATATATGCTT	10200
	TTCAGTCAGA	AATTTAAACG	ATTCAATACA	TTTTTATAGA	GATATTTTAC	TTGGGAAATT	10260
	GCTATTGACT	GGTAAAAAAA	CTGCTTATTT	TGAGCTTGCA	GGCCTATGGA	TTGCTTTAAA	10320
45	TGAAGAAAAA	GATATACCAC	GTAATGAAAT	TCACTTTTCA	TATACACATA	TAGCTTTCAC	10380
	TATAGATGAC	AGCGAATTTA	AATATTGGCA	TCAGAGGTTA	AAAGATAATA	ACGTGAATAT	10440
	TTTAGAAGGA	AGAGTTAGAG	ATATTAGAGA	TAGACAATCA	ATTTACTTTA	CCGACCCTGA	10500
50	TGGTCATAAG	CTAGAATTAC	ATACTGGCAC	ACTTGAGAAC	AGATTAAATT	ATTATAAAGA	10560
	GGCTAAACCA	CATATGACAT	TTTACAAATA	AGGTGTCATT	ATAAAAAGGC	CTCTTGAAC	10620
55	CCGTTAAAAAT	TTTAATTAAT	TATTATATAA	TAAGAGAACT	TTTCAAACAA	TACAGTTGTT	10680

	TTACTGCAAT TATTTTTC	AAATATCAAC GTTAATATAA	CTTCTATTAA GAAATACTCA	10800
	CATTCTGCCC TGCAATGCAA	ATCTCGTCAC ATATAAATAT	TTTAAATTAT TTTAAAAAAT	10860
5	GATGCACTAA ATTAGCAACG	AGCTTAGCAG TTCTATTGTC	AGCGTCATAT GTTGGATTCA	10920
	TCTCAGCAAT ACTAACTGAA	GACACCTTAT CACTTGGAAT	AATACGTTTT GCTAATTCAA	10980
10	GAACAGTATG TGGATACAAA	CCTAACACTG CCGGCGCACT	TACCCAGGC GCAAACGCAC	11040
	TATCAATGAC ATCCATACAA	ATCGTAAACA TAATGACATC	ATGTTTCATGT ACAAACGTT	11100
	CAATCATATC TTTAATTGTT	GGTGATACGT GACTCAATAA	TTCATCTGCA AAGACATAAT	11160
15	CAATCTTTTT CTCTTTAGCA	TAATCAAATA AACTTTGCGT	ATTACCACCT TGAGCAATAC	11220
	CAAGCACTAA ATAATCTGTG	TTTTCATCTT CTTCTAAAAT	TTGTCTAAAG CTCGTTCCAG	11280
	ATGTAGATTG TTGTTTCAGCA	CGTGATACAA AATGCGCATC	AATATTTATC ACACCAATAG	11340
20	ATTGTGTTGG ATAGACTTTA	CGTGTTGCTA AATATTGAGC	ATACGCAATA TCATGTCCAC	11400
	CACCTAATAA AAATGTTTGT	CTATGATTAG CAATTGACTT	CGCTGCAAGC ATAGCAAAT	11460
25	CTTTTGTAGT ATCAATTAAT	TCCTCATGAT CATGATAAAC	ATTTCCGTAA TCGACTAAAG	11520
	TTcACATTGA TTCAAATCCG	GCAAACCTGC AAATGCTTGT	TTAATCGCAT CTGGTCCTTC	11580
	TTTTGCACCA ATGCGCCCCCT	TGTTTAAAGC AACACCTTTC	TCAACAGCAT AGCCTAATAT	11640
30	ACCGACCCCT GATGGCATAc	TACTCTTTTC CAGCTTAGAC	AAATCTTCAA ATGTTACTGT	11700
	TTGAAATGT CTAAATTTTT	TCGGGTCTGT TTCACTATCT	AACCTTCCAG TCCATAAATT	11760
	TGGTTCACCT TGCTTGTAca	CAGCATTTCC CCCTCTTATT	TATGTGGCTT ATTAACAATT	11820
35	AAAGTATAAC GTATAGGAAA	TTTGAATTC AATTCATAGT	TAAATCCGTA TCTTAAAAAT	11880
	ACTTATCTAC ATTACTTTTA	CCCCTATTTT CTATGTAATA	ACGAATACTT AGCTGATTTA	11940
40	TGTTAATAAA ATACGTCAAG	ACTATTACAT TTTCATTAAAT	ATTGACATAG ACAATTTATC	12000
	TCTCGGCTTG TAATATGTAT	AATTGTTACT AAAAGATATT	TTGCTTGTTA CCTAATGGAG	12060
	GTTACATATA ATGAAGAACA	ATAAAATTTC TGGTTTTCAA	TGGGCAATGA CGATTTTCGT	12120
45	CTTCTTTGTC ATTACAATGG	CGTTATCCAT TATGCTCAGA	GATTTCCAGT CTATAATTGG	12180
	TGTCAAACAC TTTATATTTG	AAGTTACAGA TCTAGCACCA	TTAATTGCTG CAATCATTTG	12240
	TATACTCGTT TTCAAATATA	AAAAGGTCCA ACTTGcAGGT	TTAAAATTCT CAATCAGCCT	12300
50	GAAAGTAATT GAACGTCTAT	TGCTAGCTTT AATTTTACCT	TTAATTATTC TAATTATTGG	12360
	TATGTACAGC TTTAATACAT	TTGCAGATAG CTTTATTTTA	TTACAATCAA CAGGCTTATC	12420
55	AGTACCTATT ACACACATTC	TGATTGGACA TATTCTGATG	GCGTTCGTAG TAGAATTCCG	12480

5 TGTGTTGGT TTGATGTATT CAGTTTTCTC AGCAAATACA ACTTATGGTA CAGAATTTGC 12600
 TGCTTATAAC TTCCTTTATA CATTCTCATT CTCTATGATT CTTGGTGAAT TAATTAGAGC 12660
 GACTAAAGGA CGTACAATTT ATATTGCAAC GACATTCCAT GCTTCAATGA CATTCCGACT 12720
 TATTTTCTTG TTTAGCGAAG AAATCGGCGA TCTATTTTCA ATCAAAGTCA TCGCCATTTT 12780
 10 AACAGCAATC GTTGCAGTAG GATACATTGG TTTAAGCTTA ATTATCCGAG GTATTGCATA 12840
 TTTAACAACA AGACGAAACC TTGAAGAACT TGAGCCTAAT AATTATTTAG ACCATGTCAA 12900
 TGACGATGAA GAACTAATC ATACTGAGGC TGAAAAATCT TCTTCAAATA TTAAAGATGC 12960
 15 TGAAAAACA GGTGTAGCTA CTGCATCAAC GGTGGTGTG GCTAAAAATG ATACTGAAAA 13020
 TACAGTGGCT GACGAACCAA GCATTCATGA AGGTACTGAA AAAACAGAAC CTCAACATCA 13080
 CATAGGTAAT CAACTGAAT CTAATCATGA TGAAGATCAT GACATCACTT CGGAGTCAGT 13140
 20 AGAATCAGCT GaATCAGTTA AACAAAGCACC ACmAAGTGAC gATTTaACAA ACGATTCAAA 13200
 TGAAGATGAA ATAGAGCAAT CATTAnAGA ACCTGCGACT TATAAAGAAG ACAGACGTnC 13260
 25 ATCAGTTGTA ATTGATGCAG AAAACATAT CGAAAAAGCT GAAGAnCAAT CTTCAGATAA 13320
 A 13321

(2) INFORMATION FOR SEQ ID NO: 5:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8549 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

40 ATGTGTTGTA AACTTTTATG TTGAAAAGC TACTTATCTC AATGAAAACA AGTAGCATT 60
 AATAAATTAA TTAGTATACA GCTAGTTTTT CTAATTGTTT TTTAACTTGA ATTAAGTTTG 120
 ACCGTATTAG AGAGGCAGAT TGATCCATCG TTTGAATTGC TTGTCCTTCA TTTTCGTTCA 180
 45 AGCCATTACA AACAACTTCA AACTGTTGTG CCATTGATC AAGACGCGCA TGAGCTTGTG 240
 TGTTTAAAAT AAACATATCG TCATAATGTG ATGGCGAATA GATAATTCGT CGTTGTATAC 300
 AAACGTATAA AAACCTTGTC ATATCAACGG TTTTGGCATT TTTAAACCTC TGTGTTTTCC 360
 50 ACGCATGTTT GCCCTTATTT AAATAATTTG CCCTTTTTTC GCCCGAAAA AAAACACAA 420
 AAAAATAACC AACTTCCTAA ATTAATAGGT GGTGTGGTTT TGTTGATTGT AGGGGTATAA 480
 55 AAATAACCGC ATTATTAAAG ATACGGTTAC TCTGTTATCT GTAAATATAA TAGTAGTTTA 540

	AAACAGGACT CCACATAAAA ATCAACTCCT TTATATACCA TAATGATACT ATATTTTCTA	660
	GTTTATTTCA ATTTTTCAGT TTTTAAAAAT GAGTTTCTGT TTTTATTTAT ACGCTTTTCT	720
5	GTTTTCTTTT TAAATTTTAT CTTTTTGTTA TTCCATTTCAT TGTAATAATTC TATTAAATTA	780
	ACATAAAATT TTTTCATGCC TATTTTATTT GTTGATGAGA TATCAATGTA AAGACTCAAT	840
10	ATTGTTTTTA AATAGATTG ATGCAACGAC TGATAAACCG TATTACTATC TGCTATGTTA	900
	TTGGTAAAT GCATAGAAAA ATATTCTAAT TTATTCATGC AATATATATG GGTTCATTA	960
	TACTTCTTAA TGAGTGTATT TATACCTTGC AATACGTCAT TACTTTTAAT AACAAATTTCT	1020
15	TTTTCACCTG TCGAAAAAGT CCACTGTTTA TCTCCTATAT TTTCTTTAAT TGTTTTCTTG	1080
	TTGTCAAATT CTAAATTAT AGCCCGTAAA CACTCTTCTT TATAATTCTC GTTCTTGAAA	1140
	GTACGAAGCA AAATTTTAT AAATTGCGTA TTGGTGACTT TTTTATAAGT GTGATATTTT	1200
20	GCAATCTCTT TATCAGTAAA GACTGTTCTT AGTTCGTGAT TATCAAACT TAAATTCATC	1260
	TTATTCTCTA ATTCATTAAT TTTATCTTGC AAACCAACAT TTTCTAAAAT TTTCTTGTTT	1320
25	ATCTCCCCTA TATCAAACT CCTTTTCGAA ATTAATTTTG AAACTCGTC TGCCATTTCA	1380
	ACAGCCTTTT CTTTCCTTTT ATACCTTTTG TTAAATTTAT GAACCACCGT TGCAGCATAA	1440
	TACGATATCC CACCAGATAA AATAGATGAT ATTATCGGTA TGTATATATC ACCTTTCATA	1500
30	TTTCCACCTC TTTTAACACA ATTAAGTATT ATGATACACA ACTTGCGCAA AAAGATGTAG	1560
	ACAGAACATA ATGGCGAACA AAAACAACCA CCCAGTAACT AGTATGGGTG GCGTAGACTA	1620
	TAACAACCTCT ATGTTATCAA GATATATGTA TCGAGTGATG GCAAGGAAGA AGTCTCCTGC	1680
35	GGGACCAACA GTCAGATATA TGGCCTCTGC CGGGCTATAT AGTTCCTCC TACTATATAA	1740
	AAGTAAGTAT AACATAAAAA GCACCCCGTA AACTGTTATA CGGGAATGCT AAAGTCATAT	1800
	ATACTACGGG GAGTAGTATG AAAACTATGC TCTCTATCGT AAGAAAAAAC ACCCAGTGAC	1860
40	ATGCTTGGGT GAACAAGGAT AGATGTAAAT AGTTGATGCA TGTGTACACA TCATAACAAA	1920
	AAACTAGCCC GAAGCTAGCT ATAACATAAA AAAATAGGCA AGTACCGAAG TACCTGCCAG	1980
45	TTACGCACAT TTAAATCTTG AGAGTAATGT TAAAAAGTGT ATAGGAATAT TAACATCCAT	2040
	CCAAATAGTT ATTTAATAAC TGTAAGATTG CCTATAATTA ATGTAGCAAA ATTTTATTC	2100
	TAAGTAAATA CTAAATCGTG CTAAACTTAC CAAACTACT TATTCTATTA CCTGCCTTGT	2160
50	CTACCTCTCC TGTCGCTATA TAACGACGTT GTCCACTATT AGCAATATAA GTAATCCATC	2220
	TATAGCCATT GATGCAATAT GCGCCGTCAT ATTTAATTGT TGCGTTATTA GGTAATACAC	2280
55	CTGTAATTCT TGAATTAGTT GAATAGCCGT CCCTTACGTT ATTACCTTTA ACATTGGCAA	2340

	CTGGCACTGG TGGATTTTTT TGGTTTTTAG CTGATGTTTT AACATTACCA GCTACCAAAC	2460
	CACCTATAGG CTTACCATGA ATCGCACCGG CTATTAATTT AGAATACAAG TCATAGTTTT	2520
5	TCTTAATCCA ATCCATATCA TTTTATTAG TAATAAAACC TAATTCAGAT AAACGATAGT	2580
	TTATATTTAT TTCTGCTGAT ACATTAACTG TTAGTAAATC ATTACGAGGT GTTACACCTC	2640
10	TTATTTGTCC TAAGTTATTT TTAATAACAT CTTGTATACT TTTATCAATA GTATCTGCAT	2700
	TGAATTGACT TGAAATAATA ACATGCCCCAC CACTTGCACT TTCTCCTGCT GCGTCTAAAT	2760
	GAATCTCTAG AACAAATGTCA TACCCATGTG ATTTAACCCA ATATAAGCCA TAATCTTTAT	2820
15	TATTTCTTAC ATTAACACCG TAAGCAGTAT CTTGATACAT ATCTTGTGAT TGACTTGAGC	2880
	CACCATATAA TGCAACTTCG TGACCTGCAT GTCTTAAATA CTTAGCGATA TTTGGTGTTA	2940
	TATATTTACG GATAAAATCA CGTTCATTTG TTCCGTTTCC GACTGCTCCA GGATCGTTAT	3000
20	AACCATGACC GGCTACAAGC ATAATTTTTT TAGGTTTAAT TACTGCTTGC TTTTGGCAG	3060
	TTGCTTGCTT AATAACGCTT TTAGCTTTAT CTCCAACACT TACTTTATCT GGGAAATTTA	3120
25	ATCTAATAAA ATACATTGGG TCATCGTAAT AATGAACATG TCTTGTAACG GTTTCGGGAC	3180
	CCCAACCAGG TTGCGCAACG CCATTTGTCC AACCTTTACC ATTCCAATTT TGGCCAAACG	3240
	ATGTGAAAGT GTTTAGATTA GCGCTCTCAA CAATTTCAAC ATGTCCaGct CCGCCACCAT	3300
30	ACTTTGACGG GAAAACGACA ATGTCCAAC TTTGCGGTAA AAAGCTATCA TAGTTTTTAA	3360
	TTATTTGCCC GTATTTTCA ATCCTTGCTT TATTATCAA TGAATATTA TAAGCGTATA	3420
	AACCTTGTA CcTTTCGCCT GTTGCTATCA TAAAAACAT ATTTGCGTAA TCGTAACACT	3480
35	GAAATGCATA AAACAAATCA GGATTGAACT GCTTCCCTAA TGAATTATCA AACCATTTTT	3540
	CTGCTTGGTT TTTTGTTATC AACATTGGTC AACACCTACC CTAAATCATT TGTGTCGTTT	3600
	ATAFTCGTAG GTGTCATTAC TTCTTTAATT GGCGCTTGCC CTGTTGCTTT TCTATACTTG	3660
40	TTTTCAGCTT TATATTTCTT TAGCTTTTGA TTTGCCCAT TACCTTCTTG AGATGTTGGA	3720
	TTATCTTTAT ATGTAGTATA TAAAGCAACA ACTGTTAAGA TAATCGATGA AACACTTTCT	3780
45	TCATCTACTG GTATCGGACT TATACCTTTA TTCGCTAAAA ACTGATTGAC TAATGCTAAG	3840
	ATCAATACGA TGTATCTTGT TATTACTTTT GCATCCATTT GTTTGCTCCT TTTATCCAAA	3900
	ATAAAAAGCC AGTGCCGAAG CACTGACTCT TAACTATTAC TTACACTTAC TAAACCAGAA	3960
50	ACACGACCAA AAGCTATATC CTAAAATTCC CTTAAGCATG GTAATCACCT CCTTTAAATG	4020
	CCAAAAATAG TTTTAAACAA GGCTATAACA AATGTACTTA GAATCGTCCC TATTAATCCT	4080
55	AGAATCCACA TCTTGATGTC TCTAATATTT TTAGCATTTT TCTCTTTATT TTTTTCATCT	4140

	TGCGTTCTCA	GACTGTCTTC	TATTCTGTCG	AATTTTTC	ACATAGTCTT	ATCATTTTCT	4260
	TCTAATCGCG	TTAAACGCCA	ATCTTGTTTC	TGTCGTTTGG	TAAATCCAAA	CATTACACCA	4320
5	CCCACTTTAT	TCAAATTAAA	AAGCCATAAG	ATTATAACCT	ATGACTCTAG	ATTTTCTGGA	4380
	TACTTTTCTC	CTGTAATAAT	TGCATATTCC	TCTTTATCTA	TAACTTCCAT	ATCTACATAC	4440
	CACGCTATAT	CTTCTTTACT	ATATTCTTTC	AATTGATACC	ATGTTTTAAT	ATCTTCGAAT	4500
10	GTTGGTGAAA	TTAATTTAAG	CATTTTTCAGT	CTCTCCTTTA	ACCTCTTCTA	ATTTTTTATT	4560
	AAGTGTGACA	AGTTGTTTTG	CCATTAGTGC	ATTTTGCTTA	TTAACTTGCA	TCGATAACTT	4620
15	TGTACTTTGA	ACAACTTGTT	TCTGCATACT	AGCAACCATT	TTTCGTAAGA	TGTCATCAGA	4680
	AGCGACTGTG	TTTTGTTCTT	CACTGTCAAT	CTGTTGATGC	AAGTCATCTT	TTTCTTCTGA	4740
	ATAATCTTCG	TTAAAACTA	TTTCCCCATT	TGAATATTTA	AAGGCTTTAG	GTCTAAAAAC	4800
20	TTGAGAGAAA	TTTTCTGGTA	AATTTTCAAT	ATCAATACCT	TCTTCAAAGC	CACCAATGAT	4860
	AGCGTATGAA	ATTATCTCAT	TACGCTTGTT	AACTAATATT	TGCATTATTT	TCTCACTCCT	4920
	ATAATTTTGT	TAATTGTCCC	TCTATTTGCG	TTGCGACCAG	AGCCTCTTTG	ACTTCCTAAG	4980
25	TCGAAATAGA	CATCGTTTGA	TATAGTTAAA	GATGTACGAC	TAGATTTAGT	TAATCCAAAC	5040
	TCATAAACAC	CTCCACCATT	TCCATCACCA	TCTGGAAGAT	TTGAGGGATT	CAATGAAATC	5100
30	TTTCCTCCTC	CAAAAGGACT	GCCAAACTCT	GTAAAGTCAC	CACCTGGAAA	AGTCCCATAA	5160
	AAAATTAATA	AAATAAATTG	GTCTAAACTC	TCATTTAAGT	ACAATGTAGA	GCCCACACCA	5220
	TTTGCTGTTT	CATCAAAAAT	AACCGAATAC	CTTTTATTAA	ACTTGTATC	TGCGTATAAT	5280
35	TTAGCGTTAC	TTTCGGCCAT	ATTAGCTTTT	GATTGGGCAC	TTTGAACAGT	TTCAAAAGGT	5340
	GTATTGTAAT	CATTAATAGC	TAATTCTGAC	CACTCAGACC	ATGAACCCGC	TTCTTTTCTT	5400
	TTAACAAATA	CTTTATTTGT	ACCGTTCGGT	CGATAAGTCA	TACGCTTGTA	ATCTGAAGTT	5460
40	ACTACTAAAT	ATTCGACAGT	ACCGTTAGTA	CTAACACCTC	TTGGATAATT	TATAGCTTGC	5520
	GAAACATAAA	TAAATTGGGT	TGAATCACCT	ATTCTTTGTT	CTGGATTATT	AAAATCAAAT	5580
45	CCAGTAATCT	GCATTATCTT	ACCATCATCT	TTAGTAATCT	TAGCTTTTTG	CCAATTGAA	5640
	GTAGAACCAC	TTGTGACTAA	ACCACCACTA	TTCACTGACT	GCTTGAAGGC	TTCATGTTTC	5700
	TCATCCATAT	ATCGCTTTTG	CTCATCGAAT	GTTCTTGAAT	ATGCTTGCGC	TTTATTTTCC	5760
50	AAATCAGATA	TATGGCTATT	AGCAAGTTGC	TTTAATTCAT	CTATACTTGA	AGATTTTGCT	5820
	ATTTGAATAT	CTGATAGACC	TTTTTCTTTA	GCTTTTTC	TCAGACTCGC	ATAATCTTCA	5880
55	CCATTTTTTA	TAGCCTCGTC	CATTGCTTTC	GCACGATCCA	TAATAGTTTT	TTCTAATTCC	5940

	TCAACGTTAA	ATGTGATAGT	TCTCTCGACA	ACTACCACGT	CTGAATTACC	TAATTCTGCA	6060
	ACCGAAACTT	GAGCTTGATA	ACTTCCATCT	CGTTTAATTA	CATCATTAGG	TAATTGAAAT	6120
5	TTTAAAATAC	CTTTAAATGG	ATCTAATATT	TCTAGTGGAG	CAACTACCAT	GACTCCTTTA	6180
	CCTCGAATCG	CTATTCGTGC	KTTGATATTT	tCTTCACTCA	ATAATAACGG	TTGATTATTT	6240
10	TTAGTGATAT	TAAAAAGAAG	AACAGAAGAA	TCACTCTCTC	CTGTTCTAAA	AGTTATATCT	6300
	AGATTTGAAA	TATTTCCATA	ATGCGCTGTG	TTTTCTAAAT	TTATAGCTAC	AGATTTCTCT	6360
	AAATTACTCA	TTAACTTATA	ATTCTCCCTT	CGTGTAAGT	CCATGGCCCT	GAACCTGTTT	6420
15	TACTATCATA	ATTTTTCAAT	AGTATCTCAG	CAGATGCTGT	AACACTATTA	CGAACTAGCC	6480
	TATGAACAAA	GCCACCTGTG	TTTGAAGCTT	CTACATATAA	GTTCCAACCA	GCTACCCCTT	6540
	TACGTTCACT	TGGAAAATCT	GTAAAACGTT	TTGTATCATC	CGTAGTTAAA	TAAAACGACA	6600
20	TGCCTACTAT	GTAAATATCT	GACATTTTTG	TGATGAATGA	AGGTACTCTC	TCCCATTTAC	6660
	CACTATTTTT	AGGCACATAA	TTCCAGTCCG	AAATGTCTCC	AGTTCTTCCA	GAAAGCACCC	6720
25	TTTCAAAGT	CATCATATTC	CTTGCATAAC	TATTACGCGT	CAATATCTGA	ATTACATCAC	6780
	CGCCAGTTTG	TGGTGGCTTA	ACTTCCAAGA	ACCAACCTGC	ATCACGCCAT	TCTCTTGGA	6840
	ATGGGAAATC	ATCGATTTGA	ACTGTATGAT	CAGTGTATAA	ATAGTAAAGA	CCTGGCTCTG	6900
30	TTAACATCCC	AAGATTCTTA	AGTTTATCAG	GCCTCATTGG	TAAAGGTTTA	ACTCTACCAC	6960
	CTGTGTCACT	CaTGATAAAA	GGAACGCCTC	TTGAGTGAAG	TATTTCTAAA	ATACCTCTTT	7020
	GCCCAATCAT	GAAAATACGA	TGTGTTCTAT	TTCCaTCACC	ACCGACAGTA	ACACCTAGCA	7080
35	TCAAAGCTTT	TTTACCACTA	TCTTTGTCTAT	AGTATATTTG	CAAACCTTtC	TgCTTCCGCA	7140
	AATTCGCCAG	GAAATGAATC	tAgTGTTCCA	CCATAGTCAG	CATTAACCTG	ATACGCTTCT	7200
	TCTCCTGTTT	CTAAATCGAA	AGCCGTAA	TAGTTTCTAT	TATTTGGATT	ACTGTCTCCT	7260
40	GTATACCAAT	ACAAGTATTT	TTCATCAAAA	GTCACACCCT	GCATTGGTTG	GGTTTCGTTT	7320
	GTTAGTCTCA	TAGGGATACT	GATTTTATGC	AAAACTTTAT	CAATATTTTT	ATCAACATCG	7380
45	TCTAAACTTC	TTATCTCTAT	ATAAnTCATT	GAGTTTTC	GTTCCCACTG	ACTTCTAGGT	7440
	CTCTCaATTC	TGTATAGAAT	TTTATTTTCT	TTTTCATTTA	TGACAGGGGT	GATGTAGGGT	7500
	TTTTCTGGGT	GTCCTGTAAA	TACATCTTGC	ATACCATACT	TGCCATAGCT	AATTTCCACA	7560
50	TTAGGCGTAT	ACTTGAAACG	AACTAATGTA	TTCTCATTAT	TACCATTTAA	GATAAACTA	7620
	TAAATCCATA	ACTCATcATC	AATATATCTA	TAACCGTTAT	GTGTACCATG	ACCCCCACCT	7680
55	ACAATCAATG	AGCTGTCTAT	AAATTGACCA	TTAGGTCTTA	GACGACTTAG	CATATAGCCA	7740

ATTACTGCAT TTGTAAGAGG TGCAAGTTCT GTCACAAATA AAAATTCTTG CTTATCAGGT 7860
TCAAAACGAT ACTCGATATC AAGAATTTCT TGTTTGGTCT TATTTAATTC TCTTATAGTT 7920
5 TCCTCTTTAT TAATTTGAGT TTTGGTTTCC CAATCGTCTA AATGTTCTTT TAATGTGTCA 7980
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10 GGTGCCACAA CAAGTGC GTT AATTTGACTT TGTAAGATT TGTTTACTGC TGCTTGCGAT 8100
CTACCATTAT AATAAATTTG CTCAGCGAAG TGTTGAATTG TTTTAGCTyT CTGATGCAAC 8160
TTAAACTCTG TTGTCAAGCC AAGCGCAAAT TGCTCTATTC TTTGTAAGTT TTGTATTTCC 8220
15 TTAGCTCTAT AATCTCGACC TGCTAAAGCT CCCAAATCCT TTATTAAATA CAAATTTTCC 8280
ATAATGCACC TTCCTTTCTA ATAAAATAGC ACTGTACCAA GTTCCCACT ATCGTCAACT 8340
GTTATTTTCC ACAATTTACC GTTTGGGGAT TTCTGTACAA TGCTATTTTG AATAATTgcC 8400
20 TGctTCGCCT ATTTTAAAT TATCTAATTT ATTTKTATCA TTPACCGAAA TGATACCGTC 8460
TTGAGGCAAT CCATCAATAn CACTACTGCC TGCATAAGGT ATCCCATTTA TAGCTTTCCA 8520
25 ATGTGTAGCT GGAAAGTACT GTTTATCGT 8549

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AGGCGTGTAG TGA CTTACGG nTAGGAAACT ATGTATCCGA ATGATTTATT GAGACCAAAA 60
AGGCATTAAA GTCCATTGAA ATATChGGTA GCGmGTTGGT ACgTGGACGT GGGGGCCCTA 120
40 GATGTATGAG TCAACCATTa TTCAGAGAGG ACATTTAACG TAATAAATTA TAGAmACGAG 180
GGTGAAAATA ATGACAGAAA TTCAAAAACC GTATGATTTA AAAGGCAGAT CATTATTAAA 240
45 AGAAAGTGAT TTTACCAAAG CAGAATTCGA AGGACTTATT GATTTTGCAA TTACATTAAA 300
ACAGTATAAG AAAAACGGTA TTAAGCATCA CTACTTATCT GGAAAAAATA TTGCACTACT 360
ATTCGAAAAG AATTCGACGA GAACGCGTGC TCGGTTTACA GTTGCGTCTA TTGATTTAGG 420
50 TGCGCATCCA GAATTTT TAG GAAAAAATGA TATTCAATTA GGCAAAAAAG AATCTGTAGA 480
GGATACTGCG AAAGTATTAG GTAGAATGTT CGATGGTATT GAATCCGTG GTTTTTCACA 540
55 ACAAGCTGTT GAAGATTTAG CGAAGTTCTC TGGTGTAACG GTGTGGAATG GATTAACAGA 600

	TCTAGAAGGA ATAAACTTAA CTTACGTTGG AGATGGACGT AATAATATTG CGCATTTCATT	720
	AATGGTAGCA GGTGCTATGT TAGGTGTTAA TGTAAGAATT TGTACACCTA AATCATTAAA	780
5	TCCAAAAGAG GCATATGTTG ATATTGcAAA rGAAAAaGCG AGTCAaTATG GTGGTyCAGT	840
	CATGATTACG GATAATATTG CAGArcCAGT TGAAAaTwCm GATGCTATAT ATmCAGATGT	900
10	TTGGGTATCG ATGGGTGAAG AAAGTGAATT TGAACACGTA TTAATTTATT AAAAGACTAT	960
	CAAGTGAATC AACAGATGTT TGATTTAACA GGTAAAGATT CAACGATATT CTTACATTGT	1020
	TTACCAGCAT TCCATGATAC AAATACACTT TATGGACAAG AAATTTATGA AAAATATGGA	1080
15	TTAGCTGAAA TGGAA GTTAC AGACCAAATC TTTAGAACTG AACATTCAAA AGTGTTTGAT	1140
	CAAGCTGAAA ATAGAATGCA TACAATTAAG GCAGTAATGG CAGCAACATT GGGGAGTTAA	1200
	TCACTAAATG GAACGATATG AATATGATGT GTCTGATGAT ATAAGTGTCA TGTACAGACA	1260
20	CCTCATATTG GTATTAAAGG AGAAATGAAT ATGAACGAAT CAGGAGATAA CAAACTCAGT	1320
	AAATCTTCTT TAATTGGACT AGTTATAGGA TCCATGATTG GTGGCGGTGC GTTCAATATA	1380
	ATGTCTGATA TGGGCGGTAA AGCCGGTGGG TTAGCCATTA TTATTGGTTG GATTATTACA	1440
25	GCTATAGGAA TGATTTTCATT AGCGTTTCGTA TTTCAA AATT TAACCAATGA ACGGCCGGAG	1500
	CTAGACGGTG GTATTTATAG TTATGmTCAA GCAGGATTTG GCGATTTTGT AGGATTTATC	1560
30	AGTGmTTGGG GATATTGGTT CTCAGCGTTT TTAGGCAATG TTGCCTATGC AACACTATTG	1620
	ATGTCAGCAG TAGGTAACTT TTTCCCGATT TTTAAAGGAG GCAACACATT ACCAAGTGTT	1680
	ATTGTCGCCT CGTTACTACT CTGGGGTGTC CATTTCTTGA TTTTAAAGG CGTTGAAACA	1740
35	GCAGCATTTA TCAATAGTAT TGTTACTGTT GCAAAGTTAA TACCGATTTT ACTTGTAATC	1800
	ATATGCATGA TAATTGCATT CAATTTTGAC ACTTTTAAAA CAGGCTTTTT CAGTATGACG	1860
	TCAGAGGGTG TATTGCCATT TAGTTGGGCG AGCACAATGA GCCaaGtLAA AAGTACGrTG	1920
40	CTAGTGACAG TTTGGGTGTT TATCGGTATC GAAGGTGCAG TAATTTTTTC TAGTAGAGCT	1980
	nAAAATGAGA AAGATGTAGG TAGTGCCACG GTTATAGGAC TTATATCAGT TTTAATTATC	2040
45	TATyTCTTAT TAACTGTATT AGCTCAAGGC GTGATTTTGC AAAATCATAT TTCGCAATTA	2100
	GATTCGCCAA GTATGGCACA GGTGCTTGCA ACTATTGTAG GTGGTTGGGG ATCTACACTT	2160
	GTAAATATTG GTTTAATTAT TTCGGTACTA GGTGCATGGT TAGGATGGAC ACTGCTTGCT	2220
50	GGTGAATTAC CTTTCATTGT TGCAAAAGAT GGATTATTTT CAAAATGGTT TGCTAAAGAA	2280
	AATAAAAATG GAGCACCTGT AAATGCACTG CTTATTACCA ATATATTAGT ACAATTATTT	2340
55	TTAATAAGTA TGCTATTTAC ACAGAGTGCG TATCAATTTG CATTTTCACT AGCATCAAGT	2400

CGACAGCAAG CAACTACTAA ACAATGGACG ATTGGTATCA TAGCCTCAAT TTATGCTATA 2520
 TGGCTTATAT ATGCAGCAGG TATCAATTAC TTATTATTGA CGATGTTACT TTATATTCCA 2580
 5 GCTCTTCTTG TTTATACaAT CGkTCmAAAG rATWATCAGa CACGTTTGAT TAAATCAGrC 2640
 TATATTCTtTT TTATGATTAT tATCGTACTT GCAGTTATCG GGTTAATTAA GTTATTGATG 2700
 10 GGAACGATAA ATGTTTTTTTA AAAGGAGCGA CAAAAATATG AAAGAGAAAA TTGTCATTGC 2760
 ATTAGGCGGT AATGCGATAC AGACAACAGA AGCAACAGCT GAAGCACAAC AAACAGCTAT 2820
 TAGATGTGCG ATGCAAAACC TTAAACCTTT ATTTGATTCA CCAGCGCGTA TTGTCATTTC 2880
 15 ACATGGTAAT GGTCCACAAA TTGGAAGTTT ATTAATCCAA CAAGCTAAAT CGAACAGTGA 2940
 CACAACGCCG GCAATGCCAT TGGATACTTG TGGTGCAATG TCACAGGGTA TGATAGGCTA 3000
 TTGGTTGGAA ACTGAAATCA ATCGCATTTT AACTGAAATG AATAGTGATA GAACTGTAGG 3060
 20 CACAATCGTT ACACGTGTGG AAGTAGATAA AGATGATCCA CGATTTGATa ACCCAACTAA 3120
 AcCaATTGGT CCTTTTTATA CGAAAGAAGA AGTTGAAGAA TTACAAAAAG AACAGCCAGA 3180
 CTCAGTCTTT aAAGAAGATG CAGGACGTGG TTATAGAAAA GTAGTTGcGT CACCACTACC 3240
 25 TCaATCTATA CTAGAACACC AGTTAATTcG AACTTTAGCA GACGGTAAAA ATATTGTCAT 3300
 TGCATGCGGT GGTGGCGGTA TTCCAGTTAT AAAAAAGAA AATACCTATG AAGGTGTTGA 3360
 30 AGCGGTTATA GATAAGATT TTGCTAGTGA GAAATTAGCA ACGCTGATTG AAGCAGATAC 3420
 CTTAATGATT CTTACGAATG TAGAAAATGT ATTTATTAAC TTTAATGAAC CTAATCAACA 3480
 ACAAAATCGAT GATATTGATG TAGCAACACT GAAAAAAtAC GCGGCACAAG GTAAGTTTGT 3540
 35 GGAAGGATCG tGTTGCCAAA AATAGAAGCT GCGtACgtTT GTTGAAAGtG GGGaAACCAA 3600
 A 3601

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CGACACTATT AAATGAATTA GAGCACAATC TAACAAATCA AATTCATTTT TCAAAAGATG 60
 AACGACTCAC ACATATCGCT TTAAAGTTAT TCGAAACAAC CGATCCTGTT TCAACAAAGC 120
 55 AACTTGCGCA AGATGTTAAT GTTTCGCGTC GGACAATTGC AGATGATATT AAAATGATTC 180

TTATTGGTGA GGAAGATCAT TATCGTAAAG CGTATGCACA CTTTATACAT CAATATATGA 300
 AACAAAGCTGC ACCTTTTATA GAGGCGGATA TCTTTAATTC AGAATCAATC GCATTGGTTC 360
 5 GCCGTGCCAT TATTAAGACA TTAAATAGTG AAAATTATCA TTTAGTTCAG TCGGCTATCG 420
 ATGGCTTAAT CTATCATATA CTCATTGCCA TTCAGCGTTT AAATGAAAAT TTTTCGTTTCG 480
 ATATACCTAT CAATGAAATT GATAAATGGC GACATACTAA TCAGTATGCn ATTGCTTCAA 540
 10 AAATGATAGA AAACCTTAGAA CGCAGTGTA TGT 573

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TTGATATTTA TAACGTTATA TTTTAATAGT TCACCTGGAT TATTAAATAA ATAGTCCGCC 60
 25 AAATTTTCTT TTTCTTTATC AATCTGaTg TAATTAACaC TTTCCaCTTC TGTAGGAATT 120
 CTAATGTCAA CAGAAGCATT GATATAAGCT TGATGTTGCA TGCAATCACA CTCCTAATCC 180
 30 TTCATmTmAA ACGGAGAAGT AAACCCGTCA CTATTCAAAT TCAATCCTTT TGCCCAATCA 240
 ACAGGCTTAT TCATGATAGT TTCGATTTCC TTAAGTCCAT TTGAACCTCT AGGTATTTCT 300
 ACAATTACTT CATCATGGAC ATGGCCAAC TTTTAAAC CTAATGCTTC AAGCCTTGCT 360
 35 ATAGAAATCG CAAGTAAATC CCTTGCAGTT GCTTGAACAA TATTCTCGAC TAACCTCCCA 420
 CCATACGTTT TTAACCTTGA CCATTTACGG TTAAGATCTA ACCCCATAAA TTCAACAAC T 480
 TGACTACCCC AACTATTTTC ACCAACTAAA GCTTTTGGAT AAGCTAAAGC TCTTCCACTA 540
 40 GGCAGTTCAA TCATTAGAAA ACCTTTTTTC ATATAAAATC TAAGTCCATG TGTATGATGC 600
 GTCTTTCTGGG ATTTTACAGT ATTAATTGCA GCCTCTTGGC AAGCCTTCCA AAAATTAACT 660
 45 ATGTTAGGAT TTGCGTTACG CCAACTATCA ACTAAACCTT GTAACCTGTT TTCTTCAATG 720
 CCCATTTCCA ATGCACCCAT TGCTTTTAAA GCTCCAGCGC CACCTTGATA GCCTAAAGCT 780
 AATTCGGACA CTTTTCCTTT TTGTCTGAGA GGGTCGCTT TAGTTATGCT TTCTACCGGT 840
 50 ACATTAAACA TTTGAGAAGC CGATGCTTCA TATATCTTTC CGTGTGTGTT GAATACATCT 900
 AAACGCCATT GTTCTTTTGC ATACCATGCT ATGACTCTTG CCTCTATTGC AGAAAAATCA 960
 CTTACTGCTA GTTCATTACC TTCTTCAGCA GTAAATGTCG TCCTAACTAA TTGACTTAAT 1020
 55

AGATCTCTTG CTATTCTAA TTCAGTATCT GAAATATAAT GCTTTGTTAA ATTCTGAAGT 1140
 TGTACACCTC TACCTGCCCA TCTTCCAGTA CCGGCACCGT AAAATTGAAA CAGACCTCTT 1200
 5 ACCCGTTCAT CACTGCACAT C 1221

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1090 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTTTGTTTGG TATGAGGTAG CAATGACGAC GTGTCATTGG TGGAGATTGT AAAAATACAT 60
 20 AATAAAAAGA AGCGGCAATG TATACCGCTC CTTTTTTATA CTACATACCG ATTTTCAACC 120
 ATCTCTTTCT ACTTAGTAAT AAGACAATAG TATTAACAT AAATAGAAGA ACGAAGAATG 180
 ATACTATATT TATAATTCA GTAGGACACA TAAATGTTGA CTCGTTATTC AATATTTTTT 240
 25 CTACGGCACG ATACATCGTA TTGCTCGCCT CAAATGGAGC AACGATACCA AATATATTTT 300
 TATTAATGGC AACTAAGATG ACTGAACCAA TCCAATATAC AATGCTGATA CCTAAGCTGA 360
 30 TTAAAATGTT AGGTGAAACC ATACTAATCG TTCCAACAAC TAAGATATAT TGTAAGATAA 420
 CGAGTGAAAA TAAGATTATT AATAGTAAGT AATGTGAGAA ATCCGAATAT ATAATTGAAA 480
 TAATAGTGAT ACTTAGAATT ATGAACACTA AACATTCAAA AAATAACACT GCTACCTTTT 540
 35 TATAGAAGAA GGTAAAGATA TTATCGCCAA TCAATTTATA AAACAGGATA TTTTATTTCG 600
 AATACTCTTT ATTAATAAAA TATGCAATAA CAAATGAAAA TAGTAAGAAC CCTAATTGCG 660
 TTGCAACAGT ATATGAACTG AAGAAAAACT GGCTATAGCT TAAACTTTTA ACTTTGTCTA 720
 40 TACCTATTGG TAAAAAATAC CCAAGTAAGA AAAGGAATGT GAATAGCACA ACAAGCGTGT 780
 AAATAATTTT ATTGGAAATA CTTTTTTTAA ATTCTAATTT CAAAGTGGAC ACCTCAATTA 840
 45 TAAATTAATG TAATCATTTA TGACTTCTTC TTTTGATTGG TACTCTTCTA TTGAAGGTC 900
 TTTAAAAATA AAGTATTTAC CCGGCAAAGC ACTTAAATCG GATAAATTaT GTGTAATATT 960
 GATAATAGTT TTAGTTTGAT GGCTTTGAAT AAAATCATTT AAAAATTCAT AAATTTCAAT 1020
 50 AACTGTTTTT TGTCTAAAG CGTTTGTAAC TTCATCTAAT ATGATTAAAT CATGATCTTC 1080
 CAATAAGAAA 1090

(2) INFORMATION FOR SEQ ID NO: 10:

(A) LENGTH: 904 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

10	TTAGGACTAT TTTATCATAT TCATTTAAAT TACGGCTAAA AATTTTAAAA ACGGGGATTA	60
	ATATATGGAA TTAAGCTATG AAAGTTAATT GATACTTGCA TTTTACGCTG ATTTATATAA	120
	GAATAACTAT TGTATAGTTT TAAAAACGAA CGTACGTTTG CAGGAGGCGA AATCATTGGC	180
15	AATGAATAAA CAAAATAATT ATTCAGATGA TTCAATACAG GTTTTAGAGG GGTTAGAAGC	240
	AGTTCGTAAA AGACCTGGTA TGTATATTGG ATCAACTGAT AAACGGGGAT TACATCATCT	300
20	AGTATATGAA ATTGTCGATA ACTCCGTCGA TGAAGTATTG AATGGTTACG GTAACGAAAT	360
	AGATGTAACA ATTAATAAAG ATGGTAGTAT TTCTATAGAA GATAATGGAC GTGGTATGCC	420
	AACAGGTATA CATAAATCAG GTAAACCGAC AGTCGAAGTT ATCTTTACTG TTTTACATGC	480
25	AGGAGGTAAA TTTGGACAAG GCGGCTATAA AACTTCAGGT GGTCTTCACG GTGTTGGTGC	540
	TTCAGTTGTA AATGCATTGA GTGAATGGCT TGAAGTTGAA ATCCATCGAG ATGGTAATAT	600
	ATATCATCAA AGTTTTAAAA ACGGTGGTTC GCCATCTTCT GGTTTAGTGA AAAAAGGTAA	660
30	AACTAAGAAA ACAGGTACCA AAGTAACATT TAAACCTGAT GACACAATT TTAAGCATC	720
	TACATCATTT AATTTTGATG TTTTAAGTGA ACGACTACAA GAGTCTGCGT TCTTATTGAA	780
	AAATTTAAAA ATAACGCTTA ATGATTACG CnwGGgTAAA GAGCGTCAAG AGCATTACCA	840
35	TTATGAAGAA GGGATCaAAG rGTTgTtagT atGTCCAaTG ArGGAAAAGA AGTTTTGCCT	900
	GACG	904

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11271 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

50	GATTTCTAAA TCAAGATCTG TTTTACGATA ACCATTCAAA CCTTGACGTT CATCTTCTTC	60
	AGGTTGATTT TGTGCTGTG TGTCTTGTT GTCAGAAGTC GCTACTGTT TTTTATTATC	120
55	TGTTTCTTTA GTCATAACAA ACGCCTCCGT TATAAACGC TATATTTAAT GATATGTGAT	180

	TTAATAAGAC GATTCAGCAA GTTTTAAAGT ATTATTGAC TATGTTGGAT TAGGCATCTA	300
	GTCCTATAAT ATCACTGACA TTGTCAAAAT GATGATCTTT TAAGTAACGT GCGATGCCTT	360
5	TGTTTCATTTT CTTAGTTAAA CCTGGGCCTT CAATAACAAG TGATGAATAA ATTTGAATAA	420
	GTGACGCACC GTGACGCATC ATTTTGATTG CATCTTCAGT ACTGAATACG CCGCCTGTAC	480
10	CTATAATTAA AAATTACCA TTTGTTTGCT GATAAgCATA CTTAATCAAT TTTAAATTAC	540
	GTTCAAATAA TGGACGACCA CTCAAACCGC CTTCTTCGAC TTTATTAGCA GAAGTTAAAC	600
	CATCTCGTTG TCGCGTTGTG TTGCTAAGA TGATACCGTC AAATGTCTCA GTAATCGCTG	660
15	GTAATAGTGC TTTTAAGCCA TCGAAATCCA TATCAGACGT TAGTTTTTAA TAAATTGGCA	720
	CTGTTACATC ATGTTGTTTT TTAAATGCTG TTAAAGCTTG GCATAACATT GAAAATTCAT	780
	CTTTATCATG GAAGTTTTGA AGATTTTCAG TATTTGGAGA ACTGATGTTG ACTGTGAAAA	840
20	ATGAAACGTC GTGTTTAAAC GTATCAATAA CCTTTATATA ATCTTGATAA CGCGCTTCAT	900
	AAGGTGTCAT TTTATTCACA CCAACATTGA TACCAACAGG TACTTGATAA GCATTTTTAC	960
25	GCAAATGACT TAGTGCTTTG TTCATACCAA TATTATTGAA GCCCATTCTGA TTTATCAAGG	1020
	CGTCATCTTC TAATAATCTA AACATGCGTG GTTGAGGGTT ACCCGGTTGA GGTTTAGGTG	1080
	TGATACCACC TAATTCTAAA GCACCGAATC CAAGGTGTTT CAATGCTTTT GGTACTTCGC	1140
30	AAGATTTGTC GAAACCAGCT GCTAAgCCAA TTGGATTGTC GTACGTATTA CCTTGTATCG	1200
	TTTGTGATAA CGTTGGATTG TTATAAGTAA ATAGTTTATC GACGACTGGG AATAAAACCG	1260
	GaAACTTTTG TaACGTTTTT AATGCATCGA TAGTTAGTCC GTGTGCTTTT TCGGGTTTCA	1320
35	TTTTGAATAA GAAAGGTTTA ATTAATTTGT ACATGAGTAT GCTCCTATTT CATTATATTT	1380
	GAGGCTTACT ATCCTCAACT TAATATATGT GAAATATATT CTTTTAATAG ACTAGCATTT	1440
	CCATACATAA TTTCTAGTT AAAACTAAAA AGTTTTGAAA ATTGACGCAA gTTTGAATAA	1500
40	CGTTTTTAAG ATTAAATCAT CCTAATTAGG CAATATTATA GTATAAAGTA AGTAGATTGG	1560
	AAGGTGTTTG TATGAATGAA CAATGGTTAG AGCATTTACC TTAAAAGAT ATTAAAGAGA	1620
45	TTTCACCACT GAGTGGTGGT GATGTAAACG AAGCATATCG AGTCGAAACA GATACGGATA	1680
	CATTTTTCTT ACTTGTCCTA CGTGGACGTA AAGAATCATT TTATGCTGCA GAAATTGCAG	1740
	GTTTAAATGA ATTTGAACGT GCAGGTATCA CGGCACCTAG AGTAATTGCA AGTGGCGAGG	1800
50	TTAACGGTGA TGCCTATTTA GTGATGACGT ATTTAGAAGA AGGGGCTTCA GGGAGTCAAC	1860
	GCCAATTAGG GCAACTCGTA GCTCAATTAC ACAGTCAGCA ACAAGAAGAA GGCAAATTTG	1920
55	GCTTCTCATT ACCTTATGAA GGTGCGGATA TTTCTTTTGA TAATCATTGG CAAGACGATT	1980

	GGCTATGGGA TGCCAACGAT ATCAAAGTAT ATGACAAAGT GCGACGTCAA ATTGTGGCGG	2100
	AATTAGAAAA GCATCAAAGT AAACCGTCTT TATTACATGG TGACCTATGG GGTGGTAATT	2160
5	ATATGTTCTT ACAAGATGGT CGTCCGGCGT TATTTGATCC AGCGCCATTA TATGGTGACA	2220
	GAGAATTCGA TATCGGTATT ACAACGGTAT TTGGTGGTTT TACGAGCGAA TTTTATGATG	2280
10	CGTATAATAA ACATTATCCA CTCGCAAAAG GTGCATCCTA TAGACTTGAA TTTTATCGTT	2340
	TATATTTATT GATGGTCCAT TTATTGAAAT TTGGTGAGAT GTACCGTGAT AGTGTTGCGC	2400
	ATTCTATGGA TAAGATTTTA CAAGATACAA CAAGTTAGTT AAGACGTTAG ATTGAGATAA	2460
15	ATAGATAATA TGCACAGATA TTTTACAAAT GAGAAGCGAT ACAGCTGCCT CAATAAAAAT	2520
	ATTTGTGCGT TTTTATTGTT GGAAAATAAA ATTTTAAATCG CTATTGTTAA TTTCTGTAAT	2580
	GTAAAACAAG GTTGAGTTAC AATAAAAGTG ATTTTATAAC TTTTGTTC AATAAAATTCT	2640
20	AGGAATGATA CATATTTATT GATACAATAA TTTTGAATAT AATCATAAAA CAATATTTAA	2700
	GTATAATTGA ATGTTTGAAT ATCATATATT GATACAGTTT CTAATAATTT TAAAATAATT	2760
	TAAATGGAGA GAGGTGTAAA TGATGAGTAC AGTTCAAAGT GATATTTTAA AGACCAATAG	2820
25	TGCATCATCA TCTATTAAAA GCGCTGTTGA AACATGTAAT AATGTGTCGA AACCGGATAA	2880
	AGATGAAAGT ACAACAGTAA GTGGAAATAA TAATGCTCAT AGTGTGATAG ATGATTTGAT	2940
30	GAGTAAGAAT CAATCTGTTG CTGAAGCAAT ACGAACTGCG AGCGATAATA TACAAAAAGT	3000
	TGGTGAGGCT TTTGACCAAA CTGACGTAAT GATTGGTAAT GAAATTGGTA AAAATTAAAA	3060
	CGTGGTGAAG TGATGTCGAA TAACTGGAT GAAATCAATA AAATAATCAC AGCGAAACAT	3120
35	GAGCAAATGG ATGACTTATA TGATGAAAAG CGAGAGGTTA AAGCATTGAT AGATGAAAGT	3180
	GATGCGCTTA ATCATTGAT AGATCAATTA TATCAACATT TAGGTGAGCG TTATTATAGT	3240
	AGCAATATGG CTAGTCGTAT GGAACAGTTC CGCGATGAAT TTCATTTTGC GAAACGACGT	3300
40	TCAACGGAAG CGTTATACGA GCAGCAACAG CAAATTCAAC ATGGCATTCTG TAAAGTGGA	3360
	GAAGAGATGA TTGACTTGGA AATGCGAAGG AATGTTGAAA TTGAGACGGT GACAAAGGAG	3420
	GAAAATAAAT GGAAACAATA GGAAGCATT TTTATTTAAA AGAAGGTTCTG CAAAAGTTAA	3480
45	TGATTATTAA TAGAGGmCCA aTTGTAGAAA TTGAAAATCA AAAGTATATG TTTGACTATT	3540
	CTGCATGTAA ATATCCGATT GGTGTTGTAG AAGATGAAAT TTATTATTTT AACGAGGAAA	3600
50	ATATAGATTC AGTTATTTTT AAAGGTTATT CTGATCAAGA TGAGGTTAGA TTTCAAGAGT	3660
	TGTTTGAAAA TATGAAACAA AATTTGGATA GTGAAATACA ACGTGGAGAA GTTACACAAC	3720
	AATAAGAAA TACTTTTTCT TTATTGGGGT GGGACGACGA AATAAATTTT GTAAAAATAT	3780

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	ATGTCATTCA TAATCATTTG AACTAAACGT AGCAGCCTTA AATTTTAAAA AAAGACACAT	3900
	ACCAACTTCC GAAATGTAGA TGAATTCTCT ACAATAACGG AAGTTTTTCT TTTAATATTG	3960
5	AAATTTCTCA AGGATAGGTC TATACTTTAT AAATCGTAAT TATTACGATT TATAATCAAA	4020
	AACAATAACT TGAAATAGAT CATTGAGGGA GTGTTAATAT GCAACATCAT AAAGTGGCTA	4080
10	TTATCGGTGC CGGTGCTGCA GGTATAGGTA TGGCCATTAC CTTAAAAGAT TTCGGTATAA	4140
	CAGATGTCAT TATTTTAGAA AAAGGAACAG TAGGACATTC ATTTAAACAT TGGCCGAAAT	4200
	CGACCCGTAC GATCACGCCA TCATTTACGT CTAATGGATT TGGCATGCCT GATATGAATG	4260
15	CAATTTCCAT GGATACTTCA CCAGCATTTA CATTTAATGA AGAACATATT TCCGGAGAAA	4320
	CATATGCTGA ATATTTACAA GTGGTTGCCA ACCATTACGA GCTGAATATC TTTGAAAATA	4380
	CAGTTGTCAC AAATATATCT GTAGATGATG CATATTATAC GATTGCAACG ACAACAGAGA	4440
20	TATATCACGC GGATTATATC TTTGTCGCAA CAGGTGATTA TAATTTCCCT AAAAAgCCAT	4500
	TTAAATATGG TATTCATTAT AGTGAAATG AAGACTTTGA TAACTTTAAT AAGGGGCaAT	4560
	ATGTGGTTAT CGGAGGTAAT GAAAGTGGCT TTGATGCTGC ATATCAACTT GCAAAAAATG	4620
25	GCTCTGACAT CGCACTTTAT ACTAGCACAA CCGGTTTAAA TGATCCGGAT GCTGATCCTA	4680
	GTGTTAGATT GTCACCTTAT ACACGTCAGC GACTAGGTAA TGTCACTAAG CAAGGTGCTC	4740
30	GCATCGAAAT GAATGTACAT TATACAGTTA AAGATATTGA TTTTAACAAT GGACAGTATC	4800
	ATATCAGTTT TGATAGCGGA CAAAGTGTGC TTACACCTCA TGAACCAATA CTAGCAACTG	4860
	GCTTTGATGC AACAAAAAAT CCAATCGTTC AACAAATTATT TGTGACAACA AATCAAGATA	4920
35	TTAAATTAAC AACACATGAT GAATCGACAC GTTATCCGAA TATTTTTATG ATTGGTGCAA	4980
	CAGTTGAAAA TGATAATGCC AAATTATGCT ATATCTATAA ATTTAGAGCG CGATTTGCAG	5040
	TACTTGCACT TCTTTTAACA CAGCGGGAAG GCTTACCAGC TAAACAAGAT GTCATTGAAA	5100
40	ATTATCAAAA AAATCAAATG TATTTAGATG ATTATTCATG TTGTGAAGTG TCATGCACAT	5160
	GTTAGAAGTG AAATATGATA TGAGAACTGG GCATTATACG CCCATACCTA ATGAACCTCA	5220
45	TTATTTGGTT ATTAGTCATG CGGATAAACT TACCGCAACA GAAAAAGCGA AATTAAGATT	5280
	ATTAATCATA AAACAGAAAT TAGATATTTT ATTGGCAGAA AGTGTAGTTT CTTcGCCTAT	5340
	AGCGAGTGAA CATGTGATAG AACAAATTGAC ACTATTTCAA CATGAGCGAC GACATTTAAG	5400
50	ACCTAAAATA AGTGCGACAT TTTTAGCCTG GTTGTGATA TTTTAAATGT TTGCATTGCC	5460
	AATCGGTATC GCTTATCAAT TTTAGATTG GTTTCAAAAT CAGTATGTGT CAGCATGGAT	5520
55	AGAATATTTA ACTCAAACAA CATTGCTCAA TCACGATATA TTACAGCATA TATTATTTGG	5580

	ATTGATTAGT TTATCAACTG CTATAATTGA TCAAACAGGA CTCAAATCAT GGATGATATG	5700
	GGCAATTGAA CCGTCAATGT TATGGATAGG ATTACAAGGT AATGATATCG TGCCACTATT	5760
5	AGAAGGGTTT GGATGTAATG CAGCAGCTAT TTCACAAGCA GCACACCAAT GCCATACCTG	5820
	CACGAAGACA CAGTGTATGA GTTAAATAAG CTTTGGTAGT TCTTGTAGTT ATCAAATAGG	5880
10	TGCGACATTA TCTATTTTGA GTGTAGCTGG AAAGTCATGG CTATTTATGC CGTACTTAAT	5940
	ATTAGTACTT TTAGGTGGCA TCTTACATAA AGGATATGGT TGAAAAAGAA TGATCAACAA	6000
	CTTAGCGTTC CGCTACCTTA TGATAGGCAA TTACATATGC CAAATATACG TCAAATGTTG	6060
15	CTACAAATGT GGCAAAATAT ACAAATGTTT ATCGTTCAAG CGCTACCTAT TTTTATCACA	6120
	ATCTGTCTTA TTGTTAGTAT TTTATCACTA ACGCCAATTT TGAATGTTTT ATCACAATA	6180
	TTTACACCTA TATTATCGTT ATTAGGCATC TCGTCAGAAT TGTACCAGG GATTTTATTT	6240
20	TCAATGATTC GAAAAGACGG CATGCTCTTG TTTAATTTGC ATCAGGGCGC CTTATTACAA	6300
	GGAATGACAG CAACACAGTT ACTACTACTT GTGTTTMTTA GTTCAACATT TACAGCGTGC	6360
25	TCGGTCACAA TGACGATGCT TTTGAAACAT TTAGGTGGTC AGTCAGCACT AAAATTAATT	6420
	GGAAAGCAAA TGGTGACATC ATTGTCTTTA GTTATTGGTG TAGGCATCAT TGTTAAATA	6480
	GTAATGCTGA TTATTTAAAA AAAATGAACT ATAAGTGAAT ATAGAGTCAT GTCAGTCAAT	6540
30	AGGAGATCTA TCTTGGAAATA TGCTATTCTAT ATGAAGTATA AGAGGAGAGT CGCAGATGAA	6600
	AATAGTTATT ATAGGTGGGT TTTTAGGTGG CGGTAAAACG ACTGTCTTAA ATCATTTGCT	6660
	CGCTGAATCA TTAAAGGAAT CGCTGAAACC AGCAGTCATC ATGAATGAAT TTGGGAAAAT	6720
35	GAGTGTGAT GGTGCCCTTAG TATCTGAAGA CATACTTTA AGTGAAGTGA CAGAGGGGTG	6780
	TATCTGTTGT GCAATGAAAG CAGATGTATC AGAACAGTTA CATCAATTAT ATTTAAAAGA	6840
	GCAACAGAC ATTGTATTGA TTGAATGTAG TGGGATTGCA GAACCGGTCT CTGTCTTAGA	6900
40	TGCTTGTTTA ACGCCTATTT TAGCTCCGTT TACAACAATT ACACATATGA TTGGTGTAAT	6960
	AGACGCAAGC ATGTATAAAC ACATTAAATC ATTCCTAAA GACATCCAAG GCTTATTTTA	7020
45	TGAGCAATTA GCATATTGTT CTGTCTTATT TGTTAATAAA ATAGATTCAG CAGATGTTGA	7080
	AACAACGAGC AACTATTGA AAGATTTAGA AGTTATTAAC CCAGAGGCCG ATATACAAGT	7140
	CGGTATGCAT GGCAGCGTCA CTTTGCCAAT ATCAGTTAGA CAAATGACAG CAACTTCTGA	7200
50	CAATAAACAT AAGTCTTTAC ATCAAATGAT TAATCATCAA TTTGTGCAAT CACCAGTCAA	7260
	ATGTACTAAA GCAGAGTTTA TAAAACGTTT AGCATGCCTT CCGTCTCATA TTTATAGGTT	7320
55	GAAAGGGTTT ATGACATTTG AAGACACCGC ACATACGTAT CTCATTCAAT TTACACAAGG	7380

	CGGAAAGGGT	ATTTCAAAG	AAGACTATCA	ATGTTTGAA	CAGTAGTGT	ITCAGTGGAA	7500
	GAGAATGGTT	AACATGCCTT	CATGTATAAT	AACGAGTTGA	TTTGAACGTT	TAAGCGTAAA	7560
5	TAAAAATAAG	CTTGGTCAGC	CATCAAATAT	AATTTGAAAA	CTGTCCAAGC	TGTTTTATTA	7620
	GAGAACATC	AATTAACCCC	ACATATTTAA	TAATACATCA	GCAAAGCCTT	CAGGTTTTTG	7680
10	AATATAACCT	AAGTGACCGC	CTGGAATATC	TACAATAGGT	ATGCCAGTTT	CTTTATTTAT	7740
	ATAAAAGTTA	ACATCTTGTG	GGAAGGAGCC	TCTAGAATCT	GTCCCATTTA	GTAGGGTGAT	7800
	TTTATCGCTG	TATTTTGTGA	AATCATCCAA	AGTAATATCT	GAATGCGTAT	ATTGTCTAAT	7860
15	TTCAAATTCT	GACCAGAACA	TCGTACGTTT	GTAAGTTTCT	ATACGTCCTT	CTTCAGTATC	7920
	AGCAGGTTGA	GACATCATTT	TTGCATCAAT	TGGTGCAGTA	TTTAATGTTT	CGCCAAATGT	7980
	TTTCATGCCT	TTTTCTAAGC	CTTCTGTTAA	AATTTGATGC	ACAATGTCAT	CATTTTTATC	8040
20	TTTCCAATAA	GTAAGTCTG	GTAAAAATGT	ATTAATTGGT	GGTTCGTGAA	ATGCAATCTT	8100
	TTTAACGACT	TCAGGGTAAT	CTTTTAACAC	ATGCATCGCA	ACGATTGAAC	CTGAACCTGA	8160
25	ACCTAATATA	TAGACAGGTT	CATCACTTAA	TGACTTTGCA	AGTTCGGCAA	TGTCCTGTGC	8220
	GTCGCGTTTG	ACACGATAAT	CACTGTCAGG	GTTTGAAGCG	GAATCAGGGA	GTGGTTCAGT	8280
	TAACTCGCTT	TCTCCATAAT	CACGACGATC	AACGGCTACA	ACAGTAAAAT	GGTCTTTTAA	8340
30	CTGTTCTGCA	AGAGGCAGAA	AAATGTCTCC	GGTACCGTTT	GCACCAGGAA	TAAAGATGAG	8400
	CACGGGTCCT	TGTCCGACTT	GGTGGTATCG	TAATTTAGCG	CCTTGTAATT	CTAAAGTTTC	8460
	CATATTCAAT	GACCTCCATT	TGTTAATTGT	TAGGTGATAA	ACCTAATAAT	TTAGCACCAT	8520
35	TTGTATAACT	TATTTTCTCT	TTTTCTTCAT	CTGTTAAACC	CAGTTCATCT	AAAAATACAC	8580
	CTAATTTTTC	AGGCTCAATA	TATGGATAAT	CAGCAGCATA	AAGAATTCTA	TCAATACCTA	8640
	CTTCTTTCTT	GACTAAATCA	AACTGTGGCT	TCGTTAACAT	GCCACTCGGT	GTGATATAAA	8700
40	AATTATTTTT	AAAGTAATAG	CTTACAGGGT	GGTTCAAATG	TTCAGCGAAT	AAAGCTTCAT	8760
	CCATACGTTT	TAAGAAGAAT	GGGATAAACT	CACCCCAATG	TCCAATAATC	ATATTTAACT	8820
45	TTGGATAACG	ATCAAAAATA	CCAGATAATA	CTAGATGTAT	TGTATGAATG	CCGACATCAA	8880
	TGTGCCAACC	ATAACCAAAA	CAAGCAAATG	TTGCCGCAGT	TACTTCAGGA	TAATTCCTT	8940
	TATAGTATGA	TTGATAAATG	TCAGTGTAA	CTGGCGCGGG	ATGTAGATAA	ATCGGTACGT	9000
50	CTAAATTTTC	AGCTGTTTTG	AAAATAATGT	CATATTTGTC	TTGATCAAGA	AAACCATCTT	9060
	GTGCACGTCC	CATAATGAGC	GCACCTTTGA	ATCCTAAATC	ATTGATGCAA	CGTTCGAATT	9120
55	CTCGCGCTGC	GGCTTCAGGC	TCATTGATAG	GTAAAGTTGC	AAAGCCTACA	AAGCGATTGG	9180

	TCTGACCAAC	CAAATTTGAA	GGAGAACCAT	TTCCATAAGA	TAAGACTTGA	ATTTGAACGT	9300
	CTTGATTATT	CATAAATTGG	ATACGTTTCAT	CATGATGTGA	TAATTCGTCG	GCATTTGTAA	9360
5	AACCTGTCTT	TTTTTcAAGG	CCTTCTAACA	TTACTTTTCAT	CGGTACACCT	TAGGATCTG	9420
	CTGATATCGC	ATTCATCGTT	TCTTTTTTGAA	TATCTTCAAT	GACATAATGT	TCTTCAAACG	9480
10	TAATACTTTT	CATTTACTTC	GCCTCCATAT	TGTATTGCAT	GTTTATTGCA	TCTATTGCAG	9540
	AAGCATTTTT	TATATACCTC	TAATTTCAAT	GTTTGTAACA	TAAAATTGAT	CTACCAAGGC	9600
	ATCTCTCCAT	CGCCATTAAT	AAATGTACCT	GTTGGGCCAT	CTGCACCAAT	CGTTGCTAAT	9660
15	TGAATGATTG	GCTTGATTCC	TTCAGAAACG	TGTTTGGAAT	TATTACTAAA	ATCACCAACT	9720
	AAATCAGTAT	TTGTAGCGCC	TGGATCAGCA	GCATTGATTT	GCATGTTAGG	TAATCCTTTA	9780
	GCGTATTGTA	GCGTTAGCAT	TGTTACTGCC	GATTTAGACG	AACAATAAGC	TAATGAATTC	9840
20	ACTTTAGATT	CAGCTGTTTC	GGGGTTTGTA	ACCATTCCAA	ATGAACCTAA	ACCACTTGAT	9900
	ACGTTGACGA	CAACAGGTTG	TTCAGATTTT	TCTAAGAGAG	GGACGAATGT	ATTCATCATT	9960
25	CGTACGATAC	CGAATACATT	CGTTTGATAT	ACTTCTTCAA	CGTCACGAGG	TGTCAATTTG	10020
	GAAGGTGCTG	AAAATTGACC	AGATATACCT	GCATTGTTAA	TGAGGATATC	AAGACGGCCT	10080
	TCTTTTTTCAG	CAATCATGTT	ATAAGCATTT	TTGACTGAGT	AGTCACTTGT	AACATCTAAT	10140
30	TGTACATAAT	GAACACCTAA	TTTTTGTTGAT	GCTTGTTGTC	CTCTTACATC	ATTCCGAGAA	10200
	CCTATATAAA	CTTTGTAACC	CAATGCTTTA	AGTGCCTCTG	CACTTGCATA	GCCTAACCT	10260
	TTATTGCCTC	CTGTGATTAA	CACAATTTTA	GTCATTACGT	CCCACCTCAT	CTAAATAAAT	10320
35	GTTTAATAAA	TAATTTCTGT	ACGCTTCAAT	TGAAATATGG	CGATGCTCTA	TTTGGAAGGC	10380
	AAATACACTA	GTTGATAATG	ATTGCAACAG	CATATCTGTT	TTGAATTCGT	GTAAGTGTCG	10440
	TCATGCTTTT	TAAATAAGTC	ATAATAAAAA	TCAAATAATT	CTTGATAAAA	TGCGCTTTGG	10500
40	TAAAAACGTA	ATTTATTGTT	GCCTGCTTCA	ATACATTGCA	GTAGTGCCTT	ATTATCGATT	10560
	TTAAATTGTA	AAAGATAATC	TAACGACACT	TGCATAACCT	CATAATTAGA	ATGATAGTCA	10620
45	TCTTTAATTT	GCTTAAAATG	AGTGATAAAA	ATATCAAGGT	CTCTTTGTAT	GACGTAGTAG	10680
	CATAAATCGC	TTTTATCTTT	GAAATGTCGA	TACAATGTCC	CCATACCGAT	ACCTAGTTCT	10740
	TTAGCAATAC	GATTCATACT	AATGTTTTCA	ACGCCTTCTT	CATCAAAAAG	TTTGTGCGCT	10800
50	ATTTCTTCAA	TTGTTGCTT	ATTCTCTTTT	GCATCTTTTC	GCATGATTAC	ACCTACTTAA	10860
	AATCTCTTAA	AATTGACAAA	CGGATAACTC	TCCGTTTATT	ATAAAACGTG	TTAAGAAAGT	10920
	TAGCAATGAA	TTTGCAATAA	CTATTAAATA	TCATAAAAGA	AAAGAGTGTT	GATAATGTCT	10980

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ACCTTATCGG TTCAAATGAT TGCTGAAAAA CTGAATGTCA CTACAGAAGA TGTGGAAAAA 11100
 GTATTAGCTA TGACAGCGCC ACTAGGCATT TTTAGTCATC AATTACAACG ATTTATTCAT 11160
 5 TTAGTATGGG ATGTCAGAGA TGTAATAAAC GACAATATTA AAGGAAATGG ACAAACACCA 11220
 GAACCATATA CGTATTTAAA AGGTGAAAAA GAGGACTATT GGTTTTTAAG A 11271

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

20 CAACCCGTTT AGAACAAAAT AAAAACCGTA CAATTTTATC ATCTTAATGA TTATTGTACG 60
 GAAAACTTT TTTACATCAT ATCTGCATGT GCATAATCGA TATCGGTAAA TTTATTATAT 120
 TGTTCATAA AATGTAACCT AACTGTGCCT GTTGGACCGT TACGTTGCTT AGCAATGATA 180
 25 ATTTCAATTT CACCGTTTTT ATCATTCGTT TGTGGCTCGA AACCACCATC ATCGTCATCA 240
 TCTTCATCGC CGCCACGGTT ATAGTAATCA TCACGGTATA AGAATGCAAC GATATCGGCA 300
 TCTTGCTCAA TCGAACCAGA TTCACGAATA TCACTCATCA TTGGACGTTT ATCTTGTCGT 360
 TGTTC AACAC CACGAGATAA CTGACTTAAT GCGATAACTG GACATTTTAA TTCACGGGCT 420
 AATGCTTTTA ATGTACGAGA GATTTCAGAA ACTTCCTGTT GTCTGTTATC GGACGCACGT 480
 35 GAACCACTAC CTTGAATCAA CTGTAAGTAG TCAATCACA TCATGTCTAA GCCATGTTCT 540
 TGCTTTAATC GACGACATTT AGAACGTAAA TCATTAATTC GAATACCCGG TGTATCATCA 600
 ATAAAAATCT TCGTACGTGA TAATTTACCT ACCGCTATAG TAAAACGACT CCAATCTTCC 660
 40 TCAGTCATAG TACCCGTTCT TAAGCGGTTT GAGTCAACAT TTCCAGAACT ACAAATCATA 720
 CGTGTGGCTA ACTGATCAGC ACCCATCTCT AGCGAGAAAA TACCAACTGT ATACATATCT 780
 TCATGCGTTG CAACTTTTTT TGCAATATTA AGTGCGAACG CAGTCTTACC TACAGATGGA 840
 45 CGCGCTGCAA GGATAATTAA ATCATTTCCG TTGAACCCTG CTGTCATTTG GTCTAAATCT 900
 CGATATCCTG TAGGTATACC TGGTGTGTTGA CCACTATTTT GATCAAGCTC TTCAGCTGTT 960
 50 TCATACACTT GTCCTAAGAC GTCTCGAATG TCTTTAAAGC CATCGCTTTC ACGAGAAGAT 1020
 GATAGCTCTA AAATTCGACG TTCTGCATCA CTTAAAATCG CATCTAGTTC AAGTTCATCA 1080
 TTATATCCAT CATTGGCAAT ACTATCTGCA GTTTGAATCA ATCTACGTTT TAATGCATGC 1140

	TCTGCAAGAT ATTGCGGGCC ACCCGCTTcA TTCAACGTAC CTTCCGTCGA TAATTGATCC	1260
	ATCAATGTTA CAACATCAAT TTCTTTATTA TCTTCATTTA AGTGCATCAT TGCACGGAAA	1320
5	ATATGTTGAT GGGCACCCCT ATAAAACGAC TCAGGAAGCA AAACCTCCTG AGTAGTATTA	1380
	ATCAATTCTG GATCTATAAT AATTGAACCT AAGACAGACT GTTCAGCTTC ATTGTTATGC	1440
10	GGCATTGAT TTTGCTCATA CATTCTATCC ATGAATGGTT ACACCTCTTA TTTCAATCCA	1500
	ACTTTATTGT TCAACTGTGT GTACGCGAAT TGTACCTTCA ACTTCTTTAT CTAATTTAAC	1560
	AGGTACATTC GTATATCCTA GGAATGAAT TCCATTTGGT AAATCCATTT TACGTTTATC	1620
15	AATTTTAATA TCATGTTGTG CTTTTAGTGC TTCGGCAATT TGTTTTGTAC TTA CTGACCC	1680
	AAACAATTTA CCACCTTCAC CAGTTTTTGC TGaTACTTCA ACTTCAATGT TTGATAACGT	1740
	TTCTTTTAAT GCTTTAgCAT CTTCAATTTT TTGTTGGCGT TCTTGTTTTG CACGTTTTTT	1800
20	CTGTAACTCT AATTGTTTAA GGTAAECTGG TGTTGCTTCT ACAGCATAAT TCTTTTCAA	1860
	TAAGAAGTTA TTTGCATAAC CTACTGGTAC TTCTTTAACT TCACCTTTTT TACCTTTACC	1920
	TTTACCTTTA ACATCTGTG TAAAAATTAC TTTCATGCAT CTTCACTCCT ACTTAATTGT	1980
25	TCTGTAATTG CTTGTTGTAA TTGTGCTATC GCCTCTTCGA CTGTCACACC TTTAAGTTGT	2040
	GTTGCCGCAT TGGTTAAATG TCCACCGCCA CCAAGTGCTT CCATTGTTAA CTGGACATTT	2100
30	ACTGAACCGA GTGAACGCGC AGATATACCA ATCAGATTAT CTTACAGTCT CGCAACAACA	2160
	TATGATGCTT CAATACCTTC TAAACTTAAC AGTTCATCTG CTGCTTGTGC AACTGTTACT	2220
	GGATGATAAA TTTTATCGTC TGAACCATGC GCAATGGCTA TGCCATTATC TTCAACTTTT	2280
35	ACAGTTGAA TTAATTCAGA TCGATTAATG TAAGTATCCA CATCATCTTT TAAGAAATGT	2340
	TGCGTTAAAA TCGTATCTGC ACCATGTGCA CGTAAATAAC TCGCTGCATC GAATGTTCTT	2400
	GATCCTGTTT GTAATGTAAA GTTTCTTGTA TCTACAATAA TACCTGCATA CATCACTGTT	2460
40	GATTCAAGAC GTGTTAAACG TTGTTCTGTT GGTGATATT CCAGTAACTC TGTTACCAAT	2520
	TCAGCTGTG AACTTGCCTA TGGTTCCATA TATATCAACA ATGGATTAGA GATGAAGCTT	2580
45	TCACCACGTC TATGATGATC GATAACAAC TTTACGGTTTG CTTTATTTAA GACATTTTCA	2640
	TCTAAAACCA GTTCCGGTTT ATGCGTATCA ACAATCACTA CGGTTGTCTT AGATGTCATC	2700
	ATATCCCAAG CATCATCTGA TGTAATAAAT CGCTCTCTTA ACTCTGGCTT TTTATCTATT	2760
50	TCGTTTCATCA CGCGTCGTAA TGTTGGATCA ATGTCAGTCT CATTTAATAC GATGTATGCT	2820
	TCTAAATTAT TCATCATTCG AAATCTAGAC ACACCGATTG CTGCACCAAT TGCATCTAAG	2880
55	TCAGGACGTT TATGTCCCAT GATAATGACT TTGTCACCCT CTGCAAGGAT ATCTTTTAAC	2940

	CCATAGAAAC GCACATTACC ATTAATACTT TTAATTGCAA CTTGGTCGCC ACCGCGTCCT	3060
	AATGCTAAGT CTAGGCCTGA TTGTGATAAT TCACCTAAGT CGATTAAATT TTCAGTACCT	3120
5	TCACCAACAC CGATACTTAA TGTTAATTGG GCACGATAAC CAACACTTTT TTCACGTAAT	3180
	TGACTCAAGA TATCAAATTT AGATTCTTCT AAGTCAGCTA ATATTTTGTG ATTTAAATAG	3240
	GCTACGAATT GATCGGAACT GTATCTTTTG AAAAATATAT TATACTCAGT TGCCCATCGA	3300
10	CTAATGACAC GCGTTACCAT TGAGTTGATT TCCGAACGCT GCGTATCATT CATATTTTGC	3360
	GTAATCTCAT CGTAGTTATC TAAAAATAAT GTCGCAATGA TTGGTTTAGA ATTTTCATAT	3420
15	AGTTCATTTG TTTGTACTTG TTCAGTTATA TCAAAGAAAT AGAGGCAGTG ATCATTCTCA	3480
	GAATAACGTA CTTGGAAATG ATACTGATTA TATTCTATTT CAACGGATTT CACTCTATCT	3540
	AATTGCTTTA AAATGTTTGG AAATACTTCA TTTACAGATT CAGAAATGAC ATTCGCTTCC	3600
20	ATATGATCTG TCATAAATTG GTTAACCCAT TCGATGTGAT CATTTTCATC TAAAAACAATG	3660
	ATACCAATTG GTAAATGTTT GATTGCTTTA TTATTTGTTG TTGAAATTTG AGCACTCAAA	3720
	CCATCTACAT AACTATCCAT TTTCAATAAA GCTTGTCTGA ATAAAAATGAT GCTAACAATA	3780
25	ATCATCACGA CAAGAACGAT AGATGCAATT AGTGCTATAA GACTATTAAA GATAAACCAT	3840
	ACACCCATTA AAACAATTGC TGTGATGATC ATGATGACAA ATGGTATTAG TAAAGCTTTC	3900
	TTAGTGGAAT GCGGATTCAT TATTCCACCT CTATTCACTT TTTAGAAATTA TTTTTCATGA	3960
30	TTGCTTCAA ATTCAAATTT AAATCGATAA CACCAAGTAG TCCTACAATA TGTGTCGTAG	4020
	GTGTCAGTAT TGTACCGATA ACCAATAGTA AAATCGTTAC TGCAATTCGGC AAACCTTTTCG	4080
35	CTTTACCAAA GAAATGAATA ACACTTAAAC CTGAATATA CATTACTAAT GATAACACAA	4140
	GTTGGAAGTT TAAAAGAATG CTCTGGAACA CACTCGGTTG ACCTGTAAAT AATAAACATA	4200
	TGATAACAAT AATGTATATC CATAATAAAA TACCGCTCAT TTGCCACGCG AAAAGTGGCT	4260
40	TAAATACAGG TGTAGCGATT TTAAATTTTC GTAAAATCGG AAATGTAACG ATTAAGTTAA	4320
	TTAAGACGAT TAAAAATGTA ATGATAATGA TGAAACCTGG TAATTGAACG GTCGCTTGTC	4380
	TAAACCTTTC TTCTAATATT TGGGTCATAT TCGCATCGGC ACCGCTCATC GTAATCGCTT	4440
45	CATGTAATGT TTGCTTGAAA GGTTTTACTA TGCTCGCTGA TGGTGAATC CTTCCGAATG	4500
	TTTGTAGTAA CATAAAAGCG ATTAATGAAA TTAACTCAT CGCTACTGTT GTTACGTATA	4560
	ATATTCTTTC TTTAGACGTT CTTTCTTTGA GCAATTGACC AATAATTAAA CTTGCAATTA	4620
50	AGACTAATAT GATGGCACTT AAAACGAAAG TATTACCTAA AACAGTTGTT ATAATTACTG	4680
	TAATAAGTGC ACTAATCCCG AAAGATTGTA TTGATTATT CCATAAAACG ATACCTGGTA	4740

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	CAAATACCAA CGCAATCGTT GCAATTATTG TTGCTTTAGG TTGTATTTT GAAAACACAT	4860
	AAGCCACTCC CATATTTTTA ACTATAGCTA TTATTTTAAC CTCTTTAATG AAAATTAACA	4920
5	ATTTATAGAT TGTATGCTTC TATTTCAATT AATTGAATAA TAACTTTCAT GTTTTATAAG	4980
	TAATTAACAT ACTCATTTGA ATCGCTTTTG TGTGCTTTCA TTTTCAACAT GATTATTTAA	5040
10	TCCCACTACA TAGCAATCAA GCTTGATTTA GATTTACAAT ACATTTCCAC TCTCATGTAC	5100
	TCTAGATGTT TTTGAATATG ATAAGTGTGA TTTAGTGGCT TCATTCTTTG AAAATATATA	5160
	TTATTACTTA CGCTTAAAAT GCTTTAAATT TAAGAAATGA TATAAGTTAG GTGCCCGGT	5220
15	ACTAAAGTTT AGTAGGATC CATCATGCCC AACATTATCA GGCACGAAGA AATGACGATG	5280
	ATATTTAAAA CGTTCACCTA ATGCACGAAC TTGATCATCC GGATATAGCA AATCATCTAT	5340
	GAACCCCATC GTTAACACTT TTGTTTCTAA ATTTTAAAA ACATGCGTTA CGTCTGTGCG	5400
20	ACCTCGGTCA ATGTTGTGAC TATCCAATAC ATCTAGCAGT GTCAGATAAC AATTCAAATC	5460
	AAAATGTTCT TTAAATTTAT TACCTTGATG TTGTTGGTAT GCGACTACTT CATCCGGCGT	5520
	AAAACGTTCA TCATAACTTT TTGATGATCG ATATGTCAA AAACCTAATT GGCCTGCAAT	5580
25	ACTTAGACCT TCCTTACCAC CAAGATGAAT GGCTTGCCTT GCAATTTTCAT TGAAAGCTCT	5640
	ACTATAAGAT GATGTTGAC TTGTTGCAGC AAGGATAATG GCTTTATCTA CTTCAAAGT	5700
30	TTGATTGTAG AGTAGTTCCA TTGCTTGCAT ACCTCCAAGA CTTCCCCCTA TAAAAATATT	5760
	AATCTTATCA TAACCAAGGG CTTGTATACC TCGTTCATTC GCTCTGACTA TATCTCTTAA	5820
	TGTTAATTTT TTAGGAAAAT GAGGGTCGTT TAAAGTGAA CTTGAACCGA AAGGACTACC	5880
35	AATAACATCA AATGTTAAAA ATTGATAATC GTGAATGGGT ATATATCCCC CATCAATAAT	5940
	TTCTCGCCAC CAACCCGGAT AATCATCTGT TCCATATGTT AAATGATTGC CAGTTAATGC	6000
	ATGACAAACT ACAACTAATG GTTGTCCATG ATAACCGACA TGCTCATATC TCAAACGCAA	6060
40	GTAATCTATG ACTTCCCCAG ATTCTGTAAT AAATCCCCT AAATTTAAAG TATCTACTGT	6120
	GTAATTTGTC ATTGTTCTTT CCTCCTTAAA CAAAAAACT TCTCACCCTA TTGAAAAGTA	6180
	AGAAGTCTTT ATAATTATCA TTCGAGTAAC TCGTTGGTTT TAGCACCGTG CTATAAAGTC	6240
45	GGTTGCTGAA GTATCACAGG G	6261

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

	ATGCGATTAA CTCTGGAAAT ATCTTTTCCA TATTACGTh TTAAATTATT CAGCAAATTC	60
5	ATACGAGaTT CATACTCGTT yAACTTTGT TCGTCGAATT CTGTATTAGC CATTTCATCA	120
	TATAACTCAT GTTTTGCATC TTCTAAAATG TAGTAAAATT GATCAATATC TTCTTTTAAT	180
	TTGTCATATT TGTTTGGAAC TATATCGTTT ATTGTTAACA AATGGTTGCT TAGTTCATAT	240
10	AAACGATCAG TGATAGCATT TTCATCCGTT AATGTCATAT ATGCGTTATT AAGCGCTAAG	300
	CTTAATTTTT CAGAGTTTTG AATGCGTTTA ATATCTATTT CAAGTTGCTC TATTTGCGCT	360
	TCTTTTAGAT GTGCTTCAGA CAATTCTTCT AATTGGAATT TCATTAAATC TAAACGCTGT	420
15	AGCAATGCTT GGTCTGCTGA TTCTAAATCT TCTAACTCTT GCTTTTGGC TTTATAATTT	480
	TGAAAAGTTT GGTGATATTT ATCCAACAAA TCTTGATAAC GTGATTCTGC GTAATTATCC	540
20	AATAATGTTA AATGGTATTT TTGTTTCAAC AAAGACTGCG TTTTCATGTTG GCCATGAATA	600
	TCTAATAATT CTTGCATAAC TTTTCGTAAA TCTTGTAAG TAACTGTTTG ATTATTAATT	660
	TTACAAAGAC TTTTACCAGA GCTGAAAATT TCCCGTTTAA CTAATAAAAA ATCTTCATCT	720
25	ACATCAATAT CCATATTTTT CAATATATGT ATAGCATCTT TACTCTCGTC AATATCAAAT	780
	ATACCTTCGA TGACAGCCTT TTTTTCACCA TGTCTTACAA AATCAGATGA AGCTCTCATT	840
	CCAATTAATT GTCCAATTGC ATCTATAATA ATTGACTTAC CTGAACCCGT TTCACCACTT	900
30	AAAACAGTTA AACCATCAGA AAATTGAATT TCTAATTCTT CAATAATAGC AAATTGCTTG	960
	ATTGATAAGG TTTGTAACAT AAATCATCG CATCCTTATA ACAAATTGAA AATTCTTGAC	1020
35	TTGATTTTCA CACTTGCCCTC TTTGCTTCGA CAAATAATTA AACAAGTATC ATCACCACAA	1080
	ATTGTGCCTA GTAATTCTTC CCAATTGATT TGGTCTAATA TAGCTCCAAT AGATTGTGCA	1140
	TTAC E AGGTA TGTTTTTAGA ACAAGTAAAT TATCAGTACC ATCTATATTA ACAAAGGAAT	1200
40	CCATTAAATA ACGTCCCAAT TT	1222

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TTTGTTATTA TTACnTnAAA TAATTGCATT ACTTTTACT GATGGTACAA CTTTCCATCC	60
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TTCTTTTGGC ACGACATAAT TGTCTTTATC TTGAACTAAA TATCCGCCAG ATACTGAAAC 180
 AAACCTCTTCT TCGTTACTGT CTATAGTCAT ATCAATTCTT AATAATCTTA CATTCTTCTT 240
 5 TTGTTTTAAA ATATCTAATG CTTCATCTGT AAATTTTGGT GCAATAATGA CTTCCAAAAA 300
 GATACTATGC AATTGCTCTG CTAACCTCAGG TGTACAGCT CGGTTTAATG CAACAATTCC 360
 10 ACCAAATATT GATTGACTAT CCGCTTCATA CGCATGTTGA AATGCTTGTT CTATCGTGTC 420
 ACCGATACCA ACACCACATG GATTCATGTG TTTAACCGCA ACTGTAGCAG GTGTATCAAA 480
 CTTTTTAACT AAAGCTAGTG TAGCATCTGC ATCTTTAATA TTGTTATAGC TTAATTGTTT 540
 15 CCCATGTAAT TGTTTAGCGC CTGCAATCGT GTGCTTAGCA TTCGAAGTTC TCACAAAATA 600
 CGCTGATTGT TGTGGATTTT CTCCATATCT TAAAGTTTCT TTATCCCCTT TAAAGAAACG 660
 TACAATCGCT TCATCATATT CTGCAGTATG CTCAAAACT TTAATCATT AATGATTGTCT 720
 20 ATATGACTCA TCTAACGAAT CGTTTCTTAA TCGCGTCAAT ACTTCTTGAT AATCTGCCGG 780
 ATGTACAATT GTTGTTACAT GTTTATAGTT TTTAGCTGCA GCACGTAACA TTGTTGGACC 840
 ACCAATATCA ATATTTTCAA TTGCTTCGTC CATCGTCACA TCAGGGTTTG CAACAGTTTG 900
 25 TTGGAATGGA TATAAATTAA CTACTACCAT ATCAATTAAA TCTATATGTT GTTCTGATAA 960
 TTCATTAAAA TGCTGCGGTT TATTTGATC AGCTAAAATG CCACCATGAA CAGCCGGATG 1020
 T 1021

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3759 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TCATTCACTC CTAAATTGTT ATTACACTAT TACACaTAGC TAATCATCAA TGTGAAATCA 60
 CCTTCAAAGA CACTATCCAA ATCTTCAGAA GTCAAAATAA AGTTTGTAAC AGTAGTCAGT 120
 45 TTGAAAATTT CACCATCGAC AATCATTTGC CCTTCGCCTT CCAACACTGT AACTAAACAG 180
 AACTCTCTAG GCTTCATATA ATTTAACGTG CCAGAAATTT CCCATTTAAC CAATGTAAAG 240
 50 AAATCATTCG ATACAATGTG TGTACACTTA TGGTTTTCAA TAATTTTCGCT TTCAGGCAAA 300
 ATATTAGGTA ATGGTGCATT GTACTGAATA ACGTCTAAAG CTTTTTCAAT ATTTAACGGT 360
 CTATCATTAT ATTGATTATC TTGACGATTG AAATCATAAA GTCTATATGT AATGTCTGAC 420

	ATAAAAtAGa	ATTcYCCAGG	KTTTACTTTA	AtatATCyAA	gTAtCGaCtC	tATCGTTCCG	540
	TGTTGAACAT	GATTGCAAC	TTCTTCTCTA	GACTCTGCTA	ATGTCCCTAT	AACTATTTCT	600
5	GCATCTTCTT	CTGCATCTAT	AATATACCAA	CATTGAGATT	TGCCATATTG	CCCgTTTTCA	660
	TGCTCATAAG	CATAAGAATT	ATCAGGGTGC	ACATGAATAG	AAAGTGATTG	TCTTGCAATC	720
	ACTATTTTAG	TTAGAAGCGG	AAAATCTTTG	CTTGGGAAAT	CACCAAACAA	TTCACGATGT	780
10	TCTGACCAAA	TACGGTCTAA	TGTTTGACCT	TGATATGGTC	CATTAATAAT	CTCGCTCGTA	840
	CCATTGGGAT	GTGCTGACAC	ACACCAACAT	TCCCCAGTT	GTATCATTGT	CTAATTGATA	900
15	TCCAAACTCA	CTTAGACGTT	GACCGCCCCA	TAATTTTGTT	TTTAAAATTG	GTTGTAAAAA	960
	TAATGGCATT	GTTGCACCTC	CATTGTGATT	AAGTAAGCAA	TAGAAGCTCTG	ATGTTGTTGT	1020
	TCCATTATAT	TTTGATTTTG	TTCTCATTTA	CATCGTATTA	TTAACTTCCA	CATTTCAAAT	1080
20	TAAGTATTAG	TGATTGTACC	ATATTTACTA	ACATTGCACT	ACTGCCAATT	AAAAGnGCTT	1140
	CACTTAAATT	TACAGTACTT	TAACATTTTC	AAAAATTTAT	AGCATAGAGA	TTATATCTCT	1200
	CTTACATTTG	TACATATTTT	CCTTTAAATT	TACTCGCCCA	TTATACCAAT	TAATAaACAA	1260
25	CTTTAATAGT	TGTGCCATAC	ATTGTTCAAA	TTCTTTGTAA	AACGCATAGA	CAATACGTAC	1320
	TTAFTCATAC	TTATAATTCA	TCATTTTCAA	AAAATAACGA	GTTACGAAAA	AGTAACCCGC	1380
	TTCAAATCAT	ATTTACTATC	CTTATTAATC	CGTTTCATTT	TCAAATTGAG	TTAAAGCATC	1440
30	TTTAATGTCC	TGATCACCAC	TAATAATTTG	AAACTCTTGG	TGATTAAAAT	GATTGGATGT	1500
	GACAATTTCT	TTTAATACTG	TCGCAACATC	TTCTCTAGGA	ATTTACCTT	TACCATCAAA	1560
35	ATATTGTGCA	GCTTCTATCT	TTCCAGATCC	TGCTGCATTT	GTAAGTGCCC	CTGGATGTAA	1620
	AATTGTATAA	TTCAAACCTG	AAACGTCTTA	AATAGTCATC	AGCGTAATGT	TTAGCTATTG	1680
	TATATGGCTT	TAAATCACCG	CTATCATCAA	AAGCCTGACG	TCTCGAATCA	TATGTTGAAA	1740
40	CCATGACATA	GTGTTTAATA	TTGGCCTCTT	TACTCGCAAT	CATTGATTTA	ACAGCACCAT	1800
	CTAAATCGAC	AATAATTGTT	TTATCTGCAC	CCGTGTTCCC	TCCAGAACCT	ACTGAAAAGA	1860
	TAACTTTATC	GAATGGTTTA	AACGTCTCAG	TTAAAGTCTC	TATTGAATCA	TTTTCAACAT	1920
45	CAACAAGAAT	TGCTTTTATA	CCTTGTGATT	TTAACGCATT	AAGTTGATCT	GATTGCCTAA	1980
	CACCAGCAGT	AAATGGTACA	TTTTCTTTTG	CTAATTGTTG	CACTAGTAAC	GAACCTACAC	2040
	CGCCATTAGC	ACCTATAACC	AAAATATTCA	TTTACAACAC	TCTCCTATkT	ATTATTCTCT	2100
50	ATGCCATACC	ACTTTATGAG	ATATGTAAAA	CTTGTTACAA	CTATAAAAAT	CAATTGACAT	2160
	ACTACTGGGA	ACGTATTAAA	TTAATATATG	AACAAATATT	CATATGAAAG	GATTGTCATA	2220

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	tCaAGGCATT AGcGATTACA ATCGAATACG TATCaTGGAA TTGTTATCaG TCAGCGAAgC	2340
	AAGTGTGGT CACATTtCAC ATCAATTGAA TTTATCTCAA TCAAATGTCT CGCACCAATT	2400
5	AAAATTACTT AAAAGTGTGC ATCTTGTGAA AGCAAAACGA CAAGGCCAAT CAATGATTTA	2460
	TTCATTAGAT GACATCCACG TAGCAACTAT GTTAAAGCAA GCCATACATC ACGCGAATCA	2520
10	TCCTAAAGAA AGTGGGTTAT AATATGTCTC ATTACATCA TCATCATGAC CATATGCATA	2580
	GTCATGTAAC TACAAATAAT AAGAAAGTAT TGTTTATATC GTTTTAAATA ATCGGTCTAT	2640
	ATATGTTTAT CGAAATCATC GCGGTCTCC TTGCTAACAG CTTGGCATTa CTATCTGACG	2700
15	GTATCCATAT GTTTAGCGAC ACATTCTCAT TAGGTGTTGC ACTTGTCGCA TTTATTTATG	2760
	CTGAAAAGAA TGCCACAACt ACAAAAACAT TTGGTTATAA ACGTTTCGAA GTACTCGCAG	2820
	CGTTATTTAA CGGTGTAACG CTTTTTGTAa TAAGTATTTT GATTGTTTTT GAAGCGATTA	2880
20	AACGTTTCTT TGTTCTTCTT GAAGTTCAAT CAAAAGAAAT GTTAATCATT AGTATTATCG	2940
	GTTTAATTGT CAATATCGTT GTTGCAATTCT TTATGTTTAA AGGCGGCGAC ACTTCACACA	3000
	ATTTAAATAT GCGTGGTGCT TTTCTACATG TTATCGGAGA CTTATTAGGT TCAGTTGGCG	3060
25	CCATTACTGC AGCTAKTTTA ATTTGGGCAT TTGGATGGAC AATCGCCGAT CCTATCGCAA	3120
	GTATTTTAGT TTCCGTTATT ATTTTAAAAA GTGCTTGGGG TATCACAAAA TCTTCAATTA	3180
	ACATTTTAAT GGaAGGCACA CCAAGTGATG TTGATATAGA TGAAGTTATA ACTACTATTA	3240
30	AAAAGGATTC ACGAATACAA AGTGTGCATG ATTGCCATGT TTGGACAATT TCAAATGATA	3300
	TGAATGCATT GAGTTGTCAAT GTTGTGTAG ACCATACATT GACAATGAAA GAATGTGAAT	3360
35	TATTATTAGA AAaCATTGAG CATGATTTAT TACATTTAAA TATTCACCAT ATGACTATTC	3420
	AATTAGAAAC GCCTAATCAC AAACATGATG AATCGATTAT ATGTTcAGGA ACACATAGTC	3480
	ATTcACATAA CCATCATGCT CATCATCACG CGCATGTACA TTAATAATTT TAACCTACTG	3540
40	CCATTGCATC GATTAAACTT TTCAATGGCA GTAGGTTTTT TATGTCTTTA TGGCGACTTG	3600
	TTTGGTCTTT GATGATGCAA TGTTTATTAA CAAATTTTCA ACTATTATTT CTTACATTAG	3660
	TCATATTTTt GACAATTTAC TATTATAATT CTCTAACTTT AGTCACTTTA ATTAATTTT	3720
45	ATTAGATATT AATATGAAAA TAACGTGTTT TTTGTTATT	3759

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13086 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

	TAATTATCGC GCATAACAAA ACATTAGCAG GACAATTATA TAGTGAGTTT AAAGAATTTT	60
5	TTCCTGAAAA CAGGGTGGAA TACTTTGTAA GTtACTATGA TTATTATCAn CCAGAGGCAT	120
	ACGTACCGTC TACTGACACT TTTATTGAAA nAGATGCCTC AATCAnTGAT GAAATTGATC	180
10	AACTACGACA TTCTGCTACA AGTGCATTAT TTGAACGCGA TGATGTAATT ATTATTGCTA	240
	GTGTAAGTTG TATATATGGT TTAGGTAATC CTGAAGAATA TAAAGATTTA GTAGTAAGTG	300
	TTCGAGTTGG TATGGAAATG GATAGAAGTG AATTACTTAG AAAACTTGTc AGATGTGCAA	360
15	TATACACGAA ATGACATCgA TTTcCAACGA GGAACGTTTC GAGTGCCTGG TGATGTAGTG	420
	GAAATATTCC CAGCCTCTAA AGAAGAACTT TGTATAAGGG TTGAGTTTTT CGGCGATGAG	480
	ATTGACCGTA TCCGAGAAGT TAACTACCTA ACAGGTGAAG TGTGAAAGA AAGAGAACAT	540
20	TTTGGGATAT TCCCAGCTTC TCACTTCGTA ACACGTGAAG AAAAGTTGAA AGTTCCGATT	600
	GAACGTATTG AAAAAGAATT GGAAGAACGA TTGAAAGAAT TACGAGATGA GAATAAATTA	660
	CTAGAAGCGC AAAGGTTAGA ACAGCGTACC AACTATGATT TAGAAATGAT GCGAGAGATG	720
25	GGATTCTGTT CAGGAATTGA AAACATTCC GTACATTAA CTTTGGCACC ACTGGGTTTCG	780
	ACACCATATA CTTTATTGGA TTACTTTGGC GATGATTGGT TAGTAATGAT TGATGAATCA	840
	CATGTGACAT TACCGCAAGT TCGAGGCATG TATAACGGAG ACAGAGCGCG TAAACAAGTT	900
30	TTGGTGGATC ATGGGTTTAG ATTACCGAGT GCATTAGATA ACCGTCCACT TAAATTTGAA	960
	GAATTTGAAG mAAAGACAAA ACAACTTGTG TATGTATCTG CAACGCCTGG ACCATACGAA	1020
35	ATTGAACATA CGGATAAGAT GGTGGAACAA ATTATTCGTC CTACTGGTTT ACTGGATCCT	1080
	AAGATTGAGG TTAGACCTAC TGAAAATCAA ATTGACGATT TATTAAGTGA AATTCAAACA	1140
	AGAGTgAGCG TAATGAACGC GTACTTGTTA CAACGCTCAC TAAAAAGATG AGTGAAGATT	1200
40	aACCACATAC ATGAAAGaG CGGGTATTAA aGTtAATTAT CTGCATTGAG AAATCAAGAC	1260
	ATTAGAACGA ATTGAAATAA TTAGAGACTT ACGAATGGGT ACATATGATG TTATCGTAGG	1320
	TATTAATTTA TTAAGAGAGG GTATTGATAT ACCAGAAGTT TCTCTAGTTG TCATATTAGA	1380
45	TGCAGATAAA GAAGGGTTTT TACGTTCTAA CCGCTCATTa ATTCAAaCAA TAGGTAGAgC	1440
	TGCGCGTAAC GATAAaGGTG AAGTCATTAT GTATGCCGAT AAAATGACTG ATTCCGATGAA	1500
	GTATGCAATT GATGAGACAC AACGTCGTCG AGAAATACAG ATGAAACATA ATGAAAAACA	1560
50	TGGTATTACA CCTAAAACAA TTAATAAAAA AATACATGAT TTAATTAGTG CTACTGTTGA	1620
55	AAATGACGAA AATAATGACA AAGCACAAAC TGTGATACCT AAGAAGATGA CGAAAAAGA	1680

	TTTCGAGAAA GCTACAGAAT TAAGAGATAT GTTATTTGAA TTAAAAGCAG AAGGGTGACA	1800
	AGTAAATGAA AGAACCATCC ATAGTAGTAA AAGGTGCTCG TGCGCATAAC TTGAAAGATA	1860
5	TTGATATCGA ACTACCTAAA AaTAAATTAA TTGTTATGAC AGGTTTATCT GGGTCAGGTA	1920
	AATCGTCATT AGCATTTCGAT ACTATATATG CTGAAGGACA ACGACGTTAT GTTGAATCAT	1980
	TAAGTGCCTA TGCGCGTCAA TTTTITAGGCC AAATGGACAA ACCAGATGTT GATACAATTG	2040
10	AAGGATTATC GCCAGCAATT TCAATAGATC AAAAAACAAC AAGTAAAAAT CCAAGATCAA	2100
	CTGTAGCAAC AGTAACAGAA ATATATGATT ATATACGTTT GTTATATGCA CGTGTGGTA	2160
	AACCTTACTG TCCAAATCAC AATATAGAAA TTGAATCGCA AACAGTACAA CAAATGGTTG	2220
15	ACCGCATTAT GGAATTAGAG GCACGTACAA AGATTCAATT ATTAGCACCT GTCATCGCTC	2280
	ATCGTAAAGG TAGTCATGAA AAGCTAATCG AAGATATTGG TAAAAAAGGT TATGTACGTT	2340
20	TAAGAATCGA TGGCGAAATT GTTGATGTAA ATGATGTACC TACTTTAGAT AAGAACAAGA	2400
	ATCATACAAT AGAAGTTGTT GTAGACCGAT TAGTTGTTAA AGATGGAATT GAAACACGAC	2460
	TAGCTGACTC TATAGAAACT GCCTTAGAGC TTTCAGAAGG ACAATTAACA GTCGATGTCA	2520
25	TTGACGGGGA AGACCTTAAG TTTTCAGAAA GCCATGCTTG TCCTATATGT GGATTTTCAA	2580
	TCGGAGAGTT AGAACCAAGA ATGTTTAGCT TTAACAGTCC TTTTGGTGCT TGTCCGACAT	2640
	GTGATGGCTT AGGCCAAAAG TTAACAGTCG ATGTAGACTT GGTGTGTTCC GACAAAGATA	2700
30	AGACGCTAAA CGAAGGTGCA ATAGAACCTT GGATACCGAC GAGTTCTGAT TTTTATCCAA	2760
	CATTGTTAAA ACGTGTGTTGT GAAGTTTATA AAATCAATAT GGATAAACCT TTTAAAAAGT	2820
	TAACAGAACG TCAACGTGAT ATTTTATTGT ATGGTTCTGG TGACAAAGAA ATTGAATTTA	2880
35	CATTTACACA ACGTCAAGGT GGTACTAGAA AACGAACAAT GGTTTTCGAG GGTGTAGTTC	2940
	CTAAATATAAG TAGACGATTC CATGAATCTC CTTCAGAATA TACACGTGAA ATGATGAGTA	3000
	AATATATGAC TGAACCTACCT TGCGAAACTT GTCATGGAAA GCGATTGAGT CGTGAAGCKT	3060
40	TATCTGTTTA TGTAGGTGGT TTAAATATTG GTGAAGTAGT CGAATATTCA ATCAGTCAAG	3120
	CGCTGAACTA TTATAAAAAC ATTGATTTGT CAGAACAAGA TCAAGCGATT GCAAATCAAA	3180
45	TATTGAAAGA AATTATTTCC CGACTCACTT TTTTAAATAA TGTGGGACTT GAATATTTAA	3240
	CGTTAAACAG AGCTTCAGGT AACTTTTCAG GTGGTGAAGC ACAACGTATT CGATTAGCAA	3300
	CGCAAATTGG GTCGCGTTTG ACTGGTGTCT TATATGTATT AGATGAGCCA TCAATTGGAC	3360
50	TGCATCAAAG AGATAATGAT CGATTAATTA ATACACTTAA AGAAATGAGA GATTTAGGAA	3420
	ATACTTTAAT TGTAGTTGAA CACGATGATG ATACAATGCG TGCGGCTGAT TACTTAGTGG	3480

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	AGGTAATGAA	AGATAAAAAA	TCATTAACAG	GACAATACTT	GAGTGGTAAG	AAACGTATTG	3600
	AAGTACCTGA	ATATCGCAGA	CCGGCTTCAG	ATCGTAAAAT	TTCTATACGT	GGAGCTAGAA	3660
5	GCAACAATCT	TAAAGGGGTT	GATGTGGACA	TACCACTATC	AATCATGACG	GTTGTTACAG	3720
	GTGTATCAGG	TTCTGGTAAA	AGCTCATTAG	TAAATGAAGT	ATTATACAAA	TCATTAGCTC	3780
	AAAAAATTAA	TAAATCTAAA	GTAAAGCCAG	GATTGTACGA	TAAGATTGAA	GGTATTGATC	3840
10	AACCTGATAA	AATTATTGAT	ATTGATCAAT	CACCAATAGG	TAGAACGCCA	CGCTCTAATC	3900
	CAGCAACATA	TACTGGTGTG	TTTGATGATA	TACGTGATGT	GTTTGCGCAA	ACAAATGAAG	3960
	CTAAAATTCG	AGGATATCAA	AAAGGGCGTT	TTAGTTTAA	TGTAAAAGGT	GGACGCTGTG	4020
15	AAGcTTGTAA	AGGTGACGGT	ATTATTAAAA	TTGAAATGCA	TTTTTTACCT	GATGTTTATG	4080
	TTCCTTGTGA	AGTGTGTGAT	GGTAAACGAT	ATAATCGTGA	GACACTAGAG	GTTACTTACA	4140
20	AAGGTAAAAA	TATTGCTGAC	ATTTTAGAAA	TGACTGTTGA	AGAAGCAACA	CAATTTTTTG	4200
	AAAATATTCC	TAAGATTAAG	CGCAAGTTAC	AAACACTAGT	TGATGTTGGT	CTTGGATACG	4260
	TCACATTAGG	TCAACAAGCT	ACAACGTTAT	CAGGTGGTGA	GGCTCAACGT	GTGAaACTTG	4320
25	CATCTGAACT	TCATAAACGT	TCAACTGGTA	AATCTATTTA	TATCCTAGAT	GAACCGACAA	4380
	CAGGGTTACA	TGTTGACGAT	ATTAGTAGAT	TATTAAAAGT	ATTAAACCGA	TTAGTTGAAA	4440
	ATGGTGATAC	TGTTGTAATT	ATTGAACATA	ACCTAGATGT	TATCAAAACA	GCAGACTATA	4500
30	TTATAGACTT	AGGTCCTGAA	GGTGGTAGTG	GCGGTGGTAC	TATTGTTGCG	ACTGGCACAC	4560
	CCGAAGATAT	TGCTCAGACA	AAGTCATCAT	ATACAGGAAA	GTATTTAAAA	GAAGTACTTG	4620
	AACGAGATAA	ACAAAATACT	GAAGATAAAT	AAGATTAAAA	GAAGTGAAGG	ATGTTATAAA	4680
35	TTTATCCTTC	GCTTCCTTTT	ATTAATTTAG	TAATGAATAG	TAGAAAGAAA	AGATGCGTAA	4740
	AAAGaATTAT	GTTAAGATAG	GGTCAATCTA	GAGTAGTTAA	ACATAAATCG	AACTGGGAGT	4800
	GGGACAGAAA	TGATAAAGAA	TCACTAATGA	TTTATTATGT	AGTGGTTCTT	TGTCATTAGC	4860
40	CACAGCTATT	GTGTACTTAA	AAATAGGa	GCATgAGTGC	AACTCATGCA	TAAGaAATAC	4920
	TAATTTCTAA	AGAAAAAGTA	TTTCTTTATG	TTGGGGCCCC	GCCAACTTGC	ATTGTTTGTA	4980
45	GAATTTCTTT	TCGAAATTCT	TTATGTTGGG	GCCCCGCCAA	CTTGCATTGT	TTGTAGAATT	5040
	TCTTTTCGAA	ATTCTTTATG	TTGGGGCCCC	GCCAACTAAT	TCCAATATAT	CATTGTAGAG	5100
	CTTAGGTCAT	TGATTTTTTG	CTCGGACTTT	TATGGCGATA	TGAACCATGT	AAATTAAGCA	5160
50	AGCAATAAAT	TAATGATTGA	TATTGACTTG	TAAAATAATA	ACAATAATGA	ACAATTAATA	5220
	TTTATTTTAG	CTTTTCAATG	TAGATTGGTG	TTATATTTTT	GATATGATAA	GAAGAGATGT	5280

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	ACATTAAAGT TAGATTTAAT CGCTGGTGAA GAAGGACTAT CGAAGCCAAT TAAAAATGCT	5400
	GATATATCAA GACCGGGCTT AGAGATGGCA GGTTATTTT CACATTATGC GTCAGATAGA	5460
5	ATACAACTAT TAGGAACAAC GGAAGTATCG TTTTACAATT TATTACCAGA TAAGGATCGC	5520
	GCAGGTCGTA TCGGTAAACT ATGCAGACCA GAAACGCCTG CAATTATTGT GACACGTGGA	5580
	TTGCAGCCAC CAGAAGAATT AGTTGAAGCT GCAAAAGAAT TAAATACCCC ACTTATAGTT	5640
10	GCTAAAGATG CACTACAAG TTTAATGAGT CGCTTAACAA CGTTTTTAGA GCATGCACTT	5700
	GCAAAGACGA CATCTTTACA TGGTGTTTTA GTAGATGTTT ACGGTGTTGG TGTACTAATT	5760
	ACCGGTGATT CAGGAATAGG TAAAAGTGAG ACTGCGTTGG AATTAGTTAA ACGTGGGCAT	5820
15	AGATTAGTAG CAGATGATAA TG TAGAAATA CGTCAAATTA ATAAAGATGA ACTAATAGGG	5880
	AAACCACCAA AGTTAATAGA ACATCTATTA GAAATACGTG GACTAGGTAT TATCAATGTT	5940
20	ATGACTTTAT TTGGCGCGGG TTCAATATTA ACTGAAAAAC GAATTAGATT AAATATTAAT	6000
	TTGGAAGAACT GGAACAAGCA AAAGTTATAT GACCGCGTAG GTCTTAATGA AGAGACGCTA	6060
	AGTATTTTAG ATACTGAAAT CACTAAAAAA ACAATACCTG TAAGACCTGG TAGAAATGTT	6120
25	GCGGTAATTA TTGAGGTGCG TGCAATGAAC TATCGATTAA ATATCATGGG CATTAACACG	6180
	GCCGAAGAAT TTAGTGAAAG ATTAAATGAA GAAATTATCA AGAACAGTCA TAAGAGTGAG	6240
	GAGTAGGTTG AATGGGTATT GTATTTAACT ATATAGATCC TGTGGCATT TAACTTAGGAC	6300
30	CACTGAGTGT ACGATGGTAT GGAATTATCA TTGCTGTCGG AATATTACTT GGTTACTTTG	6360
	TTGCACAACG TGCACTAGTT AAAGCAGGAT TACATAAAGA TACTTTAGTA GATATTATTT	6420
	TTTATAGTGC ACTATTTGGA TTTATCGCGG CACGAATCTA TTTTGTGATT TTCCAATGGC	6480
35	CATATTACGC GGAAAATCCA AGTGAAATTA TTAAAATATG GCATGGTGGA ATAGCAATAC	6540
	ATGGTGGTTT AATAGGTGGC TTTATTGCTG GTGTTATTGT ATGTAAAGTG AAAAATTTAA	6600
	ACCCATTTCA AATTGGTGAT ATCGTTGCGC CAAGTATAAT TTTAGCGCAA GGAATTGGAC	6660
40	GCTGGGGTAA CTTTATGAAT CACGAGGCAC ATGGTGGATC GGTGTCACGC GCTTTTTTAG	6720
	AACAATTACA TTGCCTAAT TTTATAATAG AAAATATGTA TATTAACGGC CAATATTATC	6780
45	ATCCAACATT CTTATATGAA TCCATTTGGG ATGTCGCTGG ATTTATTATC TTAGTTAATA	6840
	TTCGTAAACA TTTAAAATTA GGAGAAACAT TCTTTTATA TTTAACTTGG TATTCAATTG	6900
	GTCGATTCTT TATAGAAGGA TTACGTACAG ATAGCTTAAT GCTCACAAGT AATATTAGAG	6960
50	TTGCACAATT AGTATCAATT CTTTTAATTT TAATAAGTAT AAGTTTAATT GTATATAGAA	7020
	GGATTAAGTA TAATCCACCG TTGTATAGCA AAGTTGGGGC GCTTCCATGG CCAACAAAAA	7080

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	TTATGGCGTG TATACCGTCT TGTAAATTT TCGAAAGTTT TTAAGAATGT AATTATCATT	7200
	GAATTTTCGA AATTTATTCC AAGTATGGTA CTGAAAAGAC ATATATATAA ACAACTTTTA	7260
5	AATATTAATA TCGGTAATCA ATCGTCGATA GCTTATAAAG TAATGTTAGA TATTTTTTAC	7320
	CCAGAACTGA TTACGATTGG TAGTAACAGT GTTATTGGTT ACAATGTAAC AATTTTGACG	7380
	CATGAAGCAT TAGTTGATGA ATTTGTTAT GGACCAGTGA CGATAGGATC TAACACTTTG	7440
10	ATTGGTGCAA ATGCTACCAT TTTACCCGGT ATAACGATTG GTGACAATGT AAAAGTTGCA	7500
	GCTGGTACCG TTGTTTCAA AGATATACCG GATAATGGAT TTGCATATGG CAACCCTATG	7560
	TATATAAAAA TGATTAGGAG GTGACAATTT TATGGCGCAA AAGAATAATA ATGTAATTCC	7620
15	AATGACTTTT GATGATGCAT TTTATCGTAA AATGGCTAAA CAGAAGTTTA AACAAAGAGA	7680
	ATATAAACGA GCTGCTGAAT ACTTTGAAAA AGTGTTAGAA TTGTCACCTG ATGATCTGGA	7740
20	AATTCAAATT GATTATGCAC AATGTCTAGT GCAACTTGGT ATTGCTAAAA AAGCAGAACA	7800
	TTTATTTTAT GACAATATTA TTTATAATAG GCATCTAGAA GATAGCTTTT ATGAATTGAG	7860
	TCAGCTCAAC ATTGAAGTTA ACGAACCAAA CAAGGCATTG TTGTTTGGTA TTAATTATGT	7920
25	TATTGTTAGC GACGACCAAG ATTATAGAGA TGAATTAGAT CAAATGTTTG ATGTGAAATA	7980
	TCAAAGTGAA GAACAAATTG AACTTGAAGC TCAATTGTTT GTAGTTCAA TACTATTCCA	8040
	ATATCTTTTT TCTCAAGGTC GATTAAGAAG TGCAAAGAAT TATGTCTTAC ATCAACCACA	8100
30	AGAAGTTCAA GATCATCGTG TAGTACGTAA TTTATTGGCA ATGTGTTATT TATATCTCGG	8160
	TGAATATGAT ACgGCTAAAG CATTGTACGA aGCActATTA CAAGAGGATA GTACaGATAT	8220
	ATATGCATTA TGCCATTATA CTTTGCTACT TTATAACACT AAGGAAAATG AACAATATCA	8280
35	AAAATATTTA AAAATATTAA ACAAAGTTGT ACCTATGAAT GACGATGAAA GTTTTAAATT	8340
	AGGTATTGTA TTAAGTTATT TAAAGCAGTA TCGTGCATCA CAACAATTGT TGTACCCTTT	8400
	ATATAAAAAA GGGAAATTTT TATCAATTCA AATGTACAAT GCTTTAGCAT ATAATTATTA	8460
40	TTATTTAGGT GAAGAAGACG AAAGTCATTA CTACTGGGAT AAATTGAAGC AAATTTCTAA	8520
	AGTGGAAATT GGACATGCGC CTTGGGTAAT TGAAAATAGC AAAGAAGTTT TTGACCAACA	8580
45	TATTTTGCCA TTAATTCAA GTGATGACAG TCATTATCGT TTATATGGTA TTTTTTTATT	8640
	GGATCAATTA AATGGTAAAG AAATTGTGAT GACGGAAAGT ATTTGGCAGG TTTTGAAAAA	8700
	TCTAAATAAT TATGAGAAAT TGTATTTAAC GTATTTAGTT CAAGGTTTAA CGCTCAATAA	8760
50	ATTAGACTTC ATTCATCGCG GCTTATTAAC GCTTTACCAT AATGAATTAT TTGTAAGTGA	8820
	AAATGATGTA ATGGTTGCAT GGATTAATCA AGGTGAACTC ATAATTGCTG AAAAAGTAGA	8880

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	TCGAAACGTT ACAAAGAAGC AAATTACAAC ATGGTTAGGC ATAACACAAT ATAAACTGAA	9000
	CAAAATGATT GAATTTCTCT TGAGCATATA GATTATGAA AAGTTAGATT TATTATATAA	9060
5	TGCGCATAAT GATTAATAAT GAGGAGGCGT TAATAAAATG ACTGAAATAG ATTTTGATAT	9120
	AGCAATTATC GGTGCAGGTC CAGCTGGTAT GACTGCTGCA GTATACGCAT CACGTGCTAA	9180
	TTTAAAAACA GTTATGATTG AAAGAGGTAT TCCAGGCGGT CAAATGGCTA ATACAGAAGA	9240
10	AGTAGAGAAC TTCCCTGGTT TCGAAATGAT TACAGGTCCA GATTATCTA CAAAAATGTT	9300
	TGAACACGCT AAAAAGTTTG GTGCAGTTTA TCAATATGGA GATATTAAAT CTGTAGAAGA	9360
	TAAAGGCGAA TATAAAGTGA TTAACCTTGG TAATAAAGAA TTAACAGCGA AAGCGGTTAT	9420
15	TATTGCTACA GGTGCAGAAT ACAAGAAAAT TGGTGTTCG GGTGAACAAG AACTTGGTGG	9480
	ACGCGGTGTA AGTTATTGTG CAGTATGTGA TGGTGCATTC TTTAAAAATA AACGCCTATT	9540
20	CGTTATCGGT GGTGGTGATT CAGCAGTAGA AGAGGGAACA TTCTTAACTA AATTTGCTGA	9600
	CAAAGTAACA ATCGTTCACC GTCGTGATGA GTTACGTGCA CAGCGTATTT TACAAGATAG	9660
	AGCATTCAAA AATGATAAAA TCGACTTTAT TTGGAGTCAT ACTTTGAAAT CAATTAATGA	9720
25	AAAAGACGGC AAAGTGGGTT CTGTGACATT AACGTCTACA AAAGATGGTT CAGAAGAAAC	9780
	ACACGAGGCT GATGGTGTAT TCATCTATAT TGGTATGAAA CCATTAACAG CGCCATTTAA	9840
	AGACTTAGGT ATTACAAATG ATGTTGGTTA TATTGTAACA AAAGATGATA TGACAACATC	9900
30	AGTACCAGGT ATTTTTCAG CAGGAGATGT TCGCGACAAA GGTTTACGCC AAATTGTCAC	9960
	TGCTACTGGC GATGGTAGTA TTGCAGCGCA AAGTGCAGCG GAATATATTG AACATTTAAA	10020
	CGATCAAGCT TAATTCGAAG TCGAATTAAG ATGTTGAGCT GTAAATTATT TGGATATTTA	10080
35	TTTTAATAGT GTCATCACAG CGTTAAATA ATGTCTTACT TTTAAATTAA AGCAAATTAT	10140
	ATAGAAAAC AGAAGTTAGT ACGTATCATT TGTGCGTTTC AATGAGTTCT AGTTTTTTTA	10200
	TATGTTATAT TAACTTATA ACTTTATGGG AGTGGGACAG AAATGATAAA GAGCCACTAA	10260
40	TGATTTATTA TGTAGTGGTT CTTAAACATT AGCCACAGCT AATGTGTACT TAAAAATAGG	10320
	AATACATGAG TAAACTCAT GCATAAGAAA TACTAATTTT TATAGAAAAA GTATTACTTT	10380
45	ATCGTTGTCC CACCCCAACT TGCACATTAT TGTAAGCTGA CTTCCGCCA GCTTCTGTGT	10440
	TGGGGCCCCG CCAACTTGCA CATTATTGTA AGCTGACTTT TCGTCAGCTT CTGTGTTGGG	10500
	GCCCCGCCAA CTGTCACATT ATTGTAAGCT GACTTTTCGT CAGCTTCTGT GTTGGGGCCC	10560
50	CGCCAACTTG CATTGTCTGT AGAAATTGGG AATCCAATTT CTCTATGTTG GGGCCACAC	10620
	CCCAACTCGC ATTGCCTGTA GAATTTCTTT TCGAAATTCT CTGTGTTGGG GCCCACACCC	10680

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	ACTCGCATTG CCTGTAGAAT TTCTTTTCGA AATTCTCTGT GTTGGGGCCC CTGACTAGAG	10800
	TTGAAAAAAG CTGTTGCAA GCGCATTTTC ATTCAGTCAA CTACTAGCAA TATAATATTA	10860
5	TAGACCCTAG GACATTGATT TATGTCCCAA GCTCCTTTTA AATGATGTAT ATTTTATAGAA	10920
	ATTTAATCTA GACATAGTTG GAAATAAATA TAAACATCG TTGCTTAATT TTGTCATAGA	10980
	ACATTTAAAT TAACATCATG AAATTCGTTT TGGCGGTGAA AAAATAATGG ATAATAATGA	11040
10	AAAAGAAAAA AGTAAAAGTG AACTATTAGT TGTAACAGGT TTATCTGGCG CAGGTAAATC	11100
	TTTGTTTATT CAATGTTTAG AAGACATGGG ATATTTTGT GTAGATAATC TACCACCAGT	11160
	GTTATTGCCT AAATTTGTAG AGTTGATGGA ACAAGGAAAT CCATCCTTAA GAAAAGTGGC	11220
15	AATTGCAATT GATTTAAGAG GTAAGGAACT ATTTAATTCA TTAGTTGCAG TAGTGGATAA	11280
	AGTCAAAAGT GAAAGTGACG TCATCATTGA TGTATGTTT TTAGAAGCAA GTACTGAAAA	11340
20	ATTAATTTCA AGATATAAGG AAACGCGTCG TGCACATCCT TTGATGGAAC AAGGTAAAAG	11400
	ATCGTTAATC AATGCAATTA ATGATGAGCG AGAGCATTG TCTCAAATTA GAAGTATAGC	11460
	TAATTTTGT ATAGATACTA CAAAGTTATC ACCTAAAGAA TTAAGAAGAAC GCATTCGTCG	11520
25	ATACTATGAA GATGAAGAGT TTGAACTTT TACAATTAAT GTCACAAGTT TCGGTTTTAA	11580
	ACATGGGATT CAGATGGATG CAGATTTAGT ATTTGATGTA CGATTTTAC CAAATCCATA	11640
	TTATGTAGTA GATTTAAGAC CTTTAACAGG ATTAGATAAA GACGTTTATA ATTATGTTAT	11700
30	GAAATGGAAA GAGACGGAGA TTTTCTTTGA AAAATTAATC GATTTGTTAG ATTTTATGAT	11760
	ACCCGGGTAT AAAAAAGAAG GGAAATCTCA ATTAGTAATT GCCATCGGTT GTACGGGTGG	11820
	ACAACATCGA TCTGTAGCAT TAGCAGAACG ACTAGGTAAT TATCTAAATG AAGTATTTGA	11880
35	ATATAATGTT TATGTGCATC ATAGGGACGC ACATATTGAA AGTGGCGAGA AAAAATGAGA	11940
	CAAAFAAAAAG TTGTACTTAT CGGTGGTGGC ACTGGCTTAT CAGTTATGGC TAGGGGATTA	12000
	AGAGAATTCC CAATTGATAT TACGGCGATT GTAACAGTTG CTGATAATGG TGGGAGTACA	12060
40	GGGAAAATCa GAGATGAAAT GGATATACCA GCACCAGGAG ACATCAGAAA TGTGATTGCA	12120
	GCTTTAAGTG ATTCTGAGTC AGTTTTAAGC CAACTTTTTC AGTATCGCTT TGAAGAAAAT	12180
45	CAAATTAGCG GTCACCTATT AGGTAATTTA TTAATCGCAG GTATGACTAA TATTACGAAT	12240
	GATTTTCGGAC ATGCCATTAA AGCATTAAGT AAAATTTTAA ATATTAAAGG TAGAGTCATT	12300
	CCATCTACAA ATACAAGTG GCAATTAAAT GCTGTTATGG AAGATGGAGA AATTGTTTTT	12360
50	GGAGAAACAA ATATTCCTAA AAAACATAAA AAAATTGATC GTGTGTTTTT AGAACCTAAC	12420
	GATGTGCAAC CAATGGAAGA AGCAATCGAT GCTTTAAGGG AAGCAGATTT AATCGTTCTT	12480

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GCGTTAATTC ATTCTGATGC GCCTAAGCTA TATGTTTCTA ATGTGATGAC GCAACCTGGG 12600
 GAAACAGATG GTTATAGCGT GAAAGATyAT ATCGATGCGA TTCATAGACA AGCTGGACAA 12660
 5 CCGTTTATTG ATTATGTCAT TTGTAGTACA CAAACTTTCA ATGCTCAAGT TTTGAAAAAA 12720
 TATGAAGAAA AACATTCTAA ACCAGTTGAA GTTAATAAGG CTGAACTTGA AAAAGAAAGC 12780
 ATAAATGTAA AAACATCTTC AAATTTAGTT GAAATTTCTG AAAATCATT AGTAAGACAT 12840
 10 AATACTAAAG TGTATCGAC AATGATTTAT GACATAGCTT TAGAATTAAT TAGTACTATT 12900
 CCTTTCGTAC CAAGTGATAA ACGTAAATAA TATAGAACGT AATCATATTA TGATATGATA 12960
 ATAGAGCTGT GAAAAAATG AATATAGACA GTGGTTCTAA GGTGAATCAT GTTTTAAATA 13020
 15 AGAAAGGAAT GACTGTACGA TGAGCTTTGC ATCAGAAATG AAAATGAAT TAACTAGAAT 13080
 AGACGT 13086

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

30 CATTAGTCAT GAAAATAGCC GACAACTTCA TCTGTGAAAT CACCGGCCTT TTATTTTAGC 60
 TAACTTTATT TCTGATTTTA CGATTTTAAT TGATCATACA GAGAAAGTGA TCTTTTACA 120
 ATTTCTAAAA ACTCATGATC TATATTGGAC ATTTGATGAA AATAAGACAA AATGTTTTCT 180
 35 GTTAGCTTCT CTGTTTTGG GAATGAATCA TCTTCTTAA TCCAAATCGC TAATTCGCCT 240
 AATGGTGTTT TATCATCTTT AAATGTTTGT ATATATTCGT AAAAGCTCAT AGTATTCCTT 300
 CTCTCAATTT ACTTATATAA ATCCTACCAC GAAAGCTTTC AAGAAAACAC AATTAAATGT 360
 40 CTATTTAGTG AACTTTTTAA GGTGTGTCAC TCTTTTAATG TCTGCCAATT AGGTCAATTA 420
 ATCATCACAA TGTACAATTA ACTCTATTTT CAGTTCATAT ACTCACACAC CGTTTTTGAA 480
 45 CAACACATTA ACTTCTCATT TAGATAAAAC GCAAAAAGC CTGGACCAA TACAATAGAT 540
 GCCAGACTAA GAGTCTACTA TATAAATTTA TTTAGCGTAT GGTTTACTT CGATTGCACC 600
 TTCATTTTCA TCATGAACAC CATGCTTATA ATAATCAATA TATTGTGGCT CTAAAGGCTT 660
 50 TCTGCCACGT ATAATGTCTG CTGCTTTTTT AGCTAACATT AAAACAGGTG CGTGATATT 720
 GCCATTTGTC GTACGTGGCA TAGCTGATGC ATCAACTACA CGTAAATTTT CCATACCGTG 780

ACTACAAGAT GGGTGTAATG CTGTTTCACC ATCTCTACGA ACCCAATCAA GAATTTCTTC 900
 GTCTGTTTGC ACTTCTGGTC CTGGTGAAAT TTCTCCACCA TTGAATGGAT CCATTGCTTT 960
 5 TTGAGATAAG ATATTCTTG CTACACGAAT TGCTTCTACC CATTCTTTTT TATCTTCTTC 1020
 TGTGATAAA TAATTAAAGC GGATACTTGG TTTTTCGAAT GGATCTTTAG ATTTGATTTT 1080
 CAAGCTACCA CGAGAGTTTG AATACATTGG TCCTACGTGA ACTTGATAAC CATGTGCGAC 1140
 10 CGCTGCCTTT TGACCATCAT ATCTTACAGC TATTGGTAAG AAATGGAACA TTAAGTTAGG 1200
 ATAATCAACT TCGTTATTTG AACGTACAAA TCGCCACCT TCAAATGGT TAGATGCTGC 1260
 15 TGCACCTGTA CGTGTGAAAA TCCATTGTAA ACCAATAAAT GGcATGCGCT TGAtATCTAA 1320
 GCTTGGCtGt AATGATACAG GTTCCTTACA 1350

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1376 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TAATGCTATT GGCAACACCA TATATGAAAn CTCCAAACGA TCCTAAACCG ACTATAGATT 60
 30 CACCAATTT nACAATCCAT GAATAAGTA GTGGCCATAA GAATAACAAT ATGACAACTA 120
 AAAATGTACA GTAAATGCA GTCATAATTG GAACTAGACG TTTACCACTA AAAAATGATA 180
 ATGCTAATGG TAATTCTGTT TCACTAAACT TATTGTATGC ATAAGCTGCT ATTAAACCTA 240
 35 TTACAATACC AACAAAGACA TTGCCATTAT TCATCTTTTC AAAAGCTGAA TTTATTTCCG 300
 A_rGCTTTTCAT TCCTAATAAAA GGCGCTAATT TCATTGGTGA TAATACAACT GTAACATAAA 360
 40 AATATCCTAA CGT_rGCTGCA rGCGSGACTG CACCATCATT TTTCTTTGCC ATTCCTATAG 420
 CTACACCAAT TGCAAATAAA ATACCTAATT GCTCTAAAAT CGTAGTACCT ACCGTAGTAA 480
 AGAACATTGC GATTTTCGGC GTCGCATGAA GTGCATTTAA CGTATTACCA ATTCCGGCAA 540
 45 TAATTGCTGC AGCCGGTAAA ATGGCAACTG GTAACATTAA CGAACGCCCT AAATTTTGGA 600
 AAAATTTATA CATTGAATGT CATCCTTCTT AAAATAATGT AGAAATATAA AGATTACTAA 660
 TGTAAC TAGA ATAAC TACTT CGATACTCCG TTATAGTCAC CTAGGCTTAC TAACCAGCTA 720
 50 TATTTCTACC TCAAGTTATT TTATAA ACTT TTTACAATTT CATGCAATTC TTGTTGTAAC 780
 TTTGCTGTTC GTGTTTCAAT CTCTTTTGTA ATATAATCGA TACGCTCGTT TCGTTTTAAA 840

	AAAGACCGTG AATCTTAGTA GGACCAACAT AAGCAACAGG TAATATTGGT GACTTACTTA	960
	ACATTGCAAT TGTTGAAGCA CCaCGTTTCA AAGGTGCACC TTCTTGCGAT GTGCGAGAAC	1020
5	CTGTTGGGAA GATACCAACT GTCTTATTAT CTTTCAACAA ATTGATTGGG CGTTTTAAAG	1080
	TACTAGGTCC TGGATTTCa CGATCTACAG GAAATGCATT TAAAGACGTT AAAAATTTAC	1140
	CAATCCATTT ATTTTGAAT AATTCTTTTT TAGCCATATA ATGAATTGGA TTAGGATATA	1200
10	ATGCCATACC TAGCATAATG ACTTCGTTAT AACTTTCATG CGTACAAGTT ACGACATATT	1260
	TACTATCCTT AGGAATATTA TCTTTACCGA TTACGTATAA TGATTTTGAC ATTTTAACTA	1320
15	AAATGAAATT CAAAATCTTA CTAATCACTG AATACATTGT GCCACCTACT TAACTT	1376

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

	TTGTCATACC AATATTTTGT AAAATATGGA ACACAAGTAA AGTGACGAAA CCAACGATAA	60
	AGATTTTGTT AAATTGATCT TCAATTTTCG CAGCTAATCT TATTAGATGG AAGATTAAAA	120
30	ATAAAAATAT TAAGATCAAT ATGACAGAAC CGATAAAGCC AAGTTCCTCT CCAATCACTG	180
	AAAAGATAAA GTCAGTATGA TTTTCAGGTA TATAAACTTC ACCGTGATTG TATCCTTTAC	240
	CTAGTAACTG TCCAGAACCG ATAGCTTTAA GTGATTCAST TAAATGaTAG CCATCACCAC	300
35	TACTATATGT ATAGGGGTCA AGCCATGAAT TGATTGCTCC CATTGATAC AGTTGGaCAC	360
	CTAATAAATT TTCAATTAAT GCGGGTGCAT ATAGaATACC TAAATGACT GTCATTGCAC	420
	CAACaATACC TGTAATAAAG ATAGGTGCTA AGATACGCCA TGTATACCA CTTACTAACA	480
40	TCACACCTGC AATAATAGCA GCTAATACTA ATGTAGTTCC TAGGTCATTT TGCAGTAATA	540
	TTAAAATACT TGGTACTAAC GAGACACCAA TAATTTTGAA AAATAATAAC AAATCACTTT	600
45	GGAATGATTT ATTGAATGTG AATTGATTAT GTCTAGAAAC GACACGCGCT AATGCTAAAA	660
	TTAAAATAAT TTTCATGAAT TCAGATGGCT GAATACTGAT AGGGCCAAAC GTGTACCAAC	720
	TTTTGGCACC ATTGATAATA GGTGTAATAG GTGACTCAGG AATAACGAGC AAGCCTATTA	780
50	ATAATAGACA GATTAAGAAA TACAATAAAT ATGTATAATG TTTAATCTTT TTAGGTGAAA	840
	TAAACATGAT GATACCTGCA AAAATTGCAC CTAAAATGTA ATAAAAAATT TGTCTGATAC	900

TTGCTAAAAC AGCTATAGTG GCTACTAATA CCCAGTCTAC TTTGCGAAhC aATGCTTATC 1020
 CGGCTGTTGA CGAGATGAAT AATTCATTGC AAACCTCCTTT TATACTCACT AATGTTTATA 1080
 5 TCAATTTTAC ATGACTTTTT AAAAATTAGC TAGAATATCA CAGTGATATC AGCTATAGAT 1140
 TTCAATTTGA ATTAGGAATA AAATAGAAGG GAATATTGTT CTGATTATAA ATGAATCAAC 1200
 ATAGATACAG ACACATAAGT CCTCGTTTTT AAAATGCAA ATAGCATTAA AATGTGATAC 1260
 10 TATTAAGATT CAAAGATGCG AATAAATCAA TTAACAATAG GACyAAATCA ATATTAATTT 1320
 ATATTAAGGT AGCAAACCTT GATATATCAT TGGAGGAAAA CGAAATGACA AAAGAAAATA 1380
 15 TTTGTATCGT TTTTGGAGGG AAAAGTGCAG AACACGAAGT ATCGATTCTG ACAGCACAAA 1440
 ATGTATTAAA TGCAATAGAT AAAGACAAAT ATCATGTTGA TATCATTAT ATTACCAATG 1500
 ATGGTGATTG GAGAAAGCAA AATAATATTA CAGCTGAAAT TAAATCTACT GATGAGCTTC 1560
 20 ATTTAGAAAA TGGAGAGGCG CTTGAGATT CACAGCTATT GAAAGAAAGT AGTTCAGGAC 1620
 AACCATACGA TGCAGTATTC CCATTATTAC ATGGTCCTAA TGGTGAAGAT GGCACGATTC 1680
 AAGGGCTTTT TGAAGTTTTG GATGTACCAT ATGTAGGAAA TGGTGTATTG TCAGCTGCAA 1740
 25 GTTCTATGGA CAAACTTGTA ATGAAACAAT TATTTGAACA TCGAGGGTTA CCACAGTTAC 1800
 CTTATATTAG TTTCTTACGT TCTGAATATG AAAAATATGA ACATAACATT TTAAATTAG 1860
 TAAATGATAA ATTAAATTAC CCAGTCTTTG TTAAACCTGC TAACTTAGGG TCAAGTGTAG 1920
 30 GTATCAGTAA ATGTAATAAT GAAGCGGAAC TTAAAGAAGG TATTAAAGAA GCATTCCAAT 1980
 TTGACCGTAA GCTTGTATA GAACAAGGCG TTAACGCACG TGAAATTGAA GTAGCAGTTT 2040
 TAGGAAATGA CTATCTGAA GCGACATGGC CAGGTGAAGT CGTAAAAGAT GTCGCGTTTT 2100
 35 ACGATTACAA ATCAAAATAT AAAGATGGTA AGGTTCAATT ACAAAATCCA GCTGACTTAG 2160
 ACGAAGATGT TCAATTAAACG CTTAGAAAATA TGGCATTAGA GGCATTCAAA GCGACAGATT 2220
 GTTCTGGTTT AGTCCGTGCT GATTTCTTTG TAACAGAAGA CAACCAAATA TATATTAATG 2280
 40 AAACAAATGC AATGCCTGGA TTTACGGCTT TCAGTATGTA TCCAAAGTTA TGGGAAAATA 2340
 TGGGCTTATC TTATCCAGAA TTGATTACAA AACTTATCGA GCTTGCTAAA GAACGTCACC 2400
 45 AGGATAAACA GAAAAATAAA TACAAAATTG ACTAACTGAG GTTGTATTATA TGATTAATGT 2460
 TACATTAAAG CAAATTCAAT CATGGATTCC TTGTGAAATT GAAGATCAAT TTTTAAATCA 2520
 AGAGATAAAT GGAGTCACAA TTGATTCACG AGCAATTCTT AAAAATATGT TATTTATACC 2580
 50 ATTTAAAGGT GAAAATGTTG ACGGTCATCG CTTTGTCTCT AAAGCATTAC AAGATGGTGC 2640
 TGGGGCTGCT TTTTATCAA GAGGGACACC TATAGATGAA AATGTAAGCG GGCCTATTAT 2700

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	AAACCCTAAA	GTAATTGCCG	TCACAGGGTC	TAATGGTAAA	ACAACGACTA	AAGATATGAT	2820
	TGAAAGTGTA	TTGCATACCG	AATTTAAAGT	TAAGAAAACG	CAAGGTAATT	ACAATAATGA	2880
5	AATTGGTTTA	CCTTTAACTA	TTTTGGAATT	AGATAATGAT	ACTGAAATAT	CAATATTGGA	2940
	GATGGGGATG	TCAGGTTTCC	ATGAAATTGA	ATTTCTGTCA	AACCTCGCTC	AACCAGATAT	3000
10	TGCAGTTATA	ACTAATATTG	GTGAGTCACA	TATGCAAGAT	TTAGGTTTCGC	GCGAGGGGAT	3060
	TGCTAAAGCT	AAATCTGAAA	TTACAATAGG	TCTAAAAGAT	AATGGTACGT	TTATATATGA	3120
	TGGCGATGAA	CCATTATTGA	AACCACATGT	TAAAGAAGTT	GAAAATGCAA	AATGTATTAG	3180
15	TATTGGTGTT	GCTACTGATA	ATGCATTAGT	TTGTTCTGTT	GATGATAGAG	ATACTACAGG	3240
	TATTTTCAAT	ACGATTAATA	ATAAAGAACA	TTACGATCTG	CCAATATTAG	GAAAGCATAA	3300
	TATGAAAAAT	GCGACGATTG	CCATTGCGGT	TGGTCATGAA	TTAGGTTTGA	CATATAACAC	3360
20	AATCTATCAA	AATTTAAAAA	ATGTCAGCTT	AACCTGGTATG	CGTATGGAAC	AACATACATT	3420
	AGAAAATGAT	ATTACTGTGA	TAAATGATGC	CTATAATGCA	AGTCCTACAA	GTATGAGAGC	3480
	AGCTATTGAT	ACACTGAGTA	CTTTGACAGG	GCGTCGCATT	CTAATTTTAG	GAGATGTTTT	3540
25	AGAATTAGGT	GAAAATAGCA	AAGAAATGCA	TATCGGTGTA	GGTAATTATT	TAGAAGAAAA	3600
	GCATATAGAT	GTGTTGTATA	CGTTTGGTAA	TGAAGCGAAG	TATATTTATG	ATTCGGGCCA	3660
	GCAACATGTC	GAAAAAGCAC	AACACTTCAA	TTCTAAAGAC	GATATGATAG	AAGTTTTAAT	3720
30	AAACGATTTA	AAAGCGCATG	ACCGTGTATT	AGTTAAAGGA	TCACGTGGTA	TGAAATTAGA	3780
	AGAAGTGGTA	AATGCTTTAA	TTTCATAGAG	ATTAGTCGAG	GGACCTTTTA	CTTATAAAAA	3840
	TGATTTGAAT	TAATACTAAA	AGATTACAAA	GAAGAGGTGG	TTTGTGTGTG	AAATACAAAA	3900
35	TTGCCTTTTT	CTTTTTATGT	TAAATCTATA	AATTTGAAAC	TAAATCAAGG	TTAATTCTAT	3960
	GTACACACTT	TATATAGGAA	GTAGTTTGAA	TGTTTATATA	ATGTTTTACA	AAAAGATGTA	4020
40	GTATTATAAT	GTCTAATTTT	ACATGTGTTT	CAGTAAATTT	TGTGTGGGAA	TGTTAACGAT	4080
	ATACGTATTT	TATAAAAAAT	TTTTTATAAT	GATTATTTCG	ATGATGCGTA	ACGCTTACAT	4140
	CTTATCTAAT	GCTAGCTTTT	TGACAAAAAT	ATGACAATCA	ATTAATGTGA	TTCTAATAAA	4200
45	TATTCGCAAA	TTGCTTTTAT	GCGATTAAAT	TTTTTTGGTG	GTACTATATA	GAAGTTGATG	4260
	AAATATTAAT	GAACCTTATAT	GCAAAAGTAT	ATTGAGAAAT	AAACAGGTAA	AAAGGAGAAT	4320
	TATTTTGCAA	AATTTTAAAG	AACCTAGGGAT	TTCCGATAAT	ACGGTTCAGT	CACCTGAATC	4380
50	AATGGGATTT	AAAGAGCCGA	CACCTATCCA	AAAAGACAGT	ATCCCTTATG	CGTTACAAGG	4440
	AATTGATATC	CTTGGGCAAG	CTCAAACCGG	TACAGGTAAA	ACAGGAGCAT	TCGGTATTCC	4500

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	AGAATTGGCA ATGCAGGTAG CTGAACAATT AAGAGAATTT AGCCGTGGAC AAGGTGTCCA	4620
	AGTTGTTACT GTATTCGGTG GTATGCCTAT CGAACGCCAA ATTAAAGCCT TGAAAAAAGG	4680
5	CCCACAAATC GTAGTCGGAA CACCTGGGCG TGTATCGAC CATTAAATC GTCGCACATT	4740
	AAAAACGGAC GGAATTCATA CTTTGATTTT AGATGAAGCT GATGAAATGA TGAATATGGG	4800
10	ATTCATCGAT GATATGAGAT TTATTATGGA TAAATTTCCA GCAGTACAAC GTCAAACAAT	4860
	GTTGTTCTCA GCTACAATGC CTAAAGCAAT CCAAGCTTTA GTACAACAAT TTATGAAATC	4920
	ACCAAAAATC ATTAAGACAA TGAATAATGA AATGTCGTAT CCACAAATCG AAGAATTCTA	4980
15	TACAATTGTT AAAGAATTAG AGAAATTTGA TACATTTACA AATTCCTAG ATGTTTCATCA	5040
	ACCTGAATTA GCAATCGTAT TCGGACGTAC AAAACGTCGT GTTGATGAAT TAACAAGTGC	5100
	TTTGATTCTT AAAGGATATA AAGCTGAAGG TTTACATGGT GATATTACAC AAGCGAAACg	5160
20	TTtAGAAGTA TTanAGAAAT TTAAAAATGA CCAAATTAAT ATTTAGTCG CTACTGATGT	5220
	AGCAGCaAGA GGACTIONATA TTTCTGGTGT GAGTCATGTT TATAACTTTG ATATACCTCA	5280
	AGATACTGAA AGCTATACAC ACCGTATTGG TCGTACGGGT CGTGCTGGTA AAGAAGGTAT	5340
25	CGCTGTAACG TTTGTTAATC CAATCGAAAT GGATTATATC AGACAAATTG AAGATGCAAA	5400
	CGGTAGAAAA ATGAGTGCAy TcGTCCACCA CATCGTAAAG AAGTACTTCA AGCACGTGAA	5460
	GATGACATCA AAGAAAAAGT TGAAAACCTGG ATGTCTAAAG AGTCAGAATC ACGCTTGAAA	5520
30	CGCATTCTCA CAGAGTTGTT AAATGAATAT AACGATGTTG ATTTAGTTGC TGCACTTTTA	5580
	CAAGAGTTAG TAGAAGCAAA CGATGAAGTT GAAGTTCAAT TAACTTTTGA AAAACCATTA	5640
	TCTCGCAAAG GCCGTAACGG TAAACCAAGT GGTTCTCGTA ACAGAAATAG TAAGCGTGGT	5700
35	AATCCTAAAT TTGACAGTAA GAGTAAACGT TCAAAAGGAT ACTCAAGTAA GAAGAAAAGT	5760
	ACAAAAAAAT TCGACCGTAA AGAGAAGAGC AGCGGTGGAA GCAGACCTAT GAAAGGTCGC	5820
40	ACATTTGCTG ACCATCAAAA ATAATTTATA GATTAAGAGC TTAAAGATGT AATGTCTTGA	5880
	GCTCTTTTTT GTTTTCAATA ATTGATTCTC TGTAGATATC aaAGTaCTAA CGTTTTAAAG	5940
	GTTAAATATT TAATTGGATT GAGATCTGTA TGCGGTTATA TCaTTCTGTG TAAATATGGT	6000
45	TCTCCACCAA ATGTGGTGAG TATATAATTT AAAGAACTAT TTTTAAATTA AGAATAATCG	6060
	AACATAAATA AACTTTATGA AATTTAGTA TCATGTTCTT ATAAAAACA ATAGGGCTTT	6120
	TTGctGACGC TAGTGCGGA TAAATAATAA GTTGAATATA AAAAAGATCA CTGCCAATCA	6180
50	TTCGTTTAAT GGCAGCGATC TTTTTTATTT AATTATTTCT CTTTCCACTG CAACATTTGA	6240
	TAACCAATGC GTGGATGTGT TTTAATAATA TCTTTTGGGT CCTCATGACA TTGTGAAAGT	6300

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CCATATATTC GTTTAATAT CATCTCATAA GTGAGTACTT TTCCTTTATG ATTTGACAAT 6420
 AGTTCTAACA AGCTAAATTC ATTTGGCGTC AAATGTACCT CCTGATTATT AATAACAACA 6480
 5 GATTTGGAGC CAAAGTCGAT GCTTAGCAAA CCGTTAGTAA ATACAATGTT AGTTTCTTGA 6540
 TGTGACTTAG CGATTCTCTC GATGACTCGT ATTCGTGCCC GAAGCTCATC AACATTAAAA 6600
 10 GGTTHAGTCA TATAGTCATT CGCACCGTTA TCTAAAGCTT GAATAATTGT TTGTTCTTCT 6660
 TGTCTTGCAC TTATTACAAT GATAGGAATG TCAGTATGTT GCCTGATTTC TGAAATCAAA 6720
 CATAATCCAT CTTTATCTGG TAAACCTAAA TCTAATAAAA TGACATCTGG TTTATCAATT 6780
 15 TGAATTTTAA AGTGTGCTTG TGTGGCATTG TCGGCTGTAG TTACATTGTA ATAATCTAAA 6840
 GTTAATGCAA CATCAAGTAA ATGTGTGATT GCGTGATCAT CTTCAATTAT CAATATTTTA 6900
 GATTGCATTA TACGTCTCCT TCGTTAAAGT CTGTATATAT ATTGAAATAG AATATACTGC 6960
 20 CGTGTGGTTG GTTCGGTTTA TATTGTAAGT TTGATTGATG TTTGTGTAGG ATAGTCTGTA 7020
 CTAAATATAA GCCTAGTCCC ATGCTTTCTT TTTGGTTATC TTTAAAATAT TTATTTGATC 7080
 CTGTGTAAAA AGGCTCGAAT ATCTTTTGTt GTTCTTCTAA ACTAATTCCA GGTCCTTCGT 7140
 25 CTATAACGGC AAATTCGATT TGTTCATAGC TAGCATAACG AATAGATAAA TTGATTTTGG 7200
 TGTCAGTAGA AGTGTGTTTA ACTGCATTTT CAATCAAATT GAATAAAGCT TGTAATAATCA 7260
 ACTTACTGTC AATGTGTATA AACTGTAAAT TTAAGTGGGA TGATACAGTT ATACGCTTTT 7320
 30 TTAAATGGCG ACGTTCTAAA ATACATATCG ATTTCTTATA CTA 7363

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 10470 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTAACAATCG ATAACCACAA TACTTCTATT GTAATTGTTT AACGATTTCTn CGATTAAAAT 60
 45 CATCTAAATC GTCTGGTACT CGACTTGTTA CAATATTGTT GTCTACAcTa CTGACTCATC 120
 AACTACATGT GCGCCTGCAT TTGATAAATC TTTGCGTACA TTTAATACTG CTGTAAACGT 180
 ACGACCTTTT AAATCGTCTG TATCTATTAG TATTGTGGC CCATGACAAA TGGCAAATGT 240
 50 TGGTACATCA TTTTtagTAA AGTATTTAGC AAATGTGCCA TATCGACCTT CTGTATCTCC 300
 ACGTAAATGA TCTGGTGAAA ATCCTCCAGG AATTAATAAT GCATCATAAT CTTCTGGTTT 360

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ATTTGCAGTA TCTCCAATCA CTACAGTATT AAAGCCTGCA TTCTCTAATG CCTCTTTAGG 480
 GCTTGAATAT TCTATATCTT CAAATTCGTT TGCTAGAATA ATTGCTACTT TTTTAGTCAT 540
 TGAAAATCAC CTTTCTATAT ATCATTGATA TAATTACTAT AGACAAGTAA ATCAGTGATT 600
 AAACATACAA GATATAAAAA ATATTAAGCG ACTGTGCGGA TATCTAACCC TAACACATCT 660
 TATGTGGCAT TTAAGTAGAT ACTAATTAA CCTTTTCTC AAGCTGATCT AACAATCCAA 720
 TCCATTATC TATATCTTCA ACACGTACTT CATCAGGATT TACATGATCG ATATCCTCAA 780
 TAACTTATT TAAACGCGCT TTTATCTGTT CGATTGTTG CTGTTTCTC ATAAAAAGTT 840
 AACTCCTTTT ATTTTGTGTT CTTTTTCATT ATTATCCTAA CAGAAATTGC GTTAAAGCGA 900
 TATAATCTTA GCTATATTTA TGACATTCAA ATTATTTTGA CTTTAAAAA TCCCCTTTTC 960
 AATTAATAA AATTAAGAGA TAATTTGTTA CGAGTGATAA TACGAaGkGG TaTCATACCG 1020
 ATATGAACCA AATAGAAAGA AGGAAGTTA AGACGATGAA TAGCGTCAA TTGAAGCAAC 1080
 CTGTTAGCAT TTACAATGAT CCATGGGAAG TGAAATTTAT ATACATTTAA ATTTTCATGAG 1140
 ACAATAAAGC TTGATTTAAT GCGTTTTTTT GCCTTTTTTA TTTTCCTTAT TTTTCTGTT 1200
 TTACAACAAA ATGGTATCAA AAATGGTATC ATTTGTAGTT ATTTTAGCTT CACATATTAA 1260
 AACAAACACA CTCCTAAATT AATAGGTGGT GTGGTTTTGT TGGTGTGTG GGGATAAAAA 1320
 TAACCGCATC AGTTAAGATG CGGTTATCTA GCAAGGGCCA CGTATTTATA AATACGTTTA 1380
 GAATCTCTTC GGCAACTTTG CTATAGACAG TCTATGCTGT TACTAAATTA TACCACCACA 1440
 CAAACCTACT CCCATTGAGG AACACAGAGC TTTGTGCTC GTCAGCAACG TCATATGAAT 1500
 TCTCAGTTCA TGTGTGGTG ACACTTTAAA CGGTCTGTGC CAGTAGCGAC CGAGTCATTT 1560
 CAAGAATGAC CATTTACAT TTATATTATA ACACCTGTG TGGTAACTG TATAGTTTTT 1620
 CAGTTGTATT TAAAGTTAAG TTATCTACTT CGCGCTTTCC TTGCCTTAAT TGTGAAATTA 1680
 CATATTGCGC TACGCCAGTT TGTGTTGTA TTTGGTAACC TGTATATCA CTTTGTATCA 1740
 ATTCAATTAT TTTTAATTTA TAATCACTCA TATTATCTAC GTCCATTCTT TTTATCTAAA 1800
 CAATAAAAAAT GTGTCTTTCT CCCGATAAAT AATAACAATG GTAGGCTTAA TAAAAACAAT 1860
 ATTAAATACA TTTGTTCTGT CATAATTGAA AACCTCCAAA TAATATTATA TTATATAAGT 1920
 GTAAGGAGGA GCCATCAGGC TCCAAGCATA ATGTTAATCT TTGTTGTTG GCTTTCGGTC 1980
 TAGGTAGCCG AGATGCCaTT CTCTAAGTTG TTTTAACT TCTGGAATTA TCAGTACTGC 2040
 CAATACTTGA TGTCTAGAA GTGTTTTTAT TATGTCTAGC ATGAGGCTTT TCACCTCCTT 2100
 ACACATAATT TGTAAGTCAT CAACTAACCT ACAAATATAA TTATACTAAA CAAATGTTTA 2160

	GTTATCTACA	TTTAAATCTT	GAGAGAAATG	TTAAAAAGTT	CTAGTAAAT	AATAGCACAT	2280
	TTTATCTTTA	AATGTAAATA	GAAAGCAGGT	ATGTAACGCA	CCTGCTTAAA	TAGaCATGAC	2340
5	TATGTCATTC	TAACTGATTT	CTCCCCATAA	GTCACCTAAT	ATCTGATTAG	GTGGGGCAGA	2400
	ACCATTCCAT	GTTCTAATAG	GCAAGTAATA	ACGTTGCCCC	TCCCATGTAT	ATCCTACCCA	2460
10	AACATGACCA	TCTTGTAACA	TCACTTCTGT	ATAATCACAA	TACCCACCAG	GTTGGAAC TG	2520
	ATAACCCACT	GGACAAGATA	AGAATGGCCC	CACTTTTCTT	ACTGTGATTG	GTTGATTGCC	2580
	GTTTGTGAAT	CTAGCACTTT	CTTCCATGTA	GTAAGTACCA	TATTTATTAC	GTTTCCATGC	2640
15	ACTTGCAACT	GGTTTAACTG	TATTACTTGA	AGCGCTTGAC	TCATTAGAGA	CAGTGGCAAC	2700
	CGGTATTTTA	CCATCCATGT	ACGCCCTAAT	CTGCTTGATA	AAGTAGTCTT	TAAGTTGCAA	2760
	CCGCTTGTCT	TCTGGCAATA	GACCGCGAGT	TACTGGGTCA	AAACCAGTGT	GTAAAACCGA	2820
20	ACTTCTATGA	GGGCATGATG	TTGAAGTAAA	TTCATTGTGC	AATCTGATTG	TATTTCTGTT	2880
	TGCTGGTAAT	CCCCATTTTT	TCAACAATCT	AGCGCATTCT	TGGAAAGTTG	CCTGTTCAAT	2940
	TTTTAAGAAT	GTCGCGTTAT	CTGCGCCCAT	TGATTGACAT	ACTTCAATAC	CGTAATAATA	3000
25	TTTATTACCT	ATTTGATTAG	CGGTATGCCA	ACCTACTTGT	GATTCATCTA	AGGCTTGCCA	3060
	AACTGTGTTG	CCTGATACGT	AACATGCGC	AATGCCCGCT	TCTAATCTTG	ATAAAGGTGC	3120
	ATTTACTAAT	CCGTTACGAT	ATGCTTCAGC	AGTCGCCCT	TTGCTCCCTG	CGTCGTTGTG	3180
30	TATAACTATA	CCTTAGGGT	TACTACCACG	CTTAGGTAGG	TCATAACCTT	TAACCACATC	3240
	TTTGATGATT	TTAAGTTCTA	CTGCTTTAGG	TTGTGGCTTA	GCTGTTTCTT	TTTTAGGTGC	3300
	TTGTGTAGGA	GATTGAACTG	ATCGTGGCGC	TGTCTCACTT	TTAAAATTCTG	GACGGATAAA	3360
35	CCACATAGGG	AAATCATAAG	CATGTTGTCTG	TCTTGTAAC T	TTTTCCCAAC	CCCAGCCGGG	3420
	TTGTTCGATT	CCGTCAGTCC	AGCCACCGCC	TAGCCAATTC	TGCTCATATA	CAATGATGTA	3480
40	ATCTAAAGTT	GCTTCAATTA	CCCATGCAAC	GTGACCATAT	CCAGCACCGT	AGTTGCTACC	3540
	GAATACCACC	ATGTCGCCAG	GTTGTGCTAA	GAAGTCCGGT	GTATTTTGGT	ATACAGTAGC	3600
	TAATCCGTCG	AAGTTGTTAG	CGAACGGAAT	ATCTTTTGCA	CCTAAACCTT	TTAGAAGTAA	3660
45	TCCAAACAAA	ACTTTCCAAC	CAGCATTGGC	ATAATCAAAG	CATTGAAATC	CATACCATAA	3720
	GTCCACATTG	AATTGTTTTT	CCTCAGAAGT	TTTCAACCAC	TCTATAAACT	CATTTTTAGT	3780
	TAATTTTGCT	TGCATTGTCTG	CCACCTCCAT	GATGATACTC	ATTCACATCA	AAGCCAACAT	3840
50	CGTTAGAGGC	GTCTGTGAAA	GGTTGTGATG	TATCATATTC	TTTTGGTGCT	TTCGCGCTTA	3900
	ATTCCGGCGT	TAACTACTG	TCTTGTGATG	ATTTCCACGT	AACTTGTGT	TCTTCTTTTT	3960

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	TTGGGTCAGT AATAACGCCA ATACCTGTAA GTAACGTGAG GATAGCGCCT ATAATTGCGC	4080
	TAGCTTGATT TAATTGAGTA GATAAATCTA ATCCGAATAA ATCCGTGACT TGCTTGATAA	4140
5	ATAGCAACAA TGCTCCAACCT AAACCAGTTA GTACTGCTTT GTTTTTGAAT CTCAATTTCC	4200
	AGTTAATATC CATTTGTTTG CTCCTTTTAT CCAAAATAAA AAAACGACTA AAAATTAGTC	4260
	GTTTAAATTT ATTCAATGGT CAATGTCGGA GATCCTGAAT AAACATCACT TATAGTGACG	4320
10	TACAACATCC CTGAAGGATT ACTAAAGTTG ATATTTTTAC TTGCAACTCC GCTATTGACT	4380
	CCTGATATTC CTAAATCACT TGACCCTAAA TTAGTTTGCG AAATCCTCAT TATACCGCTA	4440
	CGTACATTTT CTATTGTCAC CTGATAACTT TTATTGGGTT CAACTCCATT TATTGTCCAT	4500
15	TTTGCTGTTG ATTCTTCTAT GCTATCCGGA TATTTATTTT TAGGTAAGGG TTTTATTACA	4560
	AAAGATGAAG GCTTTTTTCCA TACTTGGATA TTTCCAGCAT ATACTTTTGT ATATTCTTCA	4620
	CCTTCGTAAA TAAACTTCTT TACATTTTTA AAATTACCTT CCATAAAAAT CACCCTTTAA	4680
20	TTAAATATAA CGTATTCGGG TCTTTTTGAT ATATATAGTT ATATTCATTT TCTGTTCTTG	4740
	TCCAAATTTT AACCGTCGGT TGAGATGCGC TTTTATAGTT ATATAAATTA TCCGCTTGTT	4800
	GTTTAGTAAA AGCTTGAGAT GACAAAACAT ACCGCTCGTC ATGATTATGA TTTTGGAG	4860
25	CATATAAATC ATTTAGTGTT TGTTTGAATT CCTCAAATC TTCTGTATTA ACTTTTGAGC	4920
	CAATCTGTTG CAATACACTT TCTGAAATAG AGTTGTTTTG TATTGCTTCT GCTAATTCTC	4980
30	TTAATGTGTT CATAGATTCA GCGCGCTAT CAACTAGTTC AGCAATTTTT GTATCCGTAT	5040
	ACGTTTTAGA GTCGTTGAGA GTTGATCTT TGATTTTTTC AACTTCTTGC AATTTATTTT	5100
	CTAACCCTTC AACATTTGCG ATATTGATTT TGTCCAATAA CTCAGGTTCT GCTTTGATAT	5160
35	CTGTATCTTT ACCATCAATT TGCCACATTT TAGTGTGAGG ATTGATTGAT ACTACAGTAC	5220
	CGTTTTIACC GGGTGCGCCT TGTTCTCCTT TTTTACCTGC TTCACCTTTT GCTCCAGGTT	5280
	GTCCCGGTTT ACCTTTATCA CCTTTCGCAC CTTTAAATCT ACTTTCATTC TTTTCGATGT	5340
40	AAGAAATGAC ATCTTTATCT ATTTTCTCTT TAAAGTCTT GCTCAATAAA TCTGTCGCGT	5400
	TATCTTTTAA AATTCTCGTA ATAGCATCAT CTACCAATTT AACATCGATT TCTTTTGCTA	5460
45	CAGCAGATTC AATACCACTA TCAACGATAT TGAAAGAAAA GTTTGCGACA TGTATTTTTT	5520
	CTTCTTCTTT CTCTAAAAAC AGCTTACAGC GAACATAACC AGCGTGTGTTG ATAACCTTTT	5580
	TAGGTATCTT GTAGGTAAGG AAACCTTTTA CAACATCGTC GATAATAAGG GGCTCATTTT	5640
50	TGAATATAGA GCCATCTTCC ATAAACAAAT GTAATCTAGG TGTTAAGCCA TGTGCTTTTA	5700
	GATCGATACG ACCTTGTTTG TCATTGATAC CTATTCTTAT AGATGCTGTA TTTTCATCTT	5760

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CAACATCTTT TATTTTGTAC ATTTACACAC CTCTTTATTT ATATTTATCC CTTGTGAAGT 5880
 AGATACCTTT TAAGCCGATT TGTTTATATA ACTTAGCGAT TGTACTTGCT TGATGTTGGC 5940
 5 ACCACTCTAT AGCAGTAGCG TATTGGTGGG TAGCTGGATT CTTAGGATTC CATCTAATTC 6000
 GGTACAATGT GTTTTGACCT TTATTGATGT AATCCTTTCT TACGAAGCTA GCACCGCCCA 6060
 10 TGATTGCTTT TGCTGGAGAT GTCCAACCTT TATTCCTTGC AAACGTCATT GCGTAGTTAG 6120
 GATTGTTGTC GTAAGCGCCA ATGCCGAAGT AGTTGTATAC TCCATCTTTT CCGTTAGCGA 6180
 AGTTACTTGT TCCATATCCA CTTTCTAAGA AAGCATGCGC GATTAAATAA ATTTCAATTAA 6240
 15 TGTTGTGCTT TTTACAAGCT TCTGCGAACG CTTTACCTTG ATTATTCAAT GTTCCCTTAC 6300
 CTTTAAGTAT CTTATTAAGT GCGCTAACTG AAACACCTTG ATACTTGCCT AAATTAAGCA 6360
 TTTGGTAGCA TTGTGTGTTA CTTTCCATA TACGCTTTAC ATTCATTGCT GAACTCGTTT 6420
 20 GTGCTCGTGT AGCGTTAsC AACCCCAAGC ATTAGATTTT TTCGGTTTAC CTCTTGCCAT 6480
 TTGTTTATCC AGTGCTTGTT TGAATGTATA AGGACTCGTT TCTGTTATGA TCTGCGGTTG 6540
 TTTAGATGCC GAACCATGTG TGGCTGTTGG TGACGAGTCT CTTACATTAG CTATATCAGC 6600
 25 GTTTTTATTA TCTACCATAA CTTTATTCT AGATTTTGTT ACTGTTGGCT TAGTTATAGA 6660
 ATTTAATAAT TTTTCTCTGT TTTTAAATAT ATTAAGTAAT GCCTTTTCTA ATGCTTCGTA 6720
 TTTATCTTTA GGAGGAACAC CGTTGTCAAT CATATTCCAA TTAACATGTT CCAACATTGA 6780
 30 ACGCCAAATG CTGTCGTCTA CTTTAAATTT TTCAATACTT AGAGGTATCT CATATTGGC 6840
 CATCATATCT ACAGCTACAA CCATTGCGTG AATCTCATTA AAAATAAATT CATTTTACT 6900
 CGCACTATAA TCTTCACATA CGTCTATAAC TATATAATCA GGTTCATTAG GAACTTCAAA 6960
 35 TACAGCTCTT CTAGGTGCCC AAATATTATG TCTATCAACA TAAAGTGGG GATATTCTAC 7020
 ATCTGTTTG TATTCTTCC TACTGTTATA TAACTTTCT ACCGAGCTCA TCGTTGTGC 7080
 40 GTTCTAATC ATTATTCCTT TAGGTTTTTC GAGTCGTCGA TTACCTTCTA CTATAAAGTG 7140
 ATAAATATAT TCTGGATAAT TAACCTCTTG GCTAGAAATA GTGTACTTTA TAGTTGTTAC 7200
 ATCTTTCCAA ATTGGAACCT TTTTATTATT TTTTTCGTTA TCATCACTAT CATCTTCTGG 7260
 45 TTTAGGTGCC GGTGTAGTTT TGTCTGGATG ATATGGTGGT CTAACAAAAT ATTTAACCCC 7320
 TCCACCTGGT CCATCATGAT AAGAGTGTTT AATTTTATAA GGTGGACTTC CTGTGCGTT 7380
 ATTTGTATAC CAGTTTTGAT CTACGCCATA CCAATAGTCT TTTGTGCATG GTCCCACTAC 7440
 50 AATGTTTACA TGTCTGCCC AACCACCAGT CCAAACACCC CAGTCGCCTG GTTGTGGTAC 7500
 AAAATCTTTT GTATTTCTAA TTATCTTGAA ATCTCTACCT CTATAATTGG ATTTTGTAGC 7560

	TAAATCCCAG CATTGTGCTC CCATTCCAGA ACCAGGTACA TCAATAGCTA TTTTGTTTTT	7680
	AGCGATATAT AACGCCCATT CAACCACTTC ACTAGCTGTG GGCTTTCTAT TTTTCGGATT	7740
5	AGGTAATCCC ATGTATGCAC CTCATTTCAA TCAAAATAAA AAGCCAGTGC CGAAGCACTG	7800
	ACTCTTAACT GTTATTTACA TTTACCAAAC CAGAAGCACG CCCAGAAGCT ATATCCTAAA	7860
	ATCCCTTTAA GCATGGTAAT CACCTCCTTT AAATACCAAA AACAGTTCTT AGTAAAGCTA	7920
10	TGACAATCGT ACTGAAGATA GTCCCTATCA AACCTAGAAT CCACATTTTT ATGTCTCTAA	7980
	TATTCCTGGC ATTCTTTTCT TTATTCTTTT CATCTTCTAC CTTGTCGCGC TTTAATTCTT	8040
	CAAAATTTCT ATCTAATTTG TCATAAATCT TTTCTTGCGC TCTAAGACTA TCTTCTATTC	8100
15	TGTCGAATTT TTCAAACATA GTCTTATCAT TTTCTTCTAA TCGCGTTAAA CGCCAATCTT	8160
	GTTTCATGTCG TTTGGTAAAT CCAAACATTA TGCCACCCAC TTTATTCAAA TTAAAAAGCC	8220
20	ACAAGCATT A CACCTGTGAC TTTTCATCTT TTGTTTCTGG ATATTTTCTT CCAGTGATTA	8280
	AAGCGTATTC TTCTTTATCG ATTAAACCCCT TGTCTACGTA CCACTTAATT TGCTCGTTTT	8340
	TATAGTAACC CCAAACATAA AAAGTTTTAA TGTCTTTAAA AGTTGGATAA ATCATCTTCA	8400
25	TTATTTAAAC GTCCCCCTCA GTACTTGTTT TGTTAGTTTT CAGTTCAGTC AACTGTTGTG	8460
	TTAACATAGC GTTTTGTTGA GCTAATTCCA TTGTTAATAC GTTTACTTGT GCCACCTGCA	8520
	TTTGCATACT CGCAACCATT CCGCGAAGTT CCTCATCACT TAAATCTGAC GCACTTTGTT	8580
30	GGTTTGATGC ATTCGGTACG TCTTCTTTTT CGAAATTGCT ATTGTATTTA ATTTGCGCGT	8640
	TAGTGAAAAC AAACCTTCTA GGTTCGAACT CTTCCTTTAAA TTTAATAGGC ACATTGTTAT	8700
	CATCTACATC TAAACTATTG CGTAAACCGC CAGTATTAAC GAATCCGATA ACTTCGTTTT	8760
35	TATCGTTTAC TGTGATTTTC ATTATTTCCA CCCATAATT TTAGTTATAG TAACTTTGTT	8820
	GGCAJTCGCT CCAGAACCTG ATGTTTTACC TAAATCAAAG TACACATCGT TATCTATTCT	8880
	TAAAGTAGTG CTACTTGTTT TGGATAGTAA GCACTCATAA ATACCGCCAC CGTTGCCGTC	8940
40	TGAGTCAACT ACATTCGCTT TACTCAATTG AATCGCGTTA GGTAATGCGG TTAGTCCGAA	9000
	TCCCTCAATA ACGCCACCTG GATAAGTTCC ACTTACCAAC AAAATAGAAT AGTTTGTGTA	9060
	CGGTTCAAGT AGATTGATTG TTGTACCTAC ACCATTGCGG CCACCGTCGA ACAATACCGT	9120
45	TGATTTATGT TCATTAGGAA CTGTCCACTG TTGCTCAAGT CTGCCGTTG TGATTGATCG	9180
	TGTGTAAATC TTTTATAGAGT TATAAGGTGT GAAGTTAAAT AGCTTGTTTG TATCATCTTT	9240
50	AACGAATACC GATAAATAAC CCTCATAACT TTCAACGCTA CCTGGTAAAT CCGGCACTCT	9300
	TGTTGCATAG TAATTACCAG CAGTTAAATA TCCCAAATCG CCTTGCGCAT TATTTAAGTT	9360

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GAATTTATCA TCTACATACT GCTTAGCTTG ATTTAAAGCG TTGTTAGACG TTTCTTCAAC 9480
 AAATTGCTTA GTTAAGTTTC CATCATTCCTT TTTATAAAAC GGGTACCATG TGCCGTAGAT 9540
 5 TTTGTATTTT GTGTACTCAT CGTTTGAATC GTCTGGGTAC CATGTTGCAC GAGCAGTATT 9600
 ATTATCAACA ACATAAACAA CTAACACACC AGATTTGCTT GATGTATAAG TTGATTTCATC 9660
 10 GAACGAAGAA CCGTCATCAA CACCATCTTG TCCAGGCTTC TCTAACGTGC CTATATCCGT 9720
 CTTTTCTGGC GCATCTGTTG CATTAGTAAT ATGAATAATC CTAGATGTGT TAACTGCGCT 9780
 TAAAACGCTA TCTATGGACT GCTCATACGA TTCAATTGCT TTACCGTAAT CATCTGTAAG 9840
 15 TTTAGACTTT TGCCAATTTC TTGTTGAATT ACCTTTAACA AGGTCAGCGC CATTGATTTG 9900
 TTGTTCAACT TCGTTAACAC GTTCAAAAAT CGCTTGCTCT TTTTCAACTA TTTTATCGAA 9960
 TTCAGCTGTA ACAGCTTGTG TTGCACTAGT TTGCGTCGCA GTAATAGCTT GTATAGCTTC 10020
 20 GTTTTGCTTG ATTTTCGATTT GTTGAATGCC TTTTGTGCGA CTATCATTCA CTTTGTCTAT 10080
 TAACGTTTGT GTATCAGCCA TATTTTGCTT TAATTGGTTA AAATCTTTAC CGACAGCTTC 10140
 GATAGTATCT TGAATAGATT TGATATAAAC AAGCTTTGTT ATACCATCAA ACCCACTAAC 10200
 25 TAAATCATTT TCAATATTGA AGCTAAATTG ACGTTCAACA ACAACATTAT TACTCCCGTT 10260
 TTGTGTAAAG AATGCCTGAG CATGCACCTT GCCTGAATGT TTTAAAAATT CATTCCGTAT 10320
 CACATACTGC AAACGCCCAT TAATTGCGTC TACTATCGTT AATTCGTCTG AAATATAAGC 10380
 30 GCCTCTATCT ACGTTATAAT CATCGGTTTT TAACACGATA GATGTTTTAA CATGTTTCAGA 10440
 ACTTATAGAT AAGGGTCTGT TATnCTTAGT 10470

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATCAGATCTT GAGAATCGAG TTATTAAGTC TATCGAAGAC TTAATAAAA TCCAACCATT 60
 45 CATGCCTACA CAAGATTTTG ATTTTAAAAC TAAAGAAATT CAATCAAACA TTTCTGAAGA 120
 AAGATTTATC GAAATGATTC AGTATTTCAA AGAGAAAATA ACAGAAGGGG ATATGTTCCA 180
 50 AGTTGTGCCA TCAAGAATTT ACAAATATGC GCATCATGCT AGTCAGCATT TAAATCAACT 240
 TTCGTTTCAA CTGTATCAAA ATTTAAAACG ACAAACCCA AGTCCATATA TGTATTATCT 300

EP 0 786 519 A2

	TCAAATTGTA	ACAACTAATC	CTATTGCAGG	TACGATTCAA	CGTGGTGAGA	CGACACAAAT	420
	AGATAATGAG	AATATGAAAC	AACTACTTAA	TGATCCAAAA	GAATGCAGCG	AACATCGTAT	480
5	GCTAGTTGAT	TTAGGACGTA	ATGATATTCA	TAGAGTAAAGT	AAAATCGGTA	CCTCAAAAAAT	540
	TACTAAATTA	ATGTTATTG	AAAAATATGA	ACATGTTATG	CATATCGTAA	GTGAAGTCAC	600
	AGGTAAAATA	AATCAAAATT	TATCGCCAAT	GACAGTTATT	GCGAATTTAT	TACCAACAGG	660
10	TACCGTTTCA	GGTGCACCAA	AATTACGTGC	AATTGAAAGA	ATATATGAAC	AATATCCACA	720
	TAAACGGGGC	GTTTATAGTG	GTGGTGTGG	ATACATAAAT	TGTAATCATA	ACTTAGATTT	780
	TGCATTAGCA	ATTGGAACGA	TGATGATAGA	TGAGCAGTAT	ATCAACGTAG	AAGCTGGTTG	840
15	TGGCGTTGTA	TATGATTCTA	TTCTTGAAAA	AGAACTGAAT	GAAACGAAAT	TGAAAGCTAA	900
	AAGCTTATTG	GAGGTGAGCC	CATGATCTTA	GTTGTAGATA	ATTATGATTG	CTTTACATAT	960
	AACCTAGTGG	ATATTGTTGC	TCAACATACT	GACGTCATTG	TTCAATACCC	TGATGATGAT	1020
20	AATGTGCTGA	ATCAATCGGT	GGACGCTGTT	ATTATATCTC	CTGGTCCAGG	GCATCCATTA	1080
	GACGATCAAC	AGTTAATGAA	AATCATATCA	ACCTATCAAC	ACAAACCCAT	TTAGGTATT	1140
25	TGTTTAGGGG	CTCAGGCACT	GACTTGTTAC	TACGGTGGAG	AAGTCATTAA	AGGCGACAAG	1200
	GTTATGCACG	GCAAAGTTGA	TACACTAAAG	GTTATATCGC	ATCATCAACA	TCTGTTATAT	1260
	CAAGATATAC	CAGAACAGTT	TTCAATTATG	AGATATCATT	CATTAATAAG	TAACCCTGAC	1320
30	AATTTTCCAG	AAGAATTGAA	AATTACTGGA	CGTACCAAAG	ATTGTATACA	GTCATTGAG	1380
	CATAAAGAAA	GACCGCATT	TGGTATTCAG	TACCATCCTG	AATCATTTGC	TACAGACTAT	1440
	GGTGTCAAAA	TAATTACAAA	TTTCATTAA	CTAGTGAAGG	AAGGATGAAA	ACCATGACAT	1500
35	TACTAACAAG	AATAAAAACT	GAAACTATAT	TACTTGAAAG	CGACATTAAA	GAGCTAATCG	1560
	ATATACTTAT	TTCTCCTAGT	ATTGGAAGTG	ATATTAAATA	TGAATTACTT	AGTTCCTATT	1620
	CGGAGCGAGA	AATCCAACAA	CAAGAATTAA	CATATATTGT	ACGTAGCTTA	ATTAATACAA	1680
40	TGTATCCACA	TCAACCATGT	TATGAAGGGG	CTATGTGTGT	GTGCGGCACA	GGTGGTGACA	1740
	AGTCAAATAG	TTTCAACATT	TCAACGACTG	TTGCTTTTGT	TGTAGCAAGT	GCTGGCGTAA	1800
45	AAGTTATAAA	ACATGGTAAT	AAAAGTATTA	CCTCaAATTC	aGGTAGTACG	GATTTGtTAA	1860
	ATCAAATGAA	CATACAAaCA	ACAACTGTTG	ATGATACACC	TAACCAATTA	AATGanAAAG	1920
	ACCTTGATTT	CATTGGTGCA	aCTGAATCAT	ATCCAATCAT	GAAGTATATG	CAACCAGTTA	1980
50	GAAAAATGAT	TGGAAAGCCT	ACAATATTAA	ACCTTGTTGG	TCCATTAAAT	AATCCATATC	2040
	ACTTAACGTA	TCAAATGGTA	GGCGTCTTTG	ATCCTACAAA	GTTAAAGTTA	GTTGCTAAAA	2100

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	AAGCAACACT ATCTGGTGAT AATTGATAT ATGAATTGAC TGAAGATGGA GAAATCAAAA	2220
	ATTACACATT AAATGCGACT GATTATGGTT TGAAACATGC GCCGAATAGT GATTTTAAAG	2280
5	GCGGTTCCACC TGAAGAAAAT TTAGCAATCT CCCTTAATAT CTTGAATGGT AAAGATCAGT	2340
	CAAGTCGACG TGATGTTGTC TTAGTAAATG CCGGTTTAAG CCTTTATGTT GCAGAGAAAT	2400
	TGGATACCAT CGCAGAAGGC ATAGAACTTG CAACTACATT GATTGATAAT GGTGAAGCAT	2460
10	TGGAAAAATA CCATCAAATG AGAGGTGAAT AATATGACGA TTTTATCAGA AATTGTTAAA	2520
	TATAAACAGT CACTTTTACA AAATGGCTAT TATCAAGACA AACTTAATAC CTTGAAAAGT	2580
	GTGAAGATTC AGAATAAAAA ATCTTTTATA AACGCAATTG AGAAAGAACC AAAGCTAGCA	2640
15	ATTATTGCAG AAATTAAATC GAAGAGTCCT ACAGTTAATG ACTTACCTGA ACGAGATTTA	2700
	TCGCAACAAA TCTCAGATTA TGACCAATAT GGTGCAAATG CCGTGTCCAT TTAACTGAT	2760
	GAAAAGTACT TTGGTGGTAG TTTTGAAAGA TTACAAGCAT TGACGACAAA AACAACATTA	2820
20	CCCGTATTAT GCAAAGACTT TATTATAGAC CCGCTTCAAA TTGATGTTGC TAAACAAGCT	2880
	GGTGCATCTA TGATTTTATT GATCGTTAAC ATCTTATCTG ATAAACAATT GAAAGATTTA	2940
25	TATAACTACG CTATATCGCA AAATCTAGAA GTGTTAGTTG AAGTACATGA TCGCCATGAA	3000
	TTAGAACGTG CCTATAAGGT TAATGCTAAA TTGATTGGTG TAAATAACAG GGACTTAAAA	3060
	CGATTTGTGA CAAATGTGGA ACATACAAAT ACTATTTTAG AAAATAAAAA AACAAATCAT	3120
30	TATTATATTT CTGAAAGTGG TATTCACGAT GCATCTGATG TAAGAAAAAT CTTGCATAGT	3180
	GGTATCGATG GCTTACTAAT AGGTGAGGCG CTTATGCGTT GTGACAATCT ATCTGAATTT	3240
	TTACCACAAC TGAAAATGCA AAAGGTGAAG TCATGATGAA ATTGAAATTT TGTGGCTTTA	3300
35	CATCAATAAA GGATGTTACA GCGGCCAGTC AATTACCTAT TGATGCGATA GGTTCATCC	3360
	ATTATGAAAA AAGTAAAAGG CATCAAACAA TTACCCAAAT AAAAAAGTTA GCGTCTGCTG	3420
	TTCCAAATCA TATCGATAAA GTATGTGTCA TGGTAAATCC TGATTTAACA ACAATTGAAC	3480
40	ACGTATTAAG CAATACGTCA ATTAACACAA TACAGTTACA CgGCACAGAA TCTATTGATT	3540
	TTATACAGGA AATTAAAAAG AAATATTCAA GCATTAAAAT CACTAAAGCT TTAGCTGCAG	3600
45	ATGgAAAAACm TwATCCCAA caTtAAtnAA tnTTAgGGGG TCCGTGG	3647

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5966 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

	CcAcCTTGAC CACCTTTACG TGGAATCTTT TcMcCTkGAG CAACaTCGaT AATaTATATT	60
5	GAAAgTCAAC AAGTTCTGGA CTAAATGTTG CTGCTAAGTT ATCGCCACCA GATTCTATGA	120
	AAATTAGTTC TATATCGTCA TGACGTTCTA ATAATTCTGC TATTGCTGCA AAGTTCATAG	180
10	ATGCATCTTC ACGAATCGCA GTATGAGGAC ATCCACCAGT TTCAACACCA ATGATACGAC	240
	TTTCAGGTAG AACTCCTGAA TTTACTAATA TCTTTTCGTC TTCTTTTGTA TATATATCAT	300
	TTGTAATAAC GCCGATACTC ATTTCTTTTG AAAGACGTTT TACAACCTTT TCAATTAATT	360
15	GTGTTTTACC TGCACCTACA GGACCACCAA TACCAATTTT AATCGGATTT GCCACAATTA	420
	TAACCTCCTA TGATATGAAA tTCTAACATT GaCGTTCTCA TGCGCCATTT GATTTAGTTC	480
	TAAACCAGGC GCTGTCATGC CAAAATCTGC TTCTTTTAAT TCGAAAATCT GCTTTCTTGT	540
20	TCCTTCTATA TAAGGAATCA TGTGAGTAAC TATCTTTTGA CCAGCAGTTT GTCCAAGTGG	600
	AATAGCACGA ACAGCATTTT GAGTTAAACT TGAAACATTT TGATATAAAT AGTAATCAAT	660
	AATCGTTTCA ATATCTACAC CTAAATGATG GCCTAGCATA GTAAAACAAA TAGCTGGATT	720
25	TnACTTTGCT TTCTTATCTT GCATTTGTTG ATGATACCAA GCAATCCATG GGCTATtATA	780
	AAGTTCTAAA GCCAATTTAA CCATGCGAGT CCCCATTTGT kTTGCACCAA CACGTGTTTC	840
30	TTTAGGTAAG TTTTGrACAr ACATCAGTTT ATCTATGTGT AATACTTTTT GTGTATCATC	900
	ATTTTCCAAT GCATCATAAA CTAAaCGCAT GGCTAAACCA TCAGAATAGG TAAGTTGCTC	960
	TTGTAAAAAC ATTTTTAACC AAGCAATAAA AGTATGATCG TCATGAATTA TATTTCTGTTG	1020
35	AATATATGTT TCAAGACCAA ATGAATGACT GAAAGCACCT GTTGGAAACT GTGAATCACA	1080
	GAACTGAAAT AATCTTAAGT GTGTATGATC AATCATGAGA ATGCCCTATA TGTCTGAAAG	1140
	CCTTATTAAC TTTACGGTCT TCTCGAACAT ATGGGATGCC TAAACTTTTT AATAAATCTT	1200
40	CAACTAAATA ATCATATTGT ACTAGCATTT CAGTCTCTGT AAATTGTGCT GGCAAATGAC	1260
	GATTTCTTAA TTGATGGGCT ATATCTCCCA TTTCTTGCAA TGTCTTGCT TGAATCACTA	1320
	AAAGATCTTC TGAATTAACA TCCACAATAA TCATATTATG GTCATCTGCG TATAAAATAT	1380
45	CTCCATATTG TAAGTCAATA GGTTGTTTTA AACGAATGCC TATTTCACTG CCATGGTCTG	1440
	TAACGACTCT TTGAATACGT TTAACAAGAT CTGAATTTTC AAGGTATACT TTTTCGACGT	1500
50	GCTTTTGTTT TTCTGAATTT GACAAATTGG CAATATTGCC TTGGATTTCT TCAACAATCA	1560
	TTCTATGTTT CTCCTAGAAT AAGAAGTATC TTTGAGTTAA TGGTAACTCA GTTGCTGCAT	1620
55	TACTTGTAAT TTTTCTCCA TCTACATATA CTTCATATGT TTGTGGATCA ACGTCTAATT	1680

	GACGCACCAT GCGTTTTAAA TTTAATGCAC GATTGATACC ATTTTCATAA GCAGTTTTAG	1800
	ACACGAATGT CATTGACGTA CTTGTAAGGT TTCCGCCGTA TTGACCATAC ATTTTACGGT	1860
5	ACTTCATCGG TTCAGATGTA GGTATAGAAC CATTTCGATC GCCATTTACG GCAGAGTTAA	1920
	TTAATCCGCC CTTTACAAC TATTTCAGGT TAACCCCAA GAAAATTGGG TCCCATAGA	1980
10	CAATGTCAGC TAGTTTGCCC GGCTCGATAG ATCCTACATA TTCAGAAATA CCATGTGTAA	2040
	TTGCTGGGTT AATTGTATAT TTAGCGATAT AACGTTTGAT GCGATTATTA TCATTATGTT	2100
	CAAAATCACC ATCTAAAGGA CCACGTTGTT CTTTCATGCG ATGTGCTACT TGCCATGTTT	2160
15	GTGTAATTAC TTCACCTACA CGGCCCATTTG CTTGTGAATC GGAACCTAATC ATACTGAATA	2220
	CACCCATATC TTGCAGAACA TCTTCTGCTG CAATCGTTTC TTTACGAATA CGTGAATCTG	2280
	CGAATGCGAT ATCTTCAGGA ATAGCCGCAT TTAATGGTG AGTAATCATT ACCATATCTA	2340
20	AATGTTTCATC TACAGTATTA TGTGTATAAG GCAAAGTTGG ATTTGTAGAT GAAGGTAAAA	2400
	TATTTGAAAA TGCAGCGGAT TTAATTAAAT CAGGCGCATG ACCGCCACCA GCACCTTCAG	2460
25	TATGGTACAT ATGAAGTACA CGGTCTTTAA CAGCAGCCAT TGTGTCTTCC ATAAATCCTG	2520
	CTTCATTTAA AGTATCTGCA TGTAATGCAA TTTGAACATC AAATTCATCA GCAACATCTA	2580
	ATGCATGACT CAAAGCAGAT GGTGTTGCAC CCCAGTCTTC ATGTACTTTT AATCCAATTG	2640
30	CTCCGGCATT GATTTGTTCA ATGAGTGCAG TTGGATTGTG TGCTTGTCCT TTACCTGTAA	2700
	AACCGACATT AATCGGTAAA CcTTCCGGCAG CTTCTAACAT TCTATGAATA TGCCATGGAC	2760
	CTGGAGTTAC AGTTGTTGCT TTAGAACCTT CTGAAGCACC AGTACCACCA CCAATATGAG	2820
35	TCGTAATACC ACTTCTAAT GCGACCTCTG CTTGTTTCAGG ATTAATAAAA TGAACATGAG	2880
	TATCAATACC ACCAGCAGTG ACGATTTTAC CTTTCAGCGGC AATGATATCT GTTGTGAAC	2940
	CTATAATAAT GTCGACATTA TCCATTATAT CTGGGTTGCC GGCATTACCT ATGGCGAAAA	3000
40	TATAACCATT TTTAATGCCT ATATCAGCTT TAACCACTTT ATCGTAATCG ATAATAACGG	3060
	CATTAGAAAT GACAAGGTCT GCAACGTTCA CGTCATCACG TGTTACACGA GGATTTTGCG	3120
45	CCATACCGTC TCTAATAGAT TTACCACCAC CAAAAGTAGC TTCTTCACCA TAAACCGCAT	3180
	AGTCTTTTTT TATTTGAGCA AATAGATTCTG TATCACCTAA ACGAATGGAA TCTCCAACAG	3240
	TTGGACCGTA TAAGCTCGTA TATTGATTTT GCGTCATTTT AAAGCTCATG ATCTTTTTCC	3300
50	TCCTTTTTTA TTCACGTTTT CAGCACCGTT ATCTCCGAAT ACACCTGCAT ATTCATCATT	3360
	TTCATCAGTT GGGCGATAGA CACGTGACTC ATCGATAGGA CCATTGACCA TACCACGAAA	3420
55	ACCAAAAATT TTACGTTTGC CAGCATATTC AACTAATTGA ACTTCTTTTT TATCCCCAGG	3480

	TTCGAAATCT	AATGCTGCAT	TTGCTTCATA	AAAATGAAAA	TGTGAGCCCA	CTTGAATTGG	3600
5	TCGATCTCCT	GTATTTTCAA	CTTCGATAAC	TGTTTCAGGA	TGATGGTTAT	TAATTTCAAC	3660
	CTCTGTACTT	TTTGTAAATA	TTTCTCCTGG	TATCATTGA	CTGCCTCCTT	TAAACAATAG	3720
	GGTGATGTAC	TGTGATTAAC	TTAGTACCAT	CGGGGAACGT	AGCCTCGATT	TCGATATCTG	3780
10	TAATCATGTG	TTCGACACCA	TCCATGACAT	CTTCTTTGTT	TAGAATTTGT	CTACCATAAC	3840
	TCATTAACTC	TGCAACGGTC	TTACCATCGC	GTGCACCTTC	TAATAATTCA	TCGCTGATT	3900
	AAGCTAATGC	CTCAGGATGA	TTTAGTTTCA	AACCACGTGC	TTTACGACGA	CGTGCAACTT	3960
15	CCGCCGCCAC	TACAATCATT	AATTTGTCTT	GCTCTCGTTG	TGTAAAATGC	AAATTAAAAC	4020
	CCCCAATTTT	ATATTAGATA	CaATTTACAA	AATTTATATT	AATCCTAATT	GTTGTGATAA	4080
	ACAAGTAATA	TACAAAGTTC	AATGTGTAAT	TAGAAAATTA	TATTTTTTAGC	ATATCCGATA	4140
20	TTGAAGCAAA	CAATCTAATC	GAAAACAAAT	AGTGGAATAT	ATTTATGTAA	AAACCAAAT	4200
	AGTTTTTAAT	ATACTTTTC	ATAGAATAGT	AGTATATTAA	TGAGTAATGA	TTCAAAGGAA	4260
25	AGGTGAAAGA	TTTGAAGATA	ATAGATGTGC	TTTTGAAAAA	TATATCTCAG	GTTGTGTTAA	4320
	TTAGTAATAA	ATGGACAGGA	TTATTTATCT	TAATAGGATT	ATTTGTAGCC	GATTGGACAA	4380
	TTGGATTAGC	GGCTATTGTA	GGTAGCATCA	TCGCCTATAC	TTTTGCGCGT	TTATAAAATT	4440
30	ATAGTGAGGC	AGAGATTAAT	GATGGGTTAG	CTGGATTAA	TCCAGTGCTA	ACTGCCATTG	4500
	CGTTAACAAT	CTTTTLAGAT	AAGTCAGGAT	TAGATATTGT	TATAACAATG	ATAGCAACTT	4560
	TATTAACGTT	ACCAGTTGCT	GCTGCAGTGA	GAGAAGTTTT	AAGACCATAT	AAAGTTCCGA	4620
35	TGCTGACGAT	GCCTTTTGTC	ATTGTGACTT	GGTTTACAAT	TTTACTTTCA	GGACAGGTTA	4680
	AATTTGTAGA	TACATCGTTA	AAGTTAATGC	CTCAAAACAT	TGAAACGGTT	AATTTTAGCA	4740
	ACAATGATAG	AATaCATTTC	ATTCAGTCAT	TATTTGAAGG	ATTGAGTCAA	GTATTTATCG	4800
40	AAGCGAGTGT	AATTGGTGGC	GTATGTATTT	TAATCGGCAT	ATTGATAGCA	TCAAGAAAAG	4860
	CAACACTCTT	AGCTGTTATA	GCTAGTTTGT	TAAGCTTTAT	CATTGTAGCT	CTATTAGGTG	4920
45	GTAATTATGA	TGATATTAAT	CAGGGATTAT	TCGGTTATAA	CTTTGTATTA	ATGGCAATCG	4980
	CACTAGGATA	TACATTTAAA	ACAGCGATTA	ACCCTTATAT	TTGACTTTT	TTAGGTGTGT	5040
	TATTAACAGT	AGTGGTGCAA	CTAGGTACAA	CAACATTGCT	TGAACCGTTT	GGCTTACCTG	5100
50	CATTAACATT	GCCATTTATT	ATCGTGACAT	GGATTTTATT	ATTTGCTGGT	ATTAAACATG	5160
	ACAAAGTAGA	TGCTTGATAG	TTAAATCAAA	CCTAATATTG	TTTGAATATC	ACCTTAAACT	5220
55	ATACAGCGAA	TTGTATAGTT	TAAGGTGTAT	TTTTATGGAT	AAAATTAAGT	GCATACTTAA	5280

GTGTAAACT AGGAATAAAT AATTTATATT GTGTGTTGTG TGGGGTGAAT AATATGAATG 5400
 ATATGGATAA TTCCTTTTATA ATAACAACGG AAATTCAAAG AAAATGGATT GAAAAATTCA 5460
 5 AAGTAATTAG AGATACATTT AAGGCTAAAG CTGAATATAA TGATCAACAT AGCCAATTTC 5520
 CATATAAAAA TATTGAATGG TTAATTAAAG AAGGTTATGG AAAATTAACG TTACCAAAAG 5580
 CATATGGTGG TGAAGGTGCG ACCATAGAAG ACATGGTTAT TTTGCAATCA TTTTtagGCG 5640
 10 AACTTGATGG TGCCACAGCA TTATCTATTG GTTGGCATGT GAGTGTGCGTA GGACAAATTT 5700
 ATGAACAGAA ATTATGGTCT CAAGATATGT TGGAGCAATT TGCTGTTGAA ATTAATAATG 5760
 GTGCATTAGT TAATAGAGCA GTTAGTGAAG CTGAAATGGG TAGTCCAACA AGAGGGGGAA 5820
 15 GACCAAGTAC ACATGCTGTT AAAGCTGATG ATGGGTATAT TTTAAATGGT GTGAAGACAT 5880
 ATACATCAAT GAGTAAAGCA CTAACACATA TTATTGTTGC TGCTTATATA GAAGAATTAG 5940
 20 AAAGTGTGG TTTTCTTCTTA GTAGAC 5966

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 17310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CTGTGTCATC GCGAAATAGT TAGGGTCATT CATTAATCCT TTTGAACGTA TTTCATCAAA 60
 35 ATATAACAAT TTCATTAGTA AAGGGGACTT GTTCAAACCA GCTATAATAC AAAATAGACC 120
 TATAGTCACA CTGCTTATAA TATAAGAGGT AACGATCACT TTTTGTCTAT TACCTAACTT 180
 AAAGETGATC ATCCCTAAAT AGAAATAAAT GACTACAAAT GCATATTTAA CTGTAGATGC 240
 40 AAGAACTTCC TTAACCGTAA TAAATATCAA ATCATCAAAA AATaGCaAC AArGCGTAAT 300
 AATCATACGA TATGTATACA AAATAATGA_m AA_{ACT}GT_mAA AAATGATTG CCTTTAATAA 360
 ATGGTTAGCG AAAAACAGTA AATAAACTAA TATTAGTAAT GTGATAAAGT CAGCTATAGA 420
 45 AACATTCACA CCGGCAATAA CCGAAGATTG CTGAATAAAA ACCGCTAAAC CGATAAGTAA 480
 CAATGTTAGT AATTTACTAT TGTGTTGATT TTCCATTATA AACGTCTTCC ACTTCTTTAA 540
 50 TCATTTTCTC CTCAGTAAAA CATTCTAAAT AACGTTTCT AGATTGATTA CTCATTTTGA 600
 TGTAATCACT GTCTATTAAA TATTTTCCA GGACTTTAGC AATAGTTTCG GGTGGTTGT 660
 TCATCATACA TATACCATTA TCAGCTACTA ATTCTGAAAT ACCGCCAACA TGA_{CT}GGCTA 720

55

TTATTAAAAT AAACGTATCG TATTGTGATA ATAAATGACT CGCATTAAATG ACATTGCCCA 840
 AAAATGTGAC ATCATTTTCT AACCCAGCTT GTACAACTTG TTGCTGACAA TCATTTAATG 900
 5 TAGGTCCATC GCCTATAAAT GTAAATGCG CATGATTACT GTTATGTAAT TTCAATATCT 960
 CTATTGCCGC GATTAGATTT TGTGGCAATT TTGGATAAGC AAATCTTGCA ATCATAACAA 1020
 10 ATTGATGCTT TGTGGGGGCA TTAATCTGTA AATCTTGTTT ATTAGGCAAC ATTCCAACATA 1080
 CTTGCCCAAT ATTGTTATGT GATTGGCTTT TTAGCGTTTG CTTAACAGCG GGAACATCTG 1140
 CAATACCAT ATGTATTGTG GTTAATTTCA ATCGATTAA TCGATATTTT AACGCTAACT 1200
 15 GTTTATCGAA ATCTGAAACA CAAATAATGC TATCTGTAAT AAGTGACATT AATTTTTTCGA 1260
 TAACTAAATA TAGAAATTTT TTAGCTGGTT TAACACCCTC TGTAAAAGCC CATCCATGTG 1320
 CAGTAAAAAC TATACGTGTG TCTTTCGATT TCGAAATGAa CTtCGCAATT CGTCCGACCG 1380
 20 TtCCAGCTTT GGAAGAATGT AAATGGATAA CATCAGGTTT AATTTTCGAG AATAACTGTG 1440
 CTAACACTTT GACAGCTAAA ATATCTTGTT TAAAGTCAAT TGGACCTACT AAATGTTTGA 1500
 TAATAATTAC ATTAACCTTT GCATCTAGTT GTTCAATCAT TGGTCCATGA TTGCCTACAA 1560
 25 TGACATAAAC ATCATTGTGT ACGCAAAAAT GGTGCGGAG TTGAATGAGA TGTGTTTGTG 1620
 CACCACCATT GTCTGCTTTA GTAATACAAT ATATAATTTT CAACTGTTAC AAACCCCTTT 1680
 AATGCTATAC TTTCAATTTT TTAACATGGC TATCTCATCA GATGAATAGT ATTTATAGCC 1740
 30 ATGCAAATCA ATGATGGCAC ATATTTCTTA ATGCCATTG ATACTGTCTC AAGGGATTCC 1800
 TCGTTATACT GTAACAATTG GTCACAATCT TTAATAATATA ACTTTTATTT GAACTTATTA 1860
 35 AGTAAATTAA GACTACCTTG AGCCTTCCCC TGTAATAACA ACCATCAATG TTCTAATTGA 1920
 TATATATAGT TCCATCATT AACTACCTTT ATGTATATAT TTCATGTCAT ATTTTCACTT 1980
 TTGTTGCGGT GTTAAGTCAT ATCCACCTTG AATTTGCGCA AGTCCTGTTA ACCCTGGTGT 2040
 40 AACAAGACAT CTTTGCTCGA AACCTATCAC TTCTGAACTA AATAATTCTA CAAATTCCGG 2100
 ACGTTCCGGG CGTGGTCCAA TAAACTCAT TTCCCCTTTA ACAACATTAA TTAGTTGTGG 2160
 45 TAATTCATCA ATGCGTGTTT TACGAATAAA CTTCCCGACA TTTGTTATAC GATCATCATC 2220
 TTTATCAGCC CATTGCGCAC CGTTTTCTC TCGTTTTTGT CACATCGAAC GTAATTTGTA 2280
 TATTTTAATT AATTTACCCA TCTTCCCAAC TCTAACCTGA CTATAAATAG GGTTTCCTGG 2340
 50 CGAATCTATG ACGATAGCAA TGGCGAATAT AACCATAATC GGTAAAGTTA AAAATAATAA 2400
 AACAATGCTT AAAATTAAGT CAATCGCAGG TTTAATTGGG TAATAGCTTT TTCTCACTTC 2460
 TTCTAGTTTG TCTAATTTTC TTTGATAGGC ATAACCCTTA TTATTATGGA CAGCTTCAAT 2520
 55

	AATTAAAGTA ATCCTTTAAA CCTGTTTCTA CTGTATATTT AGGAACAAAT CCTAATGCCT	2640
	TTAAGTTAGA AATATCTGCA TAAGAATGCT TAATATCTCC TTTTCGTGCT TCTTTAAATT	2700
5	CATGCTCGAC TGATTTTCCA TATAATTCAC CAATAATACG ATAAACCTCT AATAAATTAG	2760
	TAAAAGTGCC TGTACCAATG TTATAACCGT GTCCAATTGC ATCTTTGTGT TCCATAATTA	2820
10	AGCGTACAGA TTGAACAACA TCATATACAT ATACAAAATC TCTAGTTTGC AGTCCGTCAC	2880
	CAAAAAATGT AAATGGCTTG TTATGCTCAA ATGAATCGAA CATCTTTGAA ATCACACCTG	2940
	AATATTGTGA CTTAGGATCC TGTCTTGGCC CAAATACATT AAAAAATTTA ACAACCGCTG	3000
15	TTGGTATGTT ATATAACGAA CAATAATTTA ATGTCGTCCG TTCGCCGTAA TATTTATCTA	3060
	TTGCATATGG TGATAATGGT AAGATTAATG ATTGATCACT TTTAGGCAAA TCAGGAAGAT	3120
	CACCATAAAC AGCTGCTGAC GAAGCAAAGA TAAAACGTTT TATATGATTA TTATATTTTT	3180
20	TAATGATTTT TAACAATCTT AATGTTGCTA CGACGTTTAT TTCTTGAGAT AAGATAGGTT	3240
	TCTCAACCGA CTCAGCAACA CTAAC TAATG CTGCTAAATG AATAACATAA TCAAATTGAT	3300
25	ATGTCTTCAT GATTTGTTCA ACTGCATCAT ATTCACGAAT ATCTAATTCA AACACATGAT	3360
	CGTCAGCCAA ACTTTTAATA TTTTCTCGTT TACCTGTTCT ATAGTTATCT AGAACATAAA	3420
	CATCATAATC TTGTTGTAAA TCATCTACTA AATGCGACCC AATAAAACCA GCCCCACCAG	3480
30	TTATCAAAAC TCTTTCCAAA TCTTCCACCT CATTTATACA TTAAAAATAT ATCATAAAAA	3540
	CATAAAGTAT TGTAAGCTTT TTATCGATAT TTTTATTTA TAAAAATAAA ATGAGATAAC	3600
	TTTGTTGAATT TTTATTGAGA TAAATTAGAT AGTGGTGTTF TTGTGATGTT TTATAATATC	3660
35	TTGGGTGTGT TAATACTAAT AATGCTTTCA ACTGATGCAT TAGACTGTGA CATCATAACT	3720
	CACCTAAGAA CTTGCTTAT TAATTTTCTA CCAATACACT CCCTTCTAAG TGCCTAAAA	3780
	AATCCTTACT GCTAAGTGAT TAACTTAAC AATAAGGATT TATTTATCAT TAGTGGATGA	3840
40	TTATTAACGG AATCTCATAC CACCATCTAC AATAATTGTT TGTCCAGTAA TGTAATCAGA	3900
	GTCTTTACCA GCTAAGAAGC TCACTACATT TGAAACATCT TCTGGTTGAG AACTCTGCC	3960
45	CAAAGCAATC TGACTTGTA AATTGTTCCCA ACCCATGCT TCAGGTTTAC CTGCTTCTTC	4020
	GGCTGTTGCC ACTGCGATAC TTTCCATCAT TGGTGTGTTGA ACGATACCAG GTGCGAATGC	4080
	ATTCACAGTA ATACCTTCAG ACGCTAAATC TTGTGCGGCT ACTTGTGTTA AACCTCGCAC	4140
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	TGTTGCATTG ATAATTTTAC CGCCATGATT GAATTTTTA AATTGTTTAT GTGCGGCTTG	4260
55	AATACCCCAT AGCACACCTG CAACGTTTAC GCCATATACT GTTTTAAACT GTTCTTCAGT	4320

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	GCCAAATTGC	GCGGCAGTTT	GTCTTAcTGC	GTTAAATACA	TCATCACGGT	TTGATACATC	4440
	TGCTTTGATA	GCAATAGCTT	TTGTACCATC	ACTTGATAAT	TTAAGTGCAG	CTGCTTTTGC	4500
5	CCCTTCTTCA	TTGAAATCAA	CAACTGCTAC	TTTGAAACCA	TCTTCCACTA	AACGTTCTGC	4560
	AATTTTAAAA	CCAATCCCTT	GTGcTCCGCC	AGTTACTAAT	GCTACTTTGT	TGTTTGTCTAT	4620
10	AAAGATCACT	CCTCAAATTT	CTTTCCTTTA	ATTACATTTT	ACTCCTCTTC	ATTTGAATAG	4680
	TACAACAAAG	GTAGCTCCAT	TTAACAAAAT	ATTCAGATAT	TTAAGGTATA	GTTAAACGCA	4740
	CTACCATTAG	TGATTGGCAA	TGCGTTTTAA	TGTCGTTTTA	AAAGTTCTTA	TGTTGAATAT	4800
15	TATTTTTTTA	AGTCTCTCGA	TTAGTTTGTG	ATCAATCTTT	TTTCGAGACA	TGGTCTTTTG	4860
	ATTCAATAGG	CGGTCCGTG	TTATCACTGA	CAACTTAGT	TGTAGCTTCA	TCTTTATGTA	4920
	TTTCTTCGTT	AAATCCTTCA	AGGTTTTTAG	TCGTGGGATT	TTTAACCTCA	GGATGTTCCA	4980
20	TCATGTCTTG	ACTATCAAGT	TCCTTTTTAC	ACGTGTCTTT	ATGTGATGCT	TGATTTGCGT	5040
	TCCCTTTACT	TTTTTGAATA	GTGGTAGTAT	CTGCTGCAGC	TACTAATTTT	TTTCTACCTA	5100
	AAATAGATAT	GGCTGAAACA	AACCAGAGTA	TTGCAGATAC	AAAGTTGCAT	AATACTAAAG	5160
25	CGATAATAGC	CAATACAATT	AATATGACAC	CTTTTGAAAT	CCTTTCTTTA	AATAAGTCAG	5220
	ATGCCAATAC	GATGACAGGT	ACGATTGAAA	GTATAATTAC	AAATATAGAA	ATTATTGCCG	5280
30	ATATAACTAT	TGTTACTATT	AAATAATCAG	CTCTGCTACC	TGATAATAAA	TAGAAAAGGC	5340
	CGAAAATTAG	TCCATAGCAA	ATTACAAACC	CACATAAAGT	TATAGCCATG	AGTACTATAT	5400
	AAGCTATTTG	AAAATATAAA	CCTATCTTTA	TGAATGATTT	TTCTACATTT	TTTTCCATGT	5460
35	CTATTCCCCA	TTTATTTAAA	ATTTATACTT	TACCTTAAAT	ATTCTCTTTA	TTCTTTAGTG	5520
	ATTTTATCTT	TAGATTCAAA	TTGATTCTCT	GTACTTTCAA	TATCAACTTT	TTCAATTTTCG	5580
	TCTGTTCGATT	CATCTTTTGA	GTATTTATTG	CAAATCAGCA	AAATACCACC	AATCAGCCAT	5640
40	AAAATTGACG	AAAGGAAATT	ATATAAACAC	AGTGCAATAA	TAGCATAAAC	AATAAAAAGT	5700
	GCACCTCCGA	TTACAGAGTA	ACTTTCCATA	TAAATCGCAG	TAAAGATGGT	TGGTAAAACA	5760
45	GTGAAAAGAG	CCAATATTAA	TCCTAATAAA	AAAATTGTTT	CGTAATCAGA	TCCTCCAGCA	5820
	ATATTAATAG	ATATCATCCT	AACAAAAACG	ACACTAAAAT	ATATTTGAGC	TACGATGCCT	5880
	ATCCAAATTG	CTATTTTTC	TATAATTGAG	CTCATACTCA	TTCCCCATTT	ATTTAAAATT	5940
50	TATACTTTAC	CTTAATATAC	CTTATTTTAT	TTAATTTTTA	TATGCAAAAT	ACAAAAATGG	6000
	AGAACTTCAA	TATTTATAAA	ATATCAAAAG	TTCTCCACAC	TATATTGTTT	TATTATATTT	6060
55	TCGCTATCAA	TACGCTAAAT	CATCATATTT	CCCTCAACAT	CACAGTAAAA	CTATTGCTCC	6120

	TTCCAATTGC GCAGTTGTTT AACATCATCA TCTTGTTTAA GTAATGCCAG TGGTACTTGA	6240
	AGATTAAGAC ATCGTCTCTGA AATATTAAAG CGTGTACACAC CTGCTGGCAC AGTTTCCCCT	6300
5	TTATGAACAA CCGCTTCAAT TTCCTTATAA CTCAATGGCT GATACTTCAT GAGTACATCT	6360
	TGTTGAGAAA GACAAGGATA TGTACCTTGT GCAATTCTCT CTACAGAACA ACAACCACTA	6420
10	TAACTTGCGA CAACCTTTTC CCATACTTGA AAATGTGCTT CGCCTAAATC TTTGTATAC	6480
	AAATATTGTT CTGTATCACC ATGACACATT GTAATAAATG GCGCTTCTTG TCTTGCTCA	6540
	GTAGTCCATG GCAAGCGATG TTCTTGTTGT AACGTTTCCC ACCACACACC AAATGGAAT	6600
15	TTATGTTGCC ATGTACTAAT TGAATATTGT GTTTCATGGA TTTCTTGAC TGGAACTTTC	6660
	TTACATCCTA ACGCTTTCAA ACTTGATATC CGATGCACAC CATCTATAAC CATATATCTA	6720
	CCATGTTGCA TCGCTGTCAC TAAAATAGGA TGACGTATAA AATCATCTGC TTCAATACTA	6780
20	CTTTTCGTTT TTTCCAATCT TAAAGGTTTC AATGTTTCGT GAAGATCAAT CTTATCTACT	6840
	GGTACCAATT TTAAATGTTT ATGAATATGA TTCAATAGTT ATTCATCCTC CTTTGTTTGT	6900
	GTTAAATAAA TAAATTCAGG ATGTGGATGG CTTAAGAAAT CGTGATGTGA AATAGACCAT	6960
25	CCGTATGCAC CTGCATATTT GAAAACAATA ACGTCGCCTG TACTGATTGC GTCTATCTGT	7020
	ACTTCTCTAG CAAAGACATC TTTCGGTGTA CATAATTGAC CGACTAACGT TGTGTCCTGT	7080
30	CTCGAAATG AAACTTTTTC AAATGAATAT GGATTGTCCT TATAGCGATA AATGTCAAAA	7140
	GGATGTTTAT GTTGCCAAGA TACCGGCAGT CTAAATTGTT GCGTACCTCC TCTTAATATG	7200
	GCATACCAAG CACCATGTAC TTCTTAATG TCTAGCACTT CTGTCACATA GTAACCAATA	7260
35	TGTGCCACAA TAAAGCGCCC ACATTCAAAG TTCAATGTCA CATCTCCAT TTCTTGCTCA	7320
	ACGATAAGTG TTTTAAAACG TTCTACAAAA TTATCCCAT CAAATTGGTT AGTTAAATCT	7380
	GCAATAGTTAA CGCCTATGCC ACCACCAAGA TTGATATGTT TGAGTGGAAT TCGATGTTT	7440
40	TCAGACCATG CCTTTGCTTT TTTAAAATAA AGTTTCACTA CATCGACATG TAAATTCGAG	7500
	TCTAAATTGT TAGAAATAGA ATGAAAATGA AATCCATCTA GATGAATCTT TGGCATTGCG	7560
	AGCGCAGcTT CAATGACATC ATCAACTTCG TCTTCAGAAA TACCAAATTG TGTTGGGCGT	7620
45	CCTGCCATAT GCAACGTTGC ATTGGGAAAT GGTCTGCTA AATTAACACG CAATAAAATG	7680
	TGTTGTGTCT TATCTTCATC TTCTAAGATG GCATTTAGCC GTTGTAATTC ATGCATACTT	7740
50	TCAACATGAA TACGCTGAAC ACCTTCACTT ACTGCATATC TTAGTTCCTC GTCTGTCTTA	7800
	CCAGGGCCAC CAAAAATAAT ATGATTTGCT GGTTTAAAAG CAAGACCTTT TGCTATTTCA	7860
55	CCTTGAGATG CAACCTCGAA TCCTTCAACA TACTGACTAA TTGTATCTAG GATTTTTCGT	7920

	TGTTGCAAAT GATGTTCCAG TCCGACTAAA TCATAGATAT AATGACAAAC TGGATGAGAT	8040
	TGTGCTTTTA ATTGTTCAAT AACAGGTTGA ACTATACGCA TTAGCCTTCA TCCCCTTTCT	8100
5	GTTTAGACGT CGCTAGAGAT GCACCTAAAT GGCGATATAT TTTCCGCGA TCATCACCTA	8160
	AAATAAATGT TTGTACACCT TGTGCCTGCC ATTTTGCAAT ATCTTCATCT TCACGTGGTA	8220
10	ATGCACAAAA ATGTTTACCA TGTGCATTCA CAACTTCAAA AATATGTTGA ACATGTGATG	8280
	TTACTTGATC ATCACGCGTT TGCCATGGTA TGCCAAGTGA CTGCGATAAA TCTGCGGCAC	8340
	CTTCGACTAT CATGTCTAAA CCTTCGACTT GTGCTATATC GTCAATGGCC ATAACCCCTT	8400
15	CAACATCTTC TATCATGGCA ATCACCATAA TATGCTCATT AGCCATCTCC ATTGCATCAA	8460
	GTAATGGTGT ACGTCCAAAT CTTGCCATGC GACCACCATT CAAACTTCTT AATCCTTGCG	8520
	GGTAATAACG ACTTAATTTT ACAATATGCT CAACTGTCTC ACGATCTTTA ACGTGTGGCA	8580
20	CAATAATACC TCTCGCACCC ATATCCAACA CTTTAATGAT ATCTCTATCT ATCACTGCAG	8640
	TGACACGTAC AATTGGTATA ATATGCGCTG CTTGAGCTGC ACGAATTAAA TGCGCTAGTG	8700
	TCTCATCATT AATCGCCACG TGTCTGTAT CAATCACAAC AAAGTCATAC CCGCTTGCTG	8760
25	CGATAACCTC GATCATCAAT GGGTCCGGTA TAGAATTAAA AATGCCATAA ACTGAATCAC	8820
	CATTGTTTAA TCTATGTTTC AGAGATAGTT GTTGTCATCAT TGATACCTCC TACACCTAAT	8880
30	GGATTTGTAA CATGATGAAT TCTTAACTCG GAGTCACTTA ATAATCGACG TGTCGTTAAC	8940
	TTTTCAACTT GAATCGTAGG TTCAAACAAA TCGAAATGTT GATAGTTATT CAACTCTGGA	9000
	AATGCTTCTT GATACGCCTC GATGATGCCT TTAACCCATT GCCATTGCAG CTCCTCATCG	9060
35	ATACCATATT GCTTTTCAAT AAATAAGATG ATTTCCGCGA TATTAATAAA GAAAAATGCA	9120
	TCATGTAAAA AGTCGCGTAC TAAACGTTCTG TCATCTGTTT CAATAAATGA ATTACTATTC	9180
	ACTTTTITAT GTGCTTCTGG CATTGGCTTT AATGTCAGGT GTGAAGCAGC TTCACTTAAA	9240
40	TGctCACGCT TAAAACGAAC ACCATCATGG AAATCTTTTA AGGCAATACG TGTAGGCCAA	9300
	CCATTTTCAT GAATGAGCAT CATATTTTGT GCATGCGATT CAAAGGCAAT ACCGTGATAA	9360
45	TAAAGCATAT GAATCATTGG ACGAATCGCT ACAGCTAAAA ATTGCTTTGT CCAAGCTTCA	9420
	GAACCATATT GTTTAATCCA ATTTTCAATG AATGGTACAC CATCCTTATC ACTTGATATA	9480
	AGTGCATTAA ATGGTATCGC ATCCTCTTCA TCGATTAAAC TATGATATAT ATTTTCACGC	9540
50	CATATAACAC CTAACGCACC ATAAACTTGA GTTTGTTTAT AAGGCGAAAG TTGTGTATTT	9600
	AAATAAGACT GTCCTAAGAC TTCCCCTAGA AAAACTGTCT TTAATTCATC TTTTAAATAC	9660
55	ATATCTTGTT GCTGTATCTG CTTTAACCAA TCCGTAATTT GCGCTGCATT TTCAATTGTA	9720

	TATTTTGTCTG	TGTCTATTGG	CGACATCGTA	CGAATCGATT	GTTGAGGGTG	ATATAGCTCA	9840
	TCACTTTCCC	CTAACCATAG	TACTGTGCCA	TTAAGCCTTT	CTTCAGCCAA	ATCAACTTGG	9900
5	ATGACATGTT	CAAACTGCCA	TGGGTGTACA	GGTATCATCT	CAACATCATT	TACATGTTTG	9960
	CCAGATGCTT	CAATTGTCTG	TACAAAATGT	TCATAAGTCT	TATCGCCAAC	TTGTTGACGT	10020
	AACATTTTCG	TAAC TACAAC	ATTTCTTGAT	ACCGTCGTTT	CTACTTTATC	TTTGTGCGATA	10080
10	GCTAACCCTT	GCAGTTTAAC	GTTTGGTACA	AAATCAGGAC	CAAATTTCAA	ATTATCACTC	10140
	AACGTAAATC	CTAAACGTGA	TTTGTAACCT	GGATGATACT	GATGCCCTTC	CATCGCATAA	10200
15	AATTCATAGT	CGTTAAATGT	CTCAGGTGTT	GCTGGTGGGT	TTGATTCTCG	ATACTGCATA	10260
	CTTTGCGTAT	CTTTTAATTC	TGTCTGTAAT	AACTCGACAA	TAAATTGTTT	TAGCTTTTCA	10320
	TCATTTTTAG	GAAATGTAAA	TACAACCTCT	CTCAATAATT	GTGTATAGTC	TGTTGTTGTA	10380
20	TCTGCCTCAT	CTCCTACGAC	ACGCTCAATT	GGTGATGTGA	TACGTATACG	ATCAAAGCTA	10440
	TGTGTCTTTT	CAGCAGTAAA	ACGATACTCT	GAATCATGTC	CTTCTATTGT	AAAATGACCG	10500
	ACACCGTCTT	GATATGACGC	TTTATACACA	ACAATATTCT	CATAAATAAG	TGATGATACC	10560
25	AGTTGGTGCA	TCACTCTAGT	CTTTACACGA	TTAAGAATTG	TTTGATTTCAC	AATACGATAC	10620
	CTCCTTGTTA	TGACAAATTG	GATTTGGTAT	ATGTGTATAA	ATAGGGTTTG	CACCACAATC	10680
30	ATTCAATTTA	CTCATCAAAT	TCGCTTTAGC	CGCAATGGTC	GGCGTTTGAT	ATAAATCTTC	10740
	TACACAGTCA	ACAAATACTG	CGTTATTTCG	GTATTCTTTT	TTCCAAGTCA	TAAGACGATG	10800
	CGCTACAAGT	TGCCATAACA	CAACTTCATT	TCTAGTCGCT	TTACCAATAG	TTGATACTAA	10860
35	ATGTCCTAAG	TGATTTACTA	CAACGTAATA	TTAAGACGA	TGCCATGCTT	CATCATGTGC	10920
	ATATACAACA	GGGCTTGATG	CTGCCACAAC	ATTTGGCACA	AGCTGTTTTT	CAGTAGCAAT	10980
	CGTTCTAGAT	AGACAAATGC	CTTCAAGATC	TCTGACAAAG	CATACGTCGG	GTATGCCATC	11040
40	TTTTAATTCA	ATTAATGTAT	TTTGTACATG	TGCTTCTAGA	CTAATGCCTG	TGTTACTAAA	11100
	CAGCTTTAAT	ATCGGCAATA	ATGTACGATT	CAAATAACAT	TCAAGCCATG	CTTCTGGTGC	11160
	TAAACCACTT	TGCTCAATCA	CTTGTGATAA	CTTAGACATC	GGTGAATCAG	GCATCGTTTC	11220
45	AAATAATGAC	GCCAATACAT	GAATATCTTT	ATCAGCATGG	TAATTCGGTA	TCCCTTCACG	11280
	AACAATCATG	GCACTATTTG	TTAATAAATC	CATTTTCAGG	TCAACTGTTT	GCCCTAATGG	11340
50	ATTTCGGTAA	AATGCACGAT	ATCCTTCTTC	AAACATCAAT	TTAAAATGGG	GTGTTTCAAC	11400
	CTCATCTTTG	ACTGATGCGA	TAAC TTGCGC	GGCATCAATT	GTCCGTTCAA	TCTGTTCAAG	11460
	GTCATTCGTA	CGTATAAAAT	TAGTGATTTT	AACGTGTATC	GGTAATTTTA	AATAAATGTT	11520

55

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	GCCAAGGTCT	TTTATTAAAC	CTTGTTCACT	ATATTGCATA	TACTGTGGAT	GCTGTGCGAA	11640
	CACATTGATT	TGATAAGGAT	GTGTTGGTAA	TAAAATAAAA	TCTTTGGGTA	TCTCTGATAT	11700
5	ATCTATGTCT	GCTAATTGAT	ACAACACTTT	CTCAACCTGA	TCTTCTTTAC	CTTCTACATA	11760
	GCGCGTGAGC	AGAACATCTT	GATGCACAGC	TAAATAATGC	AATTGGAATG	ATGTATGACA	11820
10	TTCGGGTGCA	TATTTCTCTA	AATCTGCTTC	TGAAAACCCA	CTTGCACTCT	TAGGAGTCGG	11880
	ATGAAATGGA	TGACCTAAGT	ATAAAGATTG	TTCTGAAACG	ATATAACGAT	CCTCTACGTA	11940
	GTCTATTGTG	TTACTTTGCA	AATAACGTGC	CGTGCGATGA	ATGCTATTAT	CGATGTCAGA	12000
15	CATAATTTGC	GCCATATGTT	GTTGCACTGC	CGTTTGATTG	TCTGCACTTT	GAGCCATATG	12060
	TTGCAAAATA	CGCGCAATTG	CTTCTTTATA	AGTTGTTATT	TTTTTACTTT	TTCCATCGAT	12120
	AAGCCATACC	TCTGGATGAT	ACATATGATG	CCCCATCGCA	GACCAATAGC	GAAATTCACC	12180
20	CGTTAAAGTT	TCGAGCTCTG	ATAATTGTAT	AGACCATTGA	TGATTTTGAG	GTGGTACTTG	12240
	ATATAAATTT	TCTTCTCTAA	AATATTCAAT	TAAAATGCGT	TCGATAGCCG	CATACGCTGC	12300
	ATGTTGTATT	AATCTTTTAT	TTTGCACTTT	TTTGTTTCAA	CTCCCATAAAT	TTCATTAATG	12360
25	TGTGATCGTT	GATTTGATTA	GTGATGGTTG	AACAAATTAA	AAATAAACTA	CTTACTGCAA	12420
	ATACTACGCC	CATAACGATA	AACGTAGTAG	CTGGTGTAGT	ATAACTTGTA	ATGGCAGCGC	12480
30	CACTaAGACT	GCCAATAATT	TGACCAACAA	CTAACATACT	GTTTCGTCGT	CCAACAAATG	12540
	TGCCTTTAAG	TTGTTGATGA	CACGCATTCA	CGACAACAAA	CATGACACTT	TGAATCAATG	12600
	CACTATATGT	TAATCCTTGA	AGTATTCTTG	CAGCCATTAA	AAACTCTATA	TTCGTCGCTA	12660
35	AACCTTGCAG	TATCGCACTA	CAACCACATG	CAATCGTGGC	AAATATATAT	ACTGATTTAA	12720
	CATATGATTT	ATCATTAAAG	CGTCCCCATA	AAGGCGCGCT	TAATATCGAA	GCCGTCCAAA	12780
	ATGCGGACTG	TAAAAATCCA	ATCACACTAC	GGTCATCTAT	CGCTGTATGA	TTCACTGATG	12840
40	AAGCAAGTGG	TGATAATGCA	GTTAGCATGC	CATACATAGC	AAAGTTTGCT	AAAACGCCAA	12900
	CGATAATAAA	TCGACATGTT	TGTTGTGTGC	ATAATAGACA	TTGAAATGAA	CGGCGAATAC	12960
45	CTTTATTAAT	ATTTGGTGTT	TGTGATTTTG	GCATATGTGT	CGTTTCAATC	AATTTTAATG	13020
	CACCGAAAAT	ACAGACAATA	AAAGTAATAA	CGGCAATACT	CATCAGTAAC	GCACTAAAAC	13080
	CTAATATCGA	AGCTGTAACA	CCGCCAATTA	ATGGCCCCAC	AAGAGACCCT	GCGCTGACTG	13140
50	AACCTTGCAG	TCTTCCTAAT	ACCTTTCCAC	GATCTTCAGC	TGGCGCCTCT	GCACTCGCAA	13200
	ACGCACTTGA	TGCATCAACA	ACACCACCAA	ATAGTCCCTG	CAATAACCTC	ACAAGTACAA	13260
55	ACTGTAATGG	TGTCGTACAC	AATGCCATTA	AAAATAAGCA	TACCGCCAAA	CCAAGTAACG	13320

	ctATCATCGT	CGTTACAGCT	GGAGCAGCAA	TCGCTATACC	ACTCCACAAC	TGTATTTCTA	13440
5	CGACTGATAG	ATTTTGTAGT	GATGCCATAT	AAATTGGCAA	TAATGGCACA	AGTACTGTCA	13500
	GTCCAGCAAT	CGCTATAAAC	TGACTGAGCC	ATAAAATGCG	AAAGTTACTG	CGCCATATAG	13560
	ACTGATTAAT	CATATGTCAC	CATTGGATTT	GGTACGGTAG	TTAAACCTGA	AGGCATACTA	13620
10	CCTCCACCAC	TATCACGTTG	ATATAGCAAT	GGTAATAAAA	TTTGTTTGAA	TGCCCACGTC	13680
	TGTTTATCAA	ATAAAATGTG	TCTGACAGCT	AGCTGATCAG	TTGTAACCCA	GGAAATAGTT	13740
	GCCACTTCAT	TTTTTAAAT	TTGTTTTAAC	AACGACATAA	GTTTCATGCTC	ACTTACACCA	13800
15	AATAAATCTT	GAATTGCATC	AATAATGGCA	TATAGATTTA	CCGATACAGC	TAATGTTTGA	13860
	AAATAAGCAA	AGAATGTTTC	CAAATCCTCA	TTAATTAGCG	TATTAGGTGT	ATCTTCTCTG	13920
	ACGACATACT	TCGGCAATGA	AAGCTGATGT	GCTGTTAGCC	ATGGTTTATA	AATTCTGACA	13980
20	GTATCATGAT	CACGTAACAC	GCATTTTTGT	ACACGTCCAT	CTTCAAATGA	CAACAATATA	14040
	TTTTGACCAT	GCAACTCTGG	TAATGCGCCG	TATTGCATAA	ATGATAGTGT	TACCTTTAAA	14100
25	AAGACTTGCG	CGATATCTTC	AAATAACGTC	ATGACATCAT	TTTAGAAAT	ATTATCTTTT	14160
	CCACAAATCA	TTTGATATAA	AGTGCGATCA	TTTGCCGCGA	GTGCTGCCAT	TGACACTAGC	14220
	TGTTGCGTAT	CATTTTTGGC	TAGCACTTCG	GGATACTTTC	TTAGCTGAAC	AGTTAGATGA	14280
30	CCTAATTGAT	CTTTGAAAAT	ATCATTATCT	TGACCCATAT	ATGACCACCA	AGCTGTTTCA	14340
	TCACAAACCA	TGACATACTT	AGCTAGTGCT	TCATCTTTTT	CTATAAGCTG	ACGTAATAAT	14400
	TGTTCTGCTT	GTTCTCCGTT	TTTCATGTAA	CGCGTAGGCG	TTAGCCTTAA	TGCGCCTAAT	14460
35	GACTGCATTG	CAAATGGTAC	TTTGACATGG	TTATACGGTG	CGCCAATATC	AATTAATGAA	14520
	CGCATACTTG	AAGACGACAG	ATAATCTCCA	AATTTTAAAG	GTAATAGTAC	AACCAACTTT	14580
	TCACTAATCT	CTTTCGCAAA	GACGTTCCGC	AGAATATGCT	GATATTGCCA	AGGATGTACC	14640
40	GGAAATAGTA	CATAGTCATC	TATTGATAAC	CCTTGATCAT	TTAACATGTC	TGTCGCTTGT	14700
	TCTTTTATAG	GTACTGTCAA	ATTTTCTAAT	TCATCGATAT	TTGCAGTATC	GCCATGAATC	14760
45	ATATGTGTCT	TTTTAACTGC	TGCAACCATT	AAAGGAAATG	ATTGATTTAA	TTCAGCTTGA	14820
	TACACTTGAT	AATCCGCTTC	TCTTAATCCT	CTTTTTTCTT	TAGCTAATGG	ATGAAATGGA	14880
	CGATCTTTTA	AACTTGCAAA	CTGCTCTGAC	ATCACAAAAG	GATGTGACGC	TAAATCTAAT	14940
50	TCTGATAATT	GTTTAGCAAG	CTGTGTGGCA	GCAGTAGTCA	GTCCTTCTTC	AACGCGAGCC	15000
	ACTTCCCAT	CATGACTTAG	ATCACAATTC	ATATTAGCAA	TTGTTTGCCA	AAATTCAGCT	15060
55	GCCGTTAAAG	GTTGCTTAGA	CACCCCTCCC	TCTATCGTAA	TTGTTGTGA	ACTTTCGTAA	15120

TATATCAAAA GCGTTTGTCC GTTTTCTTTA GTAATCTCAC TATTCGATAC AATTCCGGCT 15240
 ATATCTTCAA ATAATAATGC ATCAACTAAA TCTCTTAATA TTATCGCTTG TGCTGTATTG 15300
 5 ACTGCTGTAT GATTCTGCAA TGTTTCAGACA CCTCGCATTG TTAATATAGG TTCAATGTTG 15360
 TCCCAATATT TTGTTGTTGT GCCTGTTGAT AAATAAAATA AGCACTTGAA ATATCTTCGA 15420
 10 TAGCCATACC CATCGGATTA AGTAATATGA TCTCATCATC GTCTTCACGT CCTGGTATGT 15480
 CACCTGTCAC AAGTTGTCCT AGTTCAGCAT GAAGAGCTTC TTTGCTGAAT TTACCTTCTA 15540
 ACACCAATTG GTTAATAGTT TTCTTTTCTC GATTACATTG TGACCAGTCA TCTACTACGA 15600
 15 CTTTGTGAGC TTTAATAAAG ACTTCTTTAT GCACATCCAT GATAGAAATG TTGCTAATAA 15660
 ATGCACCCTT TTGTAACCAA TCATATTCAA TGTATGGTTG ATCCGTTACG GTACATGTAA 15720
 TGACTACTTC ACCATTTGAT ACTGCTTCTT TAGCATTTTC TGTCGCAATA AAATTAATTT 15780
 20 CCGGACGCTG TTGTTGCCAT CTATCAACAA AGCGTGCACA TGCTTCAGAG AATTGATCGT 15840
 AAACAAACAC GCGTTCAATA TGATCGAATT GCTCTAACAT ACTTTGTAAT TGCTTGTCTC 15900
 CGATTAGCCC GCATCCAATG ATTGTTAAGT CTTTAAATCC TTTTITAGCC AAATGCTTTG 15960
 25 CTGCAATCAC TGAAACTGCT GCAGTACGCA TACTACTAAT TAAACTTGCT TCCATAACTG 16020
 CAATTGGATA ATTCGTTTCT GGATCATTCA AAATAATGAC GCCACTTGCA CGCTCCATAT 16080
 30 TACGTTTCGA TGGATTGTGCG TGCTTACTAC CTATCCACTT AATACCTGAA ATTGCGTGTT 16140
 CACCACCGAT ATGACTTGGC ATTGCAATAA TTCGATCTGC GATGTGTCCA TTTTCAGGAT 16200
 CCTGTCTTAA ATACGGCTTA AGCGGTTGTA CAAAATCATT GTGCGCATGG GCTGTTAATG 16260
 35 CTTCTGTAA TGCCTCCACA TAACTTGTG AATGATTACC TCCCGTTGT TCAATATCTG 16320
 ATCTATTTAA ATACAACATC TCTCTatTca TTCTGaTTTA ACTCCTTGTC TTGATTTTAT 16380
 TTTTCTAAC CATGTATCTG AATAAACTAA ATCTAAGTAA CGATCGCCTC GATCTGGTAA 16440
 40 AATCGTGACA ATTGTTGCAC CTTCTTCAAT TGACGTTATC AACTGCTCAA TCGCTGCAAT 16500
 AATCGAACCT GTTGAAcCTC CGGCAAATAT GCCTTCATAA TCAATCAGTT TTCGACAGCC 16560
 45 CAAAGCAGAT TGATAATCAT CTACATGGAT CACTTGATTA ATTTCTGATC TATTCAATAT 16620
 TTCGGGTACA CGACTAGCAC CGATACCAGG TAATTCTCTA TTAATAGGTT TGTCACCAAA 16680
 AATGACTGAC CCTTTCGCAT CAACAGCAAC AATTGTGCG TTTGGATGCA CTTCTTTTAT 16740
 50 TTTTCTACTC ATACCCATAA TGCTACCTGT CGTGCTGACT GGCGCGACAA AATAATCTAT 16800
 AGGTTGCTTA ATTGTTTCAA CAATCTCTGT GCCTGCACCA TGATAATGGG ATTGCCAATT 16860
 TAACTCATTG GCATATTGAT TAATCCAATA TGCATCGTCA ATAGTGGCTA ACAGTTCTTG 16920
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TACATTGGCA CCATAACTTT TAATAATTTT CAAATTTGTT GGTGATATTT TAGGATCAAC 17040
 AACACACGTG AGTTTTAATC CCTTGATTTT AGCTATCATT GCCAACGCAA TGCCTAAATT 17100
 5 ACCAGAAGTA CTTTCAATTA AATGTGTATT CTCAGTGATT AAACCATGTT TAATACCATG 17160
 TTCAATGATG TACTTGGCAG GTCGATCTTT CATGCTGCCT CCAGGATTCA TATACTCTAA 17220
 10 CTTTGCAAAC ACTTCATGTT TCGGAAATAG TTGATGAAGT TGAACCATAG GTGTTTGCCC 17280
 TACAGAATCT AACAAATGAAT CGTGACATG 17310

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5423 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ATACTAGTAA GCGCATCGGT TATTGACATC GAATTCAACT TTAACAGTTT TCATGTTCCG 60
 25 TGATGTTTCa ATAGAATGTG TGTGTTGTAC TTGCGCATT ATATTTCCAC CTAAATTACT 120
 TAAGTTTCCT GTAATACTAG AAATGTCAGG TCGTTTAAT GTAGGTTGAA ATGCATCAAC 180
 30 TACTTTATCT GCAACATTAG AACATTACG GATACTTTA CTTGAATGAT TATCTATACC 240
 TTTAACGAAA CCTAACATTG AATACATACC AACATCCATG AATTCACGTG AAGGTGAGTG 300
 AATACCTAGC GCTCTTTTGG CTGCATTTAA AGCACCTTTT GCTACACTAG CTGCTTTTTC 360
 35 AGCTAAGTCT CTAGCCATAT TACCAATACC TCTCATCAA CCACGGATCA TATCAGCACC 420
 TGCTGATACA AAGTCATCCA CAAAGCTTTT AACTTTATTT ACTGCATTTG TCATACCTTG 480
 ACTAACTTTG TTTACAACAT TAACGAATCC TTGAACAACT CTATTAAACA rGTTAATTAG 540
 40 CGTACTtTGt ATAGTAGATA CCCaTnGCAT ACCTTTAGTG ACmATGAAGT TCCAAGCTTG 600
 AGACATTTTG TCTGATATAG TTGAAACAAC TTGTGTGAAT ATGCTTACAA CTTTATTCCA 660
 45 AATTGTCGTT AATATACCAG ATAAGAACT CCAAATCGTA TTCCATATAT TAGAAATAAA 720
 ACTCCATGCC GCTTGTAACG CAGTAGATAT AGCTGTAGTG ATAGCGTTCC AAACCTTAGT 780
 TGCCACAGTA ACTATAGTGT TCCACAACGT TTGTAAGAAC GTCCAAATAG CGTTCCAAAT 840
 50 TGTATTGCG ATAGTCATAA TTGTGGTAAA CACTGTAGTT ATTACAGTGA CTAACAAATT 900
 CCAAATCGTA GTAGCGATTG TAATTATCGT ATTCCAGATT GTACTTAAGA ACGTCCAAAT 960
 AGCTGTCCAT ATCGTCATAA CTATTGTCAT TATCGTCGTG AAAACAGTTG TAATGATTGT 1020
 55

	ATAAGCGACT ATTTGATTCC AAACAATCAT TATAAAATTG TAAACATTCTG ATACTGCTGT	1140
	AGTGATAGCT GTTAAAATAG CATTCCATAC AACC GAAGCT ACAGCTTTTA ATACATTCCA	1200
5	AACATTAACC ATAAACGTTT TTATCGCATT CCAAGCATT ATAATAAAGT TTCTGAATCC	1260
	TTCATTTTTA TTCCACAATA AAACGAATAT AGCTATTAAT GCAGCAATTA CACCAATTAC	1320
10	TATTGTTATT GGACCGCCTA AAATACCAA CACAGTTACT AGTCCTGTGA TAGCATTTCT	1380
	AATTAATCCA ATCTTACCGA ATAACAATTG GAATATAACT GATATAATTT TTAATGGTCC	1440
	TTTAAATAAC ATGAACGCAC CTTTAAAAAT TGTTAATCCC GCTCTTAATA AACC GAACTT	1500
15	ACTTACTAAT GCAATGTTT TACCTATTAA TCCGCCACCC ATAAAGTTAG ATACAGCAAG	1560
	AATAATCGGT ATTAAAAATC TAAATGCACC AACTAAAGTT ATAATGACAC CAACTAATTG	1620
	TGCTGTAGCT GGATGCGCCT CAAACAAGTT AGCTATCCAA CCAGTTATTG CAACTGCAAC	1680
20	GCGTAATACT GCACTAGCTA TAGGAGCCAT TGCTGTGCG AATGCATTA ATCCTCTTGC	1740
	GATGTTTCCA ATCAATTGCA TTATTAGTGG TCCATTGTG TGTATATAAC TGACAAAGTC	1800
25	TTTAAACCTT TGAGATTGTC CTACTTGTTT AGACCATTCC CTAAACTTAG CTGTCATTTG	1860
	TTCAAGAGAT TGGAATATGC CAGTTGATGA TCCGCTGAAT GCATTCATCA AATTGTTAAT	1920
	TCCAACGAAA ACATTTTTGA AAATATTACC AATGATAGGT AAGTTTGTTT TTGTGTATTC	1980
30	AATAAAACGA GTTATCGAAT TTCTCCAGC TGCATTTA GCCCAGTTAG AGAAAGATTG	2040
	ACCTAATCTA TCCAACCAAT CAGCCGACCA TTGAAACAGT GGTGCTAATT GCGTGAATAC	2100
	ATTGACTAAT CCGTCACCAA AACCACCTGC AGCACTTAAT AGCTTGTTAA ATACCGAAAC	2160
35	ACCCGTTGTA TTCATCATAT TAAAGAATCT TGAAGCTACA CTGCTATTTT CAGCCCATT	2220
	AAGCACGCTT TGAGACGCTT CTTCATTCC TCTTGAAATA CCACTAAAAA ACGGTTGTAA	2280
	GCTCTGCATT GCAGTTTTAA CAGTATTTAA ACCATTGCA AGAGTTGTGA AGATAGCGGA	2340
40	TTGATTTTGC TTTATAATAT CAGTCCATGC TGACTTTACG CCATCTAACG CTTTTTTGTA	2400
	TTGTTTGTGTT GCTGAGCTAG CTGTAAAGT GCCATCATT AGCATCTTTA TAGCGCTGAT	2460
45	AGCCATTGCG CCAAACGCTA CAAATCCTGC TCCCGCTATT GCTACGGCAC CACCTAAAGC	2520
	AAGTACACCA CCAGTTAACA CTTTGATAGC GTTTAATAGC GCAAATACTA CAGGTACTAC	2580
	GCTCGCTATT ACAGGTATTA AGATACTAAA AGATGATGTA AGTAATCCAC CAACCATATT	2640
50	AGAACCTACA GTACCGAACA CACGGAACAT ATTAGCTAAA TTCCCCATCT GTCTTTGAAA	2700
	ATTGTCATTT GCTTTTATTA TGTAGGCATA AGCTTTCTTT AAACCATTAG TATCGACATC	2760
55	TACCTTTGTT GTTTTTTTGT TCGGCAATGC GTCTAATGAT TTTTAAACG CATAAATAGT	2820

	AAGTTCTTCT	TTAGTACGTT	TGATTTTAGA	GTTAGCAACA	CCATTGTCCA	CGTCTATAAT	2940
	AGCTTTGGCT	TTAGACCTAT	TTAATGCTTC	GAGACTAGCT	TTAGATACTT	TTAACTACTCG	3000
5	ATTGAATTTA	CTGTTATCTG	CATTGACGTC	AATATTGACA	CGTTTCTTTT	CTAATTCTGA	3060
	TAATTTAGCT	TCTGTTTCAG	CGATATCTTT	AATCAACTTT	TGTTTTTGCA	ACTTAACTTC	3120
10	TGGTGTAAC	TCTTTAGAGT	TTAGTTTGTC	TAGTTCAAAA	TTCGATTCTA	GTACCTTTTG	3180
	TTGTAAATCT	TGTATACTAG	CATCTAATTT	AGCTTTTACA	TTTTTGTTAC	TAAAGGCATC	3240
	TAAAGACTTT	TTAGCAACTT	TGATAGTTTT	TTGTAAATTT	TTATCGTTAG	CGTTTAAATC	3300
15	AACATCTTTA	GTTTGATCTG	CTACTCGTTT	AAATCTTTGC	ACAGACTTAA	CCGCACTATC	3360
	AATTTGCCTT	TTGAATTTGG	CTACACTAGC	TTCAATAGTC	GCTTTAATTT	TATATTCCGT	3420
	CACATTAACA	CCTCTCTTTC	TATTGCTTAT	TAAATTCTGC	TATAACTTTA	AAGAATTCAT	3480
20	TATTTTGTGG	TTCGTATTCA	TCACGTTGCG	TACTAAATCT	TATATCTTTA	CCTTCGTTAA	3540
	GCCGTTGGAT	ATTTTCTTCA	TAAGGCAATA	CGTCGTTTGC	ATTGTTAAAA	ACATATTCCT	3600
	CTTTAGGTTT	ATTTTCTGTC	CCAACATTTT	TAGTAGCTGC	AGCATCACGA	ATAGCAAACG	3660
25	CAAGTTTGTA	ACGTTCTGAAT	TCTTGGGTTA	GCATTCATA	CTCTTTCGCA	TACATTTCGAT	3720
	AGTTATATTC	TGTTAATGTC	ATTTGCTCAA	TAACGTTCAA	ATCTGTAATA	CCAAGTGTG	3780
30	ACATACAAGT	TATAACGATT	CTGTCGTAAG	TTATTAGGcT	TCCGCTGGTT	TTTCTTCCGT	3840
	TTCCACTACT	TCGACTAGGT	TTCGGGTCAT	AGGTCGCTTT	CCCAAcTCCG	TTAAATATC	3900
	CGAACCGAAT	TCTTCTAGTC	CGATATTTTC	TGCGATTTCa	TCTAATGCTT	CATCAATGTT	3960
35	ATTAATAGTA	ATTGCTTGTT	TTTTTAAGTG	AGATGTAGCT	GCGATTAAAA	cTTCGCCAAT	4020
	CACAACCGGA	TTTCCACTTT	CTAAACCTAC	AGGCAACATT	GATACACCTT	GACCGATAGA	4080
	AGCTTgTTCA	ACTTTTAAAC	CTAATCGGTT	ATCGATTTC	CTTAAAAATT	TAAAACCAAA	4140
40	ACTTAATTCT	AATGACTTTC	CGTTAATTTT	TACATTTCATA	ACTTAAATC	TCCATTTCATA	4200
	ATTAATTTAA	ACAAAATAAA	mArGCTTAAC	GCCCTATTTT	TATACCTCTC	TTGGTGCAAC	4260
	CGGTGGTGAA	TCTACTTTAG	GTTGTGGAAT	TGCTGTTAAA	TCTTCGCCAG	TTAATGCATC	4320
45	TGCTTTTGTA	GTGTCGTGGA	ATCTGTATcC	AGTCGCCTTA	AGTTTCTTTG	TTACAGCCTC	4380
	AGGTAGTGTT	GCAATCCAC	GTTGGAAACG	ACCATTCACT	CCATATTCAT	ATTCATATTC	4440
50	ATCAATACCG	TTAGCTTCTG	CTTTTAATTC	AAATTTATTG	TGGAAACCTT	GGAAATATTT	4500
	CGCTTTAAAT	TTAGCGGAAT	CCCCATTTTT	GCCTGGTATT	CTACTTTCAA	CTTCCCAAGC	4560
	TTCATACAAT	ACGCGATCTA	CAACTGCATC	TTCAATTTCA	TCTGCAAAAT	CGTCACCATA	4620

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GTCCATTGTA TCCTCTGTAT CTGTATCAGC TTCATGTGAT AAGCCGTATT CAGTTAAAAA 4740
 AAGCATTTTA GTAGCATCTA CTTTTTCGCC AGCTTTTCTA AATAAAATAA TACGATCATT 4800
 5 ACTATTTTTC ATATTTGCCA TTCAATATTC CTCGGTTTTT TAAAATGTTT TGTAAGATAT 4860
 CGTTACTGAT GTGTGTAGCA ATTCTTGATT GGTAGTATCA TCAACTAACT GTGTGATGTT 4920
 10 AGTATCTTCT TCTTCAAAGT CATAATCGTT TGTTTTAACG CTAGGTGTTA AATCATCAAT 4980
 ACATCTTTTA ACAAGTCCGT CATGATGTCC TAAATCATCG CTTACACTCC AAATATCAAT 5040
 AACTAAATTC GTATCGCCAG AATAACTATC AAACGTGTAC TTACTTCTAT TTGACTCCGG 5100
 15 CATTTTTTATT ACAAAAAAAG GATACGGAAT CTCTTGTTGC ATCTCTTTAC GAGAAATAAC 5160
 AGGGAATCCA TATCCTTGTA GCGTTTCATA CGCTTTATTA TAAAGTTGTA AGTTCGGTGT 5220
 CATGCTTTTA TCTCCTATTC AAACAACGCT TTCAATTCTT CTACAGTTGA TTTCCTAATC 5280
 20 ACTTCGTATA CCGGCCACAT AAAAGGTTCA GCCTCCATGT ATCGAGTACC AAATTCTAAG 5340
 AAACCACTAT AAGCTGCGTG CGATGTGATA GTGTATTGCA AATCGCCAGT TTTTTTATAT 5400
 CTGATATTGC GTGATAAATT ACC 5423

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AAACGCAGAT GTTCAATTAG AACCAGTCTA TCGTATTAAG GAAGGTATTA AACAAAAGCA 60
 AATACGAGAC CAAATTAGAC AAGCGTTAAA TGATGTGACA ATTCATGAAT GGTAACTGA 120
 40 TGAAC TAAGA GAAAAATATA AATTAGAGAC CTTGGACTTT ACTTTGAACA CATTACATCA 180
 TCCTAAAAGT AAAGAGGATT TATTACGTGC TCGTAGAACC TATGCATTTA CTGAACTGTT 240
 45 TTTATTCGAA TTACGTATGC AATGGCTAAA TAGATTAGAA AAGTCATCTG ACGAAGCAAT 300
 TGAAATTGAT TATGACATAG ACCAAGTTAA ATCATTATTAT GATCGTTTAC CTTTGAAC 360
 AACTGAAGCA CAGAAATCCA GTGTTAATGA AATTTTTAGA GATTTAAAAG CACCAATACG 420
 50 TATGCATCGA TTACTTCAAG GTGATGTAGG TTCAGGAAAA ACAGTAGTTG CTGCAATTG 480
 TATGTATGCG TTAAAACTG CTGGTTATCA ATCAGCATTG ATGGTACCAA CTGAAATTTT 540
 AGCAGAGCAA CATGCTGAAA GTTTAATGGC TTTATTGGA GATTCTATGA ACGTTGCATT 600

	TACGATTGAT	TGTTTAATTG	GAACCCATGC	TTTGATTCAA	GATGATGTGA	TTTTCCATAA	720
	TGTTGGTTTA	GTAATTACAG	ATGAACAACA	TCGATTTGGT	GTGAATCAAC	GCCAGCTTTT	780
5	AAGAGAAAAA	GGTGCAATGA	CGAATGTGTT	ATTTATGACA	GCAACGCCGA	TACCAAGAAC	840
	ACTAGCAATA	TCAGTTTTTG	GTGAGATGGA	TGTGTCTTCA	ATTAAACAAT	TACCAAAAGG	900
10	TCGTAAACCT	ATCATTACTA	CTTGGGCAAA	GCATGAGCAA	TACGATAAAG	TTTTGATGCA	960
	AATGACCTCA	GAGTTGAAAA	AAGGTCGTCA	AGCATATGTC	ATTTGCCCCG	TAATAGAAAG	1020
	TTCTGAGCAT	CTCGAAGATG	TTCAAAATGT	TGTCGCATTG	TACGAGTCTT	TACAACAGTA	1080
15	TTATGGTGTT	TCCCGTGTAG	GGTTATTGCA	TGGTAAGTTA	TCTGCCGATG	AAAAAGATGA	1140
	GGTCATGCAA	AAGTTTAGTA	ATCATGAGAT	AAATGTTTTA	GTTTCTACTA	CTGTTGTTGA	1200
	AGTAGGTGTT	AATGTACCGA	ATGCAACTTT	TATGATGATT	TATGATGCGG	ATCGCTTTGG	1260
20	ATTATCAACT	TTACATCAGT	TACGCGGTCT	TGTAGGTAGA	AGTGACCAGC	AAAGTTACTG	1320
	TGTTTAAATT	GCATCCCCTA	AAACAGAAAC	AGGAATTGAA	AGAATGACAA	TTATGACACA	1380
25	AACAACGGAT	GGATTTGAAT	TGAGTGAACG	AGACTTAGAA	ATGCGTGGTC	CTGGAGATTT	1440
	CTTGGTGTT	AAACAAAGTG	GaTTGCCAGA	TTTCTTAGTT	GCCAATTTAG	TTGAAGATTA	1500
	TCGTATGTTA	GAAGTTGCTC	GTGATGAAGC	AGCTGAACCT	ATTCAATCTG	GCGTATTCTT	1560
30	TGAAAATACG	TATCAACATT	TACGTCATTT	TGTTGAAGAA	AATTTATTAC	ATCGTAGTTT	1620
	TGACTAATTG	CCATGCTGAT	TTGTCAATTT	GAGTGCAACa	CTTCGTTAAT	TGAGTGATAT	1680
	GACACTTGAA	CTATTTAAAT	GTAAAGTGGT	ATTTTAACAA	TTTATAAATT	TTGACTAATA	1740
35	TAATAGCTAA	ATATTACAGT	TATTTGTTGA	GTCGGTTAAA	TAGAAAGTGT	TATGATATGT	1800
	GAGGAATGTT	TAAGACTAGG	TACTAAAAAA	TGAGGGGTGA	GACGTTGAAA	CTAAAGAAAG	1860
	ATAAACGTA	AGAAGCAATC	AGACAACAAA	TTGATAGCAA	TCCCTTCATC	ACAGACCATG	1920
40	AACTAAGCGA	CTTATTTCAA	GTGAGTATAC	AAACAATTCT	TtAGaTCGC	ACTTATTTAA	1980
	ACATACCAGA	ATTAAGGAAG	CGTATTAAAT	TAGTTGCTGA	AAAGAATTAT	GACCAAATAA	2040
45	GTTCTATTGA	AGAACAAGAA	TTTATTGGTG	ATTTGATTCA	AGTCAATCCa	AATGTTAAAG	2100
	CGCAATCAAT	TTTAGATATT	ACATCGGATT	CTGTTTTTCA	TAAAACTGGA	ATTGCGCGTG	2160
	GTCATGTGCT	GTTTGCTCAG	GCAAATTCGT	TATGTGTTGC	GCTAATTAAG	CAACCAACAG	2220
50	TTTTAACTCA	TGAGAGTAGC	ATTCAATTTA	TTGAAAAAGT	AAAATTAAAT	GATACGGTAA	2280
	GAGCAGAAGC	ACGAGTTGTA	AATCAAACCT	CAAAACATTA	TTACGTCGAA	GTAAAGTCAT	2340
55	ATGTTAAACA	TACATTAGTT	TTCAAAGGAA	ATTTTAAAAT	GTTTTATGAT	AAGCGAGGAT	2400

	TTAGAAGCCG TACAAAAGGC TGTGAAGAC TTAAAGATC TAGAAATTAT ACTTTTCGGT	2520
	GACGAAAAAA AGTATAATCT GAACCATGAA CGAATCGAAT TTAGACATTG TTCTGAAAAG	2580
5	ATTGAAATGG AAGATGAGCC TGTTAGAGCG ATTAAACGTA AAAAAGATAG CTCAATGGTA	2640
	AAAATGGCTG AAGCTGTGAA ATCTGGTGAA GCAGATGGAT GTGTGTCAGC AGGTAATACT	2700
10	GGTGCTTTAA TGTCAGCTGG TTTATTCAAT GTTGACGTA TTAAAGGTGT AGCTAGACCG	2760
	GCTTTAGTAG TAACATTGCC AACGATTGAT GGAAAAGGTT TTGTCTTTTT AGACGTTGGT	2820
	GCAATGCTG ATGCTAAACC TGAACACTTA TTACAGTATG CGCAACTAGG GGATATTTAT	2880
15	GCTCAAAAAA TTAGAGGTAT TGATAATCCG AAAATCTCAT TATTAAATAT AGGAACCGAG	2940
	CCAGCTAAAG GTAATAGTTT AACGAAAAAA TCATATGAGT TATTAAATCA TGATCATTCA	3000
	TTGAATTTTG TTGGGAATAT TGAAGCGAAG ACATTAATGG ATGGCGATAC AGATGTTGTA	3060
20	GTTACCGATG GCTATACTGG GAACATGGTC CTTAAAAATT TAGAAGGTAC TGCAAAATCA	3120
	ATCGGTAAAA TGTAAAAGA TACGATTATG AGTAGTACTA AAAATAAATT AGCAGGTGCA	3180
25	ATATTGAAGA AAGATTTAGC TGAATTCGCT AAAAAGATGG ATTACTCAGA ATACGGTGGT	3240
	TCCGTATTAT TAGGATTGGA AGGTACTGTA GTTAAAGCAC ACGGTAGTTC AAATGCTAAA	3300
	GCTTTTTATT CTGCAATTAG ACAAGCGAAA ATCGCAGGAG AACAAAATAT TGTACAAACA	3360
30	ATGAAAGAGA CTGTAGGTGA AtCAAATGaG TaAAACAGCA ATTATTTTTTC CGGGACAAGG	3420
	TGCCCAAAAA GTTGGTATGG CGCAAGATTT GTTAAACAAC AATGATCAAG CAACTGAAAT	3480
	TTTAACCTCA GCAGCGAACA CATTAGACTT TGATATTTTA GAGACAATGT TTAGTGATGA	3540
35	AGAAGGTAAA TTGGGTGAAA CTGAAAACAC ACAACCAGCT TtATTGaCGC aTAGTTCGGC	3600
	ATTATTAGCA GCGCTAAAAA ATTTGAATCC TGATTTTACT ATGGGGCATA GTTTAGGTGA	3660
	ATATFCAAGT TTAGTTGCAG CTGACGTATT ATCATTTGAA GATGCAGTTA AAATTGTTAG	3720
40	AAAACGTGGT CAATTAATGG CGCAAGCATT TCCTACTGGT GTAGGAAGCA TGGCTGCAGT	3780
	ATTGGGATTA GATTTTGATA AAGTCGATGA AATTGTGAAG TCATTATCAT CTGATGACAA	3840
45	AATAATTGAA CCAGCAAACA TTAATTGCCC AGGTCAAATT GTTGTTTCAG GTCACAAAGC	3900
	TTTAATTGAT GAGCTAGTAG AAAAAGGTAA ATCATTAGGT GCAAAACGTG TCATGCCTTT	3960
	AGCAGTATCT GGACCATTCC ATTCATCGCT AATGAAAGTG ATTGAAGAAG ATTTTTCAAG	4020
50	TTACATTAAT CAATTTGAAT GGCGTGATGC TAAGTTTCCT GTAGTTCAAA ATGTAAATGC	4080
	GCAAGGTGAA ACTGACAAAG AAGTAATTAA ATCTAATATG GTCAAGCAAT TATATTCACC	4140
	AGTACAATTC ATTAACCTCA CAGAATGGCT AATAGACCAA GGTGTTGATC ATTTTATTGA	4200

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	AACATCAATT	CAAACCTTAG	AAGATGTGAA	AGGATGGAAT	GAAAATGACT	AAGAGTGCTT	4320
	TAGTAACAGG	TGCATCAAGA	GGAATTGGAC	GTAGTATTGC	GTTACAATTA	GCAGAAGAAG	4380
5	GATATAATGT	AGCAGTAAAC	TATGCAGGCA	GCAAAGAGAA	AGCTGAAGCA	GTAGTCGAAG	4440
	AAATCAAAGC	TAAAGGTGTT	GACAGTTTTG	CGATTCAAGC	AAATGTTGCC	GATGCTGATG	4500
10	AAGTTAAAGC	AATGATTAAA	GAAGTAGTTA	GCCAATTTGG	TTCTTTAGAT	GTTTTAGTAA	4560
	ATAATGCAGG	TATTACTCGC	GATAATTTAT	TAATGCGTAT	GAAAGAACAA	GAGTGGGATG	4620
	ATGTTATTGA	CACAACTTA	AAAGGTGTAT	TTAACTGTAT	CCAAAAAGCA	ACACCACAAA	4680
15	TGTTAAGACA	ACGTAGTGGT	GCTATCATCA	ATTTATCAAG	TGTTGTTGGA	GCAGTAGGTA	4740
	ATCCGGGACA	AGCAAATAT	GTTGCAACAA	AAGCAGGTGT	TATTGGTTTA	ACTAAATCTG	4800
	CGGCGCGTGA	ATTAGCATCT	CGTGGTATCA	CTGTAAATGC	AGTTGCACCT	GGTTTTATTG	4860
20	TTTCTGATAT	GACAGATGCT	TTAAGTGATG	AGCTTAAAGA	ACAAATGTTG	ACTCAAATTC	4920
	CGTTAGCACG	TTTTGGTCAA	GACACAGATA	TTGCTAATAC	AGTAGCGTTC	TTAGCATCAG	4980
	ACAAAGCAAA	ATATATTACA	GGTCAAACAA	TCCATGTAAA	TGGTGGAAATG	TACATGTAAAT	5040
25	ATATTTGAGC	TAAAGCTCAT	TGACGCAGTG	GTTGACTGGT	CATCCAATGG	AGAATTGTCT	5100
	GACCTAGTCA	ACTTTGCGGG	GGAAATTCTA	AGCAACCTAG	ATAAGGTTCC	AGAATTTCTC	5160
30	CCTAAGAAAC	ACTAATCAAT	aaATTGWTA	GTGTTTCTAA	AATTTCTACT	TGTTTTTIAG	5220
	AATTTAAAT	GGGAAAATAT	AGTAGTCTAT	GTATAGGCAT	TTTTAAAGGA	GGTGAATCGA	5280
	CGTGGAAT	TTGATAAAG	TAAAGATAT	CATCGTTGAC	CgTTTAGGTG	TAGACGCTGA	5340
35	TAAAGTAACT	GAAGATGCAT	CTTTCAAAGA	TGATTTAGGC	GCTGACTCAC	TTGATATCGC	5400
	TGAATTAGTA	ATGGAATTAG	AAGACGAGTT	TGGTACTGAA	ATTCCTGATG	AAGANGCTGA	5460
	AAAAETCAAC	ACTGTTGGTG	ATGCTGTTAA	ATTTATTAAC	AGTCTTGAAA	AATAATAAAT	5520
40	CTTACATCTG	GGTCGTCAGT	ATTGTCGACT	CAGTTTTTTT	CTTTAATTAT	CAATAGTTTT	5580
	AACGTAAAAT	TAAAGATGAT	TCAAGAGCAA	CACATAAAGG	AGATAAAATA	ATGTCTAAAC	5640
	AAAAGAAAAG	TGAGATAGTT	AATCGTTTTA	GAAAGCGCTT	TGATACTAAA	ATGACAGAGT	5700
45	TAGGCTTTAC	TTATCAAAAT	ATTGATTTAT	ACCAACAAGC	ATTTTCGCAT	TCGAGTTTTA	5760
	TTAATGATTT	TAATATGAAT	CGTTTAGACC	ATAATGAGCG	TTTAGAGTTT	TTGGGTGATG	5820
50	CGGTATTAGA	ATTGACGGTT	TCACGATATT	TATTTGATAa	ACATCCCAAC	TTGCCAGAAG	5880
	GGAATTTAAC	AAAAATGCGT	GCCaCTATTG	TATGTGAGCC	CtCACTkGTA	ATATTTGCGA	5940
55	ATAAAATTGG	ATTGAACGAA	ATGATTTTAC	TTGGTAAAGG	TGAAGAGAAA	ACAGGGGGAC	6000

ATCAAGGACT AGATATAGTT TGGAAATTTG CTGAGAAAGT CATTTTCCCA CATGTAGAAC 6120
 AAAATGAGTT ATTAGGCGTG GTAGATTTTA AAACACAATT CCAAGAATAT GTGCACCAGC 6180
 5 AAAATAAAGG TGATGTAACC TATAATTTAA TAAAAGAAGA GGGACCGGCA CATCATCGTC 6240
 TATTCAC TTC A 6251

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4920 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

20 ACCTACTGAA GTTGCTAATT TTTTGGAGCA ACTAAGCACT GAAATTGAAC GTCTTAAAGA 60
 AGATAAAAAA CAACTTGAAA AAGTAATCGA AGAGAGAGAT ACTAATATTA AGTCTTATCA 120
 AGACGTGgCA TCAATCTGTA AGTGaTGCTT TGATACAAGC TCAAAAAGCT GGTGAAGAAA 180
 25 CTAAGCAAGC TGCAGAGAAA CAAGCTGAAG CGATTATAGC TAAGGCAGAA GCGCAAgcTA 240
 ATcAAATGGT TGGTGACGCG GTAGAAAAAG CACGCCGTTT AGCATTCCAG ACTGAAGATA 300
 30 TGAAACGTCA ATCAAAAGTA TTTAGATCGC GTTTCGGTAT GTTAGTTGAA GCGCAATTAG 360
 ACTTATTAAA AAACGAAGAT TGGGATTACT TGTGTAATTA TGATTTAGAC GCTGAACAAG 420
 TGACGCTTGA AAATATTCAT CATTTGCATG AAAATGATTT AAAGCCAGAT GAAGTTGCAG 480
 35 CAAATGCACA AAATAATGCA TCAAATACAC CAGACAATAA TCAACAATCC AATGATTCAG 540
 AAACAATAA GAAGTAAGAA TTAAATAAAG ACAGACGCGT AATATACATT TAACTTTTCA 600
 CAGCGAATTA GGTAATGGTG AGAGCCTAGT AAAAGCATGT ATGTTATATC ACTGGCTTTT 660
 40 TAATATTTAA ATAATGTAAT GAGAGAACTC TAAGTTGAGT TAATAAGGGT GGTACCGCGA 720
 GCAATCGTCC CTTTAAATTT AACTTAGAGT TTTTAAATT TTTAAGGAGT GAAAAAATG 780
 45 GATTACAAAG AAACGTTATT AATGCCTAAA ACAGATTTC CAATGCGAGG TGGTTTACCA 840
 AACAAGGAAC CGCAAATTCA AGAAAAATGG GATGCAGAAG ATCAATACCA TAAAGCGTTA 900
 GAAAAAATA AAGGTAACGA AACATTCAAT TTACATGATG GCCCACCATA CGCGAATGGT 960
 50 AACTTACATA TGGGACATGC CTTGAACAAA ATTTTAAAAG ACTTTATTGT ACGTTATAAA 1020
 ACTATGCAAG GGTTCATATG ACCATACGTA CCAGGTTGGG ATACACATGG TTTACCAATT 1080
 GAACAAGCAT TAACGAAAAA AGGTGTTGAC CGAAAGAAAA TGTCAACAGC TGAATTCCGT 1140

	TTAGGTGTTT	GTGGTGACTT	TAATGATCCA	TATATTACAT	TAAAACCTGA	ATACGAAGCT	1260
	GCACAAATTC	GTTTTTTTGG	AGAAATGGCA	GATAAAGGTT	TAATTTATAA	AGGTAAAAAG	1320
5	CCAGTTTATT	GGTCTCCTTC	AAGTGAGTCT	TCATTAGCAG	AAGCAGAAAT	TGAATATCAC	1380
	GATAAACGTT	CAGCATCAAT	TTACGTTGCA	TTTGACGTTA	AAGATGACAA	AGGTGTCGTT	1440
10	GATGCAGATG	CTAAATTTAT	TATCTGGACA	ACAACGCCAT	GGACAATTCC	ATCAAATGTT	1500
	GCGATTACCG	TTCATCCTGA	ATTAAAAATAT	GGTCAATACA	ATGTAAATGG	cGAAAAATAT	1560
	ATTATTGCAG	AAGCCTTGTC	TGACGCTGTA	GCAGAAGCAC	TGGATTGGGA	TAAAGCATCA	1620
15	ATCAAATTAG	AAAAAGAATA	CACAGGTAAA	GAATTAGAGT	ATGTTGTAGC	ACAACATCCA	1680
	TTCTTAGACA	GAGAATCGTT	AGTGATTAAT	GGTGATCATG	TTACTACAGA	TGCTGGTACA	1740
	GgTTGTGTAC	ATACAGCACC	AGGTCACGGG	GAAGATGACT	ATATTGTTGG	TCAAAAATAT	1800
20	GAATTGCCAG	TAATTAGTCC	AATCGATGAT	AAAGGTGTAT	TTACTGAAGA	AGGCGGCCAA	1860
	TTTGAAGGGA	TGTTCTATGA	TAAAGCTAAT	AAAGCCGTTA	CTGATTTATT	AACAGAAAAA	1920
	GGTGCACTAT	TAAATTAGA	CTTTATTACA	CATAGCTATC	CACACGACTG	GAGAACAAAA	1980
25	AAACCTGTAA	TCTTCCGTGC	TACACCACAA	TGGTTTGCCT	CAATCAGTAA	AGTAAGACAA	2040
	GATATTTTAG	ATGCAATCGA	AAATACAAAC	TTCAAAGTAA	ATTGGGGTAA	AACACGTATT	2100
30	TACAATATGG	TTCGTGACCG	TGGCGAATGG	GTTATTTCTC	GTCAACGTGT	GTGGGGTGTA	2160
	CCGTTACCAG	TATTTTATGC	TGAAAATGGC	GAAATTATCA	TGACGAAAGA	AACAGTGAAT	2220
	CATGTTGCTG	ATTTATTTGC	AGAACACGGT	TCAAATATTT	GGTTTGAAAG	AGAAGCGAAA	2280
35	GACTTACTAC	CAGAAGGATT	TACACATCCA	GGCAGCCCTA	ACGGTACATT	TACTAAAGAA	2340
	ACAGACATTA	TGGACGTTTG	GTTTGATTCT	GGTTCATCAC	ACCGTGGCGT	GTTGGAAACA	2400
	AGACCGGAAT	TAAGTTTCCC	AGCGGATATG	TATTTAGAAG	GTAGTGACCA	ATATCGTGGT	2460
40	TGGTTCAACT	CTTCTATCAC	AACTTCAGTT	GCTACAAGAG	GAGTATCACC	TTATAAATTC	2520
	TTACTTTCTC	ATGGTTTTGT	TATGGACGGT	GAAGGTAAGA	AAATGAGTAA	ATCTTTAGGT	2580
45	AATGTGATTG	TACCTGACCA	AGTGGTTAAA	CAAAAAGGTG	CTGATATTGC	GAGACTTTGG	2640
	GTAAGTAGTA	CGGACTATTT	AGCTGATGTT	AGAATTTCTG	ATGAAATTTT	AAAACAAACA	2700
	TCTGATGTTT	ATCGTAAAT	CAGAAATACA	TTAAGATTTA	TGTTAGGTAA	CATTAACGAT	2760
50	TTCAATCCTG	ACACAGATAG	CATTCCTGAA	TCAGAGTTAT	TAGAAGTGGA	TCGTTACTTG	2820
	CTAAATCGTT	TACGTGAATT	TACTGCAAGT	ACGATTAAACA	ACTATGAAAA	CTTTGACTAC	2880
55	TTAAATATTT	ATCAAGAAGT	TCAAACTTTT	ATCAATGTTG	AGTTAAGTAA	TTTCTATTTG	2940

	CAAACAGTGT	TATATCAAAT	TTTAGTTGAT	ATGACGAAGT	TGTTAGCACC	AATCTTAGTG	3060
5	CATACAGCTG	AAGAAGTTTG	GTCTCATACA	CCACATGTTA	AAGAAGAAAG	TGTTCACTTA	3120
	GCAGACATGC	CTAAAGTTGT	AGAAGTAGAT	CAAGCTTTAT	TGGATAAATG	GCGTACATTT	3180
	ATGAATTTAC	GTGATGATGT	GAACCGTGCA	TTAGAACTG	CTCGTAATGA	AAAAGTTATT	3240
10	GGTAAATCAT	TAGAAGCTAA	AGTTACGATT	GCTAGTAACG	ATAAATTTAA	TGCATCTGAA	3300
	TTCTTAACTT	CATTTGATGC	ATTACATCAA	TTATTTATCG	TGTCACAAGT	TAAAGTTGTA	3360
	GATAAGTTAG	ACGATCAGGC	AACAGCTTAT	GAACATGGTG	ATATTGTCAT	CGAACATGCA	3420
15	GATGGTGAAA	AATGTGAAAG	ATGTTGGAAC	TATTCAGAGG	ATCTTGGTGC	TGTTGATGAA	3480
	TTGACGCATC	TATGTCCACG	ATGCCAACAA	GTTGTAAAT	CACTTGTATA	ATTGAAATTG	3540
	TATAAGTAC	TCATACAGAT	GATATAAATT	AAAGCTCTCT	TCATAATCAT	GTTGTAGTTT	3600
20	TTGTTGACAT	GATGAAGAGA	GTTTTTTTGT	GAATAAAAAA	ATGACCAAGT	TACCGGTCAT	3660
	ATATGTAAAA	AATGTGCGAT	TTACTAAAAT	AAAAATTATT	CAGGAATGGT	ACAAATTCTC	3720
25	TGAGGCATAT	AAATGCGTTA	TAGTTGCTAT	TCTCAATTAT	GTTGCGGATA	ATTTTAAGTA	3780
	AAAGTAAGCA	CAGATATTGA	ATTTGATAGG	AGTTAATTGA	ATGTATCATA	ACAGTAACGC	3840
	AAACTTTGTC	AATGGTATCA	CTTTAAATGT	GAGAGATAAG	AATGAATTAA	AGCCATTTTA	3900
30	TGAGGACATA	TTAGGATTAA	ATATTATAAA	TGAGACATTA	ACATCGATAC	AATATGAAGT	3960
	AGGTCAAAAT	AATCATGTCA	TTACACTTGT	TGAATTACAA	AATGGACGTG	AACCTTTAAT	4020
	GTCCGAAGCG	GGA CTGTTTC	ATATCGCAAT	TAAACTACCT	CAAATTAGTG	ATTTAGCTAA	4080
35	TTTACTAATT	CATTTAAGCG	AATATGATAT	TCCAGTTAAC	GGAGGTATAC	AGCCTGCTTC	4140
	GTTATCATT	TTTTTTGAAG	ACCCGGAAGG	AAACGGTTTT	AAATTTTATG	TTGATAAAGA	4200
	CGAAGCGCAA	TGGACGAGGC	AAAATAATTT	AGTAAAAATT	GATATTAGAC	CATTAAATGT	4260
40	ACCGAGATTA	GTGAGTCATG	CAACAAAATT	GTTATGGTTA	GGTATTCAG	ATGACGCTAT	4320
	TATAGGTGCA	TTGCATATTA	AGACAATTCA	TTTATCAGAG	GTAAAAGAGT	ACTACCTCGA	4380
45	TTATTTTGGA	TTAGAGCAAT	CGGCATATAT	GGATGATTAT	TCAATATTTT	TAGCATCGAA	4440
	TGGCTATTAT	CAACATTTGG	CCATGAATGA	TTGGGTATCA	GCAACGAAAC	GTGTAGAAAA	4500
	TTTTGATACG	TATGGATTAG	CAATTGTTGA	CTTTCATTAT	CCTGAAACAA	CACATTTAAA	4560
50	TTTACAAGGT	CCGGATGGTA	TCTATTATCG	CTTTAATCAT	ATCGAAGTTG	AAGATTAGTA	4620
	TATACTTTGA	ATGGACGAAC	CATATAATGA	ATCGTTTTTA	ATGATCTTTT	TATACAAGTT	4680
55	ATGAAGGAGG	CTGGGACATT	AAGTTCCTAG	GCAATGTAAA	AAGCTGATTT	CTATTAATTA	4740

TTTTCTTAT ATTAATTGCC ATTAAATACAA AACCTAGCTC TCGTTTAACT TTATTTATTC 4860
 CTCGAACTGA CATTGnGTG AACTCAAAAT nGCCTACTTn CTAAATTAC CAATATCTAT 4920

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TGGATTGCCA TTACATGGAC AAGATTTAAC TGAATCAATT ACACCATATG AAGGTGGTAT 60
 CGCTTTTGCA AGTAAACCAT TAATTGATGC TGATTTTATT GGTAAATCTG TATTAAAAGA 120
 TCAAAAAGAA AATGGTGCAC CAAGAAGAAC AGTGGGATTA GAATTACTTG AAAAAGGAAT 180
 TGCAAGAACT GGTATGAAG TTATGGATTT AGATGGAAAT ATTATTGGAG AAGTAACTTC 240
 AGGAACACAG TCTCCATCAT CAGGAAAATC AATTGCACTT GCAATGATAA AAAGAGATGA 300
 GTTTGAAATG GGTAGAGAGT TGCTTGTTC AAGTTCGTAAG CGTCAATTAA AAGCGAAAAT 360
 TGTTAAGAAA AATCAAATTG ATAAATAATT AAAAAGGGGT GTGCATTGTG AGTCATCGTT 420
 ATATACCTTT AACTGAAAAA GACAAGCAAG AAATGTTACA AACAATTGGT GCAAAATCTA 480
 TAGGAGAATT ATTCCGTGAT GTACCAAGTG ACATTTTATT AAATAGAGAT TTAAATATTG 540
 CTGAAGGCGA ACGGAGAACA ACGTACTTGA GAAGATTnAA TCGCATTGCA AGCAAGAGTA 600
 TCACTAGAGG AACGCGTACA TCGTTT 626

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

nGGAAGTGGT GTATATATTT GTAATGAGTG TATTGAATTA TGCTCAGAAA TCGTCGAAGA 60
 AGAATTAGCT CAAAACACTT CTGAAGCGAT GACAGAATTA CCTACTCCTA AAGAAATTAT 120
 GGATCATTTA AACGAATATG TTATTGGTCA AGAAAAAGCT AAAAAATCTT TAGCTGTAGC 180
 TGTTTATAAC CACTATAAGC GTATTCAACA ATTAGGACCA AAAGAAGATG ATGTTGAATT 240

AACCTTAGCC AAGACGTTGA ATGTACCATT TGCAATTGCA GATGCGACAA GTTTAACTGA 360
 AGCTGGTTAT GTAGGCGATG ATGTTGAAAA TATCTTGTTG AGATTAATTC AAGCAGCTGA 420
 5 CTTTGACATT GATAAAGCCG AAAAAGGTAT TATTTATGTA GATGAAATTG ATAAAATTGC 480
 ACGTAAATCT GAAAACACAT CTATAACACG TGACGTTTCA GGTGAAGGTG TTCAACAAGC 540
 10 ATTGCTTAAA ATCTTAGAAG GTACGACTGC AAGTGTTCGG CCACAAGGTG GACGCAAACA 600
 TCCAAACCAA GAAATGATTG AAATTGATAC AACAAATATC TTATTTATTC TTGGTGGTGC 660
 CTTTGATGGT ATTGAAGAAG TGATTAAGCG CCGTCTTGGT GAAAAAGTTA TTGGTTTCTC 720
 15 AAGCAATGAA GCTGATAAAT ATGACGAACA AGCATTATTA GCACAAATTC GCCCAGAAGA 780
 TTTGCAAGCC TATGGTTTGA TTCCTGAATT TATCGGACGT GTGCCAATTG TAGCTAATTT 840
 AGAAACATTA GATGTAAC TGTTGAAAA CATCTTAACG CAACCTAAAA ATGCACTTGT 900
 20 GAAACAATAT ACTAAAATGC TGGAAATTAGA TGATGTGGAT TTAGAGTTCA CTGAAGAAGC 960
 TTTATCAGCA ATTAGTGAAG AAGCAATTGA AAGAAAAACA GGTGCGCGTG GTTTACGTTT 1020
 AATCATAGAA GAATCGTTAA TCGATATTAT GTTTGATGTG CCTTCTAACG AAAATGTAAC 1080
 25 GAAGGTAGTT ATTACAGCAC AAACmATTAA TGAGaACTG AACCAG 1126

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4392 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATTGACTTCT TAGCAATnAA TaTGAGTGAA GAACGTACTG TTGAAGTACC AGTTCAATTA 60
 40 GTTGGTGAAG CAGTAGGCGC TAAAGAAGGC GGCCTAGTTG AACCAACCATT ATTCAACTTA 120
 GAAGTAACTG CTAATCCAGA CAATATTCCA GAAGCAATCG AAGTAGACAT TACTGAATTA 180
 45 AACATTAACG ACAGCTTAAC TGTGCTGAT GTTAAAGTAA CTGGCGACTT CAAAATCGAA 240
 AACGATTGAG CTGAATCAGT AGTAACAGTA GTTGCTCCAA CTGAAGAACC AACTGAAGAA 300
 GAAATCGAAG CTATGGAAGG CGAACAACAA ACTGAAGAAC CAGAAGTTGT TGGCGAAAGC 360
 50 AAAGAAGACG AAGAAAAAAC TGAAGAGTAA TTTAATCTG TTACATTAAA GTTTTATATAC 420
 TTTGTTTAAAC AAGCACTGTG CTTATTTTAA TATAAGCATG GTGCTTTTGT TGTATTATA 480
 AAGCTTAATT AAACTTTATT ACTTTGTACT AAAGTTTAAT TAATTTTAGT GAGTAAAAGA 540

	CTTACTAAGC TAAAGAATAA TGATAATTGA TGGCAATGGC GGAAAATGGA TGTTGTCATT	660
	ATAATAATAA ATGAAACAAT TATGTTGGAG GTAAACACGC ATGAAATGTA TTGTAGGTCT	720
5	AGGTAATATA GGTAAACGTT TTGAACTTAC AAGACATAAT ATCGGCTTTG AAGTCGTTGA	780
	TTATATTTTA GAGAAAAATA ATTTTTCATT AGATAAACAA AAGTTTAAAG GTGCATATAC	840
10	AATTGAACGA ATGAACGGCG ATAAAGTGTT ATTTATCGAA CCAATGACAA TGATGAATTT	900
	GTCAGGTGAA GCAATTGCAC CGATTATGGA TTATTACAAT GTTAATCCAG AAGATTTAAT	960
	TGCTCTATAT GATGATTTAG ATTTAGAACA AGGACAAGTT CGCTTAAGAC AAAAAGGAAG	1020
15	TGCGGGCGGT CACAATGGTA TGAAATCAAT TATTAAGATG CTTGGTACAG ACCAATTTAA	1080
	ACGTATTCGT ATTGGTGTGG GAAGACCAAC GAATGGTATG ACGGTACCTG ATTATGTTTT	1140
	ACAACGCTTT TCAAATGATG AAATGGTAAC GATGGAAAAA GTTATCGAAC ACGCAGCAGC	1200
20	CGCAATTGAA AAGTTTGTTG AAACATCACG ATTTGACCAT GTTATGAATG AATTTAATGG	1260
	TGAAGTGAAG TAATGACAAT ATTGACAACG CTTATAAAAG AAGATAATCA TTTTCAAGAC	1320
25	CTTAATCAGG TATTTGGACA AGCAAACACA CTAGTAACTG GTCTTTCCCC GTCAGCTAAA	1380
	GTGACGATGA TTGCTGAAAA ATATGCACAA AGTAATCAAC AGTTATTATT AATTACCAAT	1440
	AATTTATACC AAGCAGATAA ATTAGAAACA GATTTACTTC AATTTATAGA TGCTGAAGAA	1500
30	TTGTATAAGT ATCCTGTGCA AGATATTATG ACCGAAGAGT TTTCAACACA AAGCCCTCAA	1560
	CTGATGAGTG AACGTATTAG AACTTTAACT GCGTTAGCTC AAGGTAAGAA AGGGTTATTT	1620
	ATCGTTCCTT TAAATGGTTT GAAAAAGTGG TTAACTCCTG TTGAAATGTG GCAAATCAC	1680
35	CAAATGACAT TCGGTGTTGG TGAGGATATC GATGTGGACC AATTTCTTAA CAAATTAGTT	1740
	AATATGGGGT ACAAACGGGA ATCCGTGGTA TCGCATATTG GTGAATTCTC ATTGCGAGGA	1800
	GGTATTATCG ATATCTTTCC GCTAATTGGG GAACCAATCA GAATTGAGCT ATTTGATACC	1860
40	GAAATTGATT CTATTCGGGA TTTTGATGTT GAAACGCAGC GTTCCAAAGA TAATGTTGAA	1920
	GAAGTCGATA TCACAACGTC AAGTGATTAT ATCATTACTG AAGAAGTGAT CAGCCATCTT	1980
45	AAAGAAGAGT TAAAACTGC ATATGAAAAT ACAAGACCCA AAATAGATAA ATCAGTGC GC	2040
	AATGATTTGA AAGAAACGTA TGAAAGCTTT AAATTATTCTG AAAGTACATA CTTTGATCAT	2100
	CAAATACTAC GTCGCTTAGT AGCGTTTATG TATGAAACAC CTTGACAAT TATTGAGTAT	2160
50	TTCCAAAAAG ATGCAATCAT TGCAAGTTGAT GAATTTAATC GTATTAAAGA AACTGAAGAA	2220
	AGTTTAACAG TAGAGTCTGA TTCGTTTATT AGCAATATTA TTGAAAGTGG TAATGGATTT	2280
55	ATAGGACAAA GTTTTATAAA ATATGATGAT TTTGAAACAT TGATTGAAGG CTATCCTGTC	2340

	TCATGTAAAC CTGTCCAACA ATTTTATGGG CAATATGACA TTATGCGTTC TGAATTTCAA	2460
	CGATATGTTA ATCAAACTA TCATATCGTG GTTTTGGTCG AAACCGAAAC TAAAGTTGAA	2520
5	CGTATGCAAG CGATGTTAAG TGAAATGCAT ATTCCATCAA TAACAAAATT GCATCGCTCA	2580
	ATGTCATCGG GGCAAGCAGT GATTATTGAA GGCAGTTTAT CTGAAGGATT TGAACCTACCT	2640
10	GATATGGGAT TAGTTGTCAT TACTGAGCGT GAgcTTTTTA AATCAAAACA GAAAAAGCAA	2700
	CGAAAACGTA CGAAAGCTAT CTCAAATGCT GAAAAAATTA AGTCTTACCA AGATTTAAAT	2760
	GTGGGAGATT ATATTGTTCA TGTGCATCAT GGTGTTGGTA GATATTTAGG TGTGAGACG	2820
15	CTCGAAGTGG GGCAACGCA TCGTGATTAT ATTAAATTGC AATATAAAGG TACGGATCAA	2880
	CTATTTGTTC CAGTAGATCA AATGGATCAA GTTCAAAAAT ATGTAGCTTC GGAAGATAAG	2940
	ACGCCAAAAT TAAATAAACT CGGTGGCAGT GAATGGAAAA AAACAAAAGC TAAAGTTCAA	3000
20	CAAAGTGTTG AAGATATTGC TGAAGAGTTG ATTGATTTAT ATAAAGAAAG AGAAATGGCA	3060
	GAAGGTTATC AATATGGGGA AGACACAGCT GAGCAAACAA CATTTGAATT AGATTTTCCA	3120
25	TATGAACTTA CGCCTGACCA AGCTAAATCT ATCGATGAAA TTAAAGATGA CATGCAAAAA	3180
	TCGCGTCCAA TGGATCGCTT GCTATGTGGT GATGTTGGTT ATGGTAAAAC TGAAGTTGCA	3240
	GTGAGAGCAG CATTCAAAGC TGTAATGGAA GGAAAGCAGG TTGCATTTTT AGTTCCTACA	3300
30	ACTATTTTAG CTCAGCAACA TTATGAGACG TTAATTGAGC GTATGCAAGA TTTTCCTGTT	3360
	GAAATTCAAT TAATGAGTCG TTTTAGAACG CCTAAAGAGA TAAAACAAAC TAAGGAAGGA	3420
	CTTAAAACTG GATTTGTTGA CATAGTTGTT GGTACACACA AATTACTTAG TAAAGATATA	3480
35	CAGTATAAAG ATTTAGGGCT GTTGATTGTA GATGAAGAAC AACGATTTGG TGTACGCCAT	3540
	AAAGAGCGTA TTAAAACATT AAAACATAAT GTAGATGTAC TAACATTGAC TGCAACCCCA	3600
	ATAGCTAGAA CATTGCATAT GAGTATGCTA GGTGTGCGG ATTTGTCAGT GATTGAAACG	3660
40	CCGCCAGAAA ATCGTTTCCC AGTTCAAACA TATGTATTAG AACAGAACAT GAGTTTTATC	3720
	AAAGAAGCTT TAGAAAGAGA ACTATCCCGT GATGGCCAAG TGTTTTATCT TTATAATAAA	3780
45	GTGCAATCCA TTTATGAAA ACGAGAACAA CTCCAGATGT TAATGCCAGA TGCTAACATT	3840
	GCAAGTGCTC ATGGACAAAT GACAGAGCGC GATTTAGAAG AAACGATGTT AAGTTTTATC	3900
	AATAATgAAT ATGATATTTT AGTAACGACG ACGATTATTG AAACAGGTGT CGATGTCCCA	3960
50	AATGCAAATA CTTTGATCAT TGAAGATGCA GATCGCTTTG GATTGAGTCA GTTGATCAA	4020
	TTAAGAGGTC GTGTTGGTCG TTCAAGTCGT ATTGGTTATG CATACTTCTT ACATCCAGCA	4080
55	AATAAGGTAC TAACTGAGAC TGCAGAAGAT CGATTACAAG CGATTAAAGA ATTTACGGAG	4140

TTAGGTAAAC AACAGCACGG CTTTATTGAT ACAGTTGGAT TTGATTGTGA CAGTCAAATG 4260
 TTAGAAGAAG CTGTAAATGA AAAACGTGGT ATTAAGGAAC CAGAATCTGA GGTGCCAGAA 4320
 5 GTCGAAGTTG ATTTAAACTT GGATGCATAT TTGCCAACAG AATATATTGC AAATGAACAA 4380
 GCTAAAATTG AA 4392

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 729 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

20 TTTCTTTTGA ATCTATATCG AGGTGGTTGG TAGGTTTCATC TAAAATAAGT ACATTGTCAC 60
 GTTGCAACAT AAGTAGTGCT AGTTGTAAAC GTGCTTTTTT ACCACCAGAT AAATCATTAA 120
 25 TTATCTTTTT AACATCGTCT TGTACAAATA AGAAACGTCC AAGAACTGCT CGAATATCTT 180
 TTTCATTTCAT TAACGGATAT TGATCCCACA CATAATCTAA AATCGTTTTA CTAGATTTAA 240
 ATTCTGCTTG CTTTTGATCA TAATAACCAA TTTGTAAATT TGCGCCGAAA GTAATATCGC 300
 30 CATTAAAGCGC TTTTGTGTTGA TTAGCAATAG TTTTAATTAA GGTGCGATTTT CCAATACCAT 360
 TTGCCCCAAT GATTGCTATA TGATCGCCTT TAGAGACCTC TATACTCATA GGTTTGGTAA 420
 TTGCAGTTTG ATAACCGATT TCTAAATTTT TTACATGCAT GACGTCATTA CCTGTATTCC 480
 35 GGTCAAAGCC AAATTGAATA TTTGCACTTT TGGCATCTAA CATTGGTTTA TCAATGCGTT 540
 CCATTTTTTC TAAAATCTTA CGTCTACTTT TTGCCATTCC ACTTGTTGAA GCACGGGTAA 600
 TATTTTCTC AACAAAAGTT TCTAATCGTT TTATTTCTGC TTGTTGACTT TCATATTCTT 660
 40 GCATTGTTTT TTGATAATAT AAATCCCGTT GCTGTATAAA TTCCTCGTAA TTACCAACAT 720
 AGCGTTTGA 729

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13856 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

	TGATGTTTTCG ATACATTGTG TGCACCTTGT GGATATACTT TAAAGGTTGT GTCGTATGTT	120
	TCCTTACTAT CTTTAGCTTC AGATTCTGT GATTCAACCG TTTTATATTT TTCAAGTGCA	180
5	TGTCCTTCAA TATCAACTCG TGAATAATG CGATTCAACC ATGCTGGTAA ATACCACGAA	240
	CCTTTTCCAA ACAATTTCTG TAATGCAGGA ATTAACATCA TtCTGACTAC GAAGGCATCA	300
10	AAGAGTACAC CAAACGCTAA TGCCATACCC ATTGATTTAA TCATGACATC TTCTTGGAAT	360
	ACAAACGCAA AGAAGACACT AAACATAATT AATGCAGCTG CTACAATAAC AGGACCGCTT	420
	TCTTTCAATC CTACTTTGAT AGAATAATCA TTATCCCCTG TTTTACTATm yyCTTCATGr	480
15	ATTCGCGACA TAAGGAAGAC TTCATAATCC ATCGCTAATC CAAATAAGAT ACCTATAGTA	540
	ATAACCGGTA AAAATGCTAG CATTGGTCCT GTCGTTTCAA TACCRAACAG ACCTTTCATA	600
	AAACCATCTT GCATTACTAA TGTTGTAAAT CCTAATGTTG CCATTAATGA CAAGACGAAT	660
20	CCTAAACTG CTTTTAATGG TATTAGAATT GAACGGAAGA CAATCATTAA TAAGAAAAAT	720
	GCTAATACAA CAATGACTGA GGCAAATAAA GGTATCGCCT CATTTAACTT TTTAGACATA	780
	TCAATATTAA TGACACTTTG TCCCGAAATC TCCGTTTTGA ACCCATATTT ATCTTGTGCA	840
25	TCTTTATGAT AATCTCGTAA ATCATGCACT AAATCATTTG TACTCTCTGC ATTAGGCCCT	900
	TGCTTAGGTA TCACGACCAT CAAAGCGTAA TCATTATCTT TACTCATTTG TGGTGGCGTA	960
30	ACGATATCTA CATTTTTCTT ATCTTTAATA TCTTTATATA CAGACTGTAA ATCTTGTGTG	1020
	AATCCTTGTG GATCATCCTT TTTATCTTTC ACATTTATCA ACATCGGTAT TTGGCCATTA	1080
	AATCCTTCAC CAAATTTATC CGAGATAATA TCGTAAGCTT TTTTCTGTGT AGAATCTGCT	1140
35	GGTTTAACAC CGTCATCTGG AATACCAAGT CGCATATGAC TAACTGGTAT TGCAGCTGCT	1200
	ACTAATATGA TTAAACCTAG TAATACTGCC GCAAGTGCAT TTCCTGTAAT AAATTTAGAC	1260
	CATGGCGTAT CAATATCTTT TTTGAATTTA GACTGTAATT TATTCACTTT AATGCGTTtA	1320
40	TGGAAAATGC TTATTAATGC AGGTAATAAA GTTAAAGCGC TAAGTACTGC AAAACAACA	1380
	CTAATTGCCG AAGCAAATCC CATTACCGCT AAGAAGTCAA TGCCTACTAA TGATAAACCA	1440
45	CATACTGCAA TTACAACTGT TACACCAGCA AAAACAACCTG CACTACCTGC TGTTCCATT	1500
	GCAAGACCAA TGCCTTTAAT GTAATCTGTT TCAGTTTCA TAACTTGTCG ATATCTGAAT	1560
	AAAATAAATA ATGCATAATC GATACCAACT GCTAGTCCAA TCATTACGGC TAATGTCAGT	1620
50	GTGACATTTG GTATATCGAA TGCATAAGTT AACAACTGA TAATACCTAC ACCAGAGGCT	1680
	AGACCAATCA ATGCACTTAT AATTGGTAAT CCTGCAGCAA TGAAGTGAACC GAATGTGATT	1740
55	AACAGTACAA CAAATGCAAC AATAATACCA ACTAGTTCAG AATTACCGCC TACTTCTGTA	1800

	AAATGACTTT TAACATTATC TCTAGAGCCA TCTTTTAAAG ATGTTTGACT AACGTCATAT	1920
	GTGATATCTG CAAATGCAGT TGTTTTATCT TTACTAATTT GCTTATTTTC ATAAGGATCT	1980
5	GATATTTTAT CAATGTGCTT GTCATCTTTT TTAATATCAT CTAACGTTTT CTTAATATCT	2040
	TTAGTAATGT TCGGTTGCAC AATACCATCA TCTTTAGTCG TCTTAAAGAC AACACGTATT	2100
10	TGTGCCTTTT CACTATCTTG ATTAAAATGT TTTTCAATCT TTTTATTCGT ATCTAACGAC	2160
	TCTAATCCTG TCATTTTAAT ATCATGTGCA AATTTGCGTG CATTTGTAGC AAGTGGTATC	2220
	AATATTGCAG CTACAATCAC TATCCATGCA ATGACCGCGG ACCATTTATG TTTTGCGATG	2280
15	AATGTCCCCA TCTTATATAA AAATTTTGCC AAAGTATATT GCCTCCTTTT AAAATCAACG	2340
	TTATAGTTTA AATATACAGT GTAGATTATT GTTCGATTAT AGTATCTATC CCCGACCTCT	2400
	TAAAGAATCA ATTGGAAAAT TTTGTATATT AAACACACA CAAAGGAGAA ATGTAGATGA	2460
20	AAGAGACTGA TTTACGAGTT ATAAAGACAA AAAAAGCATT GTCGAGTAGC TTGCTACAAT	2520
	TGTTAGAACA GCAATTATTC CAAACGATTA CTGTCAATCA AATTTGCGAC AACGCACTCG	2580
25	TACACCGTAC AACATTTTAT AAACATTTT ATGATAAATA TGATCTTCTA GAGTACTTGT	2640
	TCAATCAATT GACTAAAGAC TACTTTGCTA GAGATATCAG TGACCGTCTT AATCATCCAT	2700
	TCCAAACGAT GAGTGATACG ATTAATAATA AAGAGGATTT GAGAGAAATC GCAGAATTCC	2760
30	AAGAAGAAGA CGCTGAATTT AATAAAGTAT TAAAAAATGT CTGCATTAAA ATTATGCATA	2820
	ACGATATCAA AAATAATAGA GACCGTATCG ATATTGACAG CGACATCCCA GATAATCTCA	2880
	TATTTTATAT TTATGACTCG TTGATTGAAG GTTTTATACA TTGGATAAAA GATGAAAAAA	2940
35	TTGATTGGCC TGGCGAAGAT ATTGATAACA TTTTCCATAG ATTAATCAAT ATTAAGATTA	3000
	AATAGTAGAT GAGAAACTCA TGAGCGTTAC CAACATTCAT AATAAAAACG ATAGTGKACA	3060
	CGTTAATGAA TTCGTGTA CTATCGTTT TTTATTTTTA TCGTGCTTAT CGCTATTAAA	3120
40	ACAACTGATA CACAACACAT AAACATGAA GAAAAAATA AATCCGCTAT CTAAATGACT	3180
	TTGACTCAGT TGTTTAAATG ACCAAATTGC TAATACAATT CCCATTATTA TTGAAATAAC	3240
45	GTATCTCACA TTCTTATACC TATAATCCTT TTCTAAAAAT ATGGTTGCTA TTACTTAATT	3300
	TTTAAAGTTA TAAATAAAAA GAGCCAACCG CAATGGATGG CCCTTGTTCA TTATGAAGCA	3360
	TTAGAACATT TCTGAAACAA CCTTTTGTTT TAAGAAGTGT AATAAGTAGT CTGGACTACC	3420
50	TGTTTTAGCG TCCGTACCTG ACATTTTGAA ACCACCAAAT GGATGGTATC CAACAACCTGC	3480
	TGAAGTACAG CCTCTGTAA GGTATAAATT GCCTACATCA AATTCGTTTA CCGCTTTAAT	3540
55	CCAATGCTCG CGATTATTTG TAATCACTGC ACCAGTTAAA CCGTAATCTG TATCATTTGC	3600

	TTCTTCTTGC ATGATTCTAT CTTTAGATTT AAGTCCTGAA ATGATTGTTG GTTCTACAAA	3720
	GTAACCTTTT GAATCATCAG TGCCGCCACC TTGTTCTAAT TTACCTTCTT CTTTACCAAT	3780
5	CTCAATATAA TTTTAAATCT TATCAAATTG TTTTATTATTA ATAAGTGGGC CCATATACGT	3840
	ATTGTCTACA GTATTGCCCA ACGTTAATTC TTTTGTTAAT TTGATTGATT TCTCTAATAC	3900
10	TTCGTCATAA ACGTCTTTAT GCACAATTGC ACGTGAACAT GCTGAACATT TTTGACCAGA	3960
	AAAACCAAAT GCTGACGTTA CAATAGCTTC TGCTGCCATA TCTGTATCAA TATTTTCATC	4020
	AACTACAATG GCATCTTTAC CACCCATTTT AGCGATAACA CGTTTCAAGA AGTTTGTACC	4080
15	TTCTTGAACA ACGGCACTAC GTTCATAAAT TCTAGTACCT GTCGCACGTG ATCCTGTAAA	4140
	TGTAACGAAA TCGGTATCTT TATGATCAAC TAAGTAATCA CCAATTTCTT TCGGATCACC	4200
	AGGAACAAAG TTAAGTACGC CTTTGGGTAA TCCTGCTTCT TCTAAAATTT CCATTAATTT	4260
20	ATAAGCGATA TAAGGTGTAT CCTCAGCAGG TTTCAATAAC ACTGTATTAC CTGCCACAAC	4320
	TGGTGCTAAA GTTGTACCAG CCATAATCGC AAACGGGAAG TTCCACGGCG GAATTGTAAC	4380
	ACCTGTACCA ATTGATTAT AGAAATATTT ATTGTGTTCA CCTTCACGAT CAAGTACTGG	4440
25	CTTACCTTGA GCCAAGTCCA TCATTGAACG TGCATAGTAT TCAATAAAAT CAATACCTTC	4500
	AGCTGCATCA CCAACTGCTT CATCCCATGG CTTACCTGCT TCATAAACCA TAATTGCTGC	4560
30	AATTTCCGCT TTTCGACGAC GAATAATTGC CGAAACACGT AACATAAGCT CTGCACGATC	4620
	ATTTGCTGAC CATGTTTTCC AAGATTTATA AGCTTCGTTT GCTGCTTTAA ACGCATCTTC	4680
	AACATCTTGT TTTGTTGCCT TTGATGCATT TGCAATCACT TGTGATGTGT CTGCAGGATT	4740
35	GATTGATTTA ATTTTGTGAT CTTTGAAAAT CTTCTCTCCA TTAATCACTA ATGGTATGTC	4800
	TTGACCTAAT TCTTTTCCA CGTCTTTCAA TGCTTTCTTA AACATATCCA CATTTTCTTG	4860
	GACTGAAAAA TCGTAACCAG GTTCATTTTT AAATTCTACT ACCATGTACA CTTACCCCTT	4920
40	ATAAATTTTG AAAGTGGTTT AACCCTTTGA TTTAATGATA TAACATCATT TAACTCATT	4980
	TTACTATGAT TAAGGTTAGT TTTGCAATCG CTTTCATTTT TATGTTTTAT CACTTATTCT	5040
45	CAAGTATTTT GAAATTGATT GGTTACTTTT TAAAATTTAT ATGGGTCGCA ACTGCTACTT	5100
	TATCGTTTCG TCATTTAATG TTTCGGATGG TAGGTCATTA TCAATTTTAC GAACGACTTT	5160
	ACAAGGGTTT CCAACCGCTA AGCTGTGTGG CGGAATATCT TTAGTGACAA CACTACCAGC	5220
50	ACCAATCACA CTGCCTTCTC CAATCGTCAC CCCTGGTAAC ACGGCTACAT GACCGCCAAA	5280
	CCAAGTATTA CTGCCAATAT GAATGGGTCC GGCTTTTCA AAACCTTCAT TTCTATGATG	5340
55	GAAATTAAGT GGATGTGTGG CTGTGTAGAA TCCACAATTA GGTCTATATA AAACATTATC	5400

	TCCTAGTTTA	ACGTTCCAAC	CATAATCTGT	ATCAAAAGGA	ATCGAAATAC	TTACATTGTC	5520
	TGTTGTTGTT	TGAAATAATT	GATCAATTAA	TTCCTTTCTT	TTATTTGTAG	CACTCGGTCT	5580
5	TGTATGATTT	AATTCAAAGC	AAATATCTTT	CGCTCGTGCA	CGTTCATTGA	TTAAGTATTG	5640
	ATCAAAGTTT	GCATCGTACC	ATTTTTCTGC	TAACATTTTT	TCTTTTTCAG	TCATTACACC	5700
10	TTTCAACTCC	TAATAACTTA	TTTACTTGTT	TAAAAGTTAA	TCAAATAAAC	CTTCGCCTAT	5760
	GCAACTAATA	CGCTATAACA	TTATGAAATC	ATGACCTTAT	CACCCITTATC	TATACAATTC	5820
	TCGCATCAAA	TACTGCTAAA	GTAGTAGATA	AATTCAATAC	TACAGACGCA	TTCAATTTTTT	5880
15	AATCTATTAA	CGTACAATGT	GAGTAAGAGA	AATATAAAGG	AGTATGATAG	CGATGAGAAT	5940
	ATTAATTACA	GGCACAGTTG	CTATCTTAAT	CATTCTAGGT	TTGGTCAAAA	CGATACAAGA	6000
	TTACGAAATG	ACAAACGACA	CGAGTCGTCA	GTTGTCAGAC	AACAAAGATG	ATGATAAAGT	6060
20	CATCCATCTT	AATAATTTTA	AAAATTTACA	TGCGAAAGAA	TTTAACCCAT	CTGATTTCTT	6120
	TTAAGTCACC	TAAGAATTGC	AAATCCAGAA	GTCAATTAAG	TTTTACCTTT	CATTCATACA	6180
25	TCCTTTAATA	TTAATTACGA	CTTCTTTTAT	ATAGATGCTA	AGTAGAGAGA	TTGTTGTGCA	6240
	ATGTTTGAC	GGCAATCTCT	CTTTTTCTTT	TTAAATTGG	TAAAAGTAAA	ACGCAACGAT	6300
	TGACTTATAT	ACCTATAGGG	GGTACATTAG	ACGTGTAACA	ATGAATCACA	GGGAGGCAAT	6360
30	AATGTGGCTA	ATACGAAAAA	AACAACATTA	GATATCACTG	GTATGACTTG	TGCCGCATGT	6420
	TCAAATCGTA	TCGAAAAGAA	ACTGAATAAA	CTTGATGACG	TTAATGCCCA	AGTGAATTTA	6480
	ACTACAGAGA	AAGCAACTGT	TGAGTATAAC	CCTGATCAAC	ATGATGTCCA	AGAATTTATT	6540
35	AATACGATT	AACATTTAGG	TTACGGTGTC	GCTGTAGAAA	CTGTGGAATT	AGACATTACA	6600
	GGTATGACTT	GTGCTGCATG	CTCAAGCCGT	ATTGAAAAAG	TGTTAAATAA	AATGGACGGC	6660
	GTTCAAAATG	CAACGGTCAA	TTTAACAACA	GAGCAAGCTA	AAGTTGACTA	TTATCCTGAA	6720
40	GAAACAGATG	CTGATAAACT	TGTCACTCGC	ATTCAAAAAT	TAGGTTATGA	CGCGTCTATT	6780
	AAAGATAACA	ATAAAGATCA	AACGTCACGC	AAAGCTGAAG	CGCTACAACA	TAAATTGATT	6840
45	AAGCTTATCA	TATCAGCAGT	ATTATCTTTA	CCACTATTAA	TGTTAATGTT	TGTACATCTT	6900
	TTCAATATGC	ATATACCAGC	ACTATTTACG	AATCCATGGT	TCCAATTTAT	TTAGCTACA	6960
	CCTGTACAAT	TTATTATTGG	ATGGCAATTT	TATGTAGGTG	CTTATAAAAA	CTTAAGAAAT	7020
50	GGTGGCGCCA	ATATGGATGT	ACTTGTTGCT	GTTGGTACAA	GTGCAGCATA	TTTTTACAGT	7080
	ATTTATGAAA	TGGTTCGTTG	GCTAAATGGC	TCAACAACGC	AACCGCATTT	ATACTTTGAA	7140
55	ACAAGCGCCG	TACTAATTAC	CTTAATCTTA	TTGCGTAAGT	ATTTAGAAGC	TAGAGCGAAG	7200

	TTAAAAGATG	GTAATGAAGT	GATGATTCTT	CTAAATGAAG	TACATGTTGG	AGATACACTT	7320
	ATCGTTAAAC	CAGGTGAAAA	GATACCTGTT	GATGGCAAAA	TTATTAAAGG	TATGACTGCC	7380
5	ATCGACGAAT	CTATGTTAAC	AGGTGAATCT	ATCCCTGTTG	AGAAGAATGT	TGATGATACT	7440
	GTAATTGGTT	CAACGATGAA	CAAAAACGGT	ACTATTACTA	TGACAGCAAC	AAAAGTTGGC	7500
	GGGGACACTG	CGTTGGCAAA	TATTATTAA	GTTGTCGAAG	AAGCTCAAAG	TTCTAAAGCG	7560
10	CCGATTCAAC	GATTGGCAGA	TATTATTTCT	GGTTATTTCT	TTCTATCGT	TGTTGGTATC	7620
	GCACTATTAA	CATTTATCGT	GTGGATTACT	TTAGTTACAC	CAGGTACATT	TGAACCTGCA	7680
15	CTTGTTGCGA	GTATTTCCGT	TCTCGTCATT	GCTTGTCAT	GCGCATTGGG	ACTTGCTACA	7740
	CCAACCTCTA	TTATGGTAGG	TACTGGTCGC	GCTGCTGAAA	ATGGTATTTT	ATTTAAAGGT	7800
	GGCGAGTTTG	TTGAACGCAC	ACATCAAATT	GATACCATCG	TTTTAGATAA	GACGGGTACC	7860
20	ATTACAAATG	GTCGTCCAGT	CGTGACAGAT	TATCATGGTG	ACAATCAAAC	GCTACAACATA	7920
	CTTGCTACTG	CTGAAAAAGA	TTCTGAACAC	CCATTGGCAG	AAGCCATTGT	CAATTATGCA	7980
	AAAGAAAAGC	AATTAATATT	AACTGAGACA	ACAACATTTA	AAGCAGTACC	TGGCCATGGT	8040
25	ATTGAAGCAA	CGATTGATCA	TCACCATATA	TTGGTTGGTA	ACCGTAAATT	AATGGCTGAC	8100
	AATGATATTA	GCTTGCCTAA	GCATATTTCT	GATGATTTAA	CACATTATGA	ACGAGATGGT	8160
30	AAAACCTGCTA	TGCTCATTGC	TGTTAATTAT	TCATTAAGTG	GTATCATCGC	AGTGGCAGAT	8220
	ACTGTCAAAG	ATCATGCCAA	AGATGCTATA	AAACAATTGC	ATGATATGGG	CATTGAAGTT	8280
	GCCATGTTAA	CTGGCGATAA	TAAAAACACT	GCTCAAGCCA	TTGCAAAACA	AGTAGGCATA	8340
35	GATACTGTTA	TTGCAGATAT	TTTACCAGAA	GAAAAAGCTG	CACAAATTGC	GAAACTACAG	8400
	CAACAAGGTA	AGAAGGTTGC	GATGGTTGGT	GACGGTGTA	ATGATGCACC	TGCATTAGTT	8460
	AAAGCTGATA	TCGGTATCGC	CATTGGTACA	GGTACAGAAG	TTGCCATTGA	AGCAGCTGAT	8520
40	ATTACTATTC	TTGGTGGCGA	CTTGATGCTT	ATTCCTAAAG	CCATTTATGC	AAGTAAAGCA	8580
	ACCATTCGTA	ATATTCGTCA	AAATCTATTT	TGGGCATTCT	GCTATAATAT	TGCCGGTATC	8640
45	CCTATAGCTG	CATTGGGCTT	ACTTGCGCCA	TGGGTTGCTG	GTGCTGCAAT	GGCACTAAGT	8700
	TCAGTAAGTG	TTGTCACAAA	CGCACTTAGA	TTGAAAAAGA	TGCGATTAGA	ACCACGCCGT	8760
	AAAGATGCCT	AGATTCCTTA	ATAATGAAGG	ATTCGTTGGT	GATTCTGAGA	TAGGCTACTG	8820
50	ATTGGCTCTA	TAATGTCGCG	GTTTAYAGTt	GGATCTTCGC	TCCAAC TGCA	TATATAGTnA	8880
	CACTTTTCGC	TTGGCGAATT	AGTGTATCTT	ACCTAATAGc	TCCGCCTATT	AGGTTCCATC	8940
55	ATTATTATAA	ATAATAAGTA	CACTACGGtT	TACAGTTGGA	TCTTCGCTCC	AACTGCATAA	9000

	GAAATTTTAA ATGTTGAAGG TATGAGCTGT GGTCACTGCA AAAGTGCTGT TGAATCTGCA	9120
	TTAAATAATA TTGACGGTGT CACTTCAGCT GACGTTAACC TTGAAAATGG TCAAGTAAGT	9180
5	GTTCAATATG ATGACAGTAA AGTTGCTGTA TCTCAAATGA AAGACGCAAT TGAAGATCAA	9240
	GGTTACGATG TCGTTTAATT AGGCAATATT CAACGTCATC AACACCAAAT TAAAAAATCG	9300
10	AACTGATGAG AATCCCAACA ATCCAAATTA TCTCATCAGT TCGATTTTTA ATTTACTCGT	9360
	AACCTAGTAT CTCCAGTCTG CAATACATCT AATGTTGCAT CTAATGCATC GACAATTAGA	9420
	TTTTTAACTG CAGCTTCAGT ATAAACGCA ATATGTGGTG TTAATATGAC ATCTTCCCTG	9480
15	TCAATCAACG ATTCTAACAA TGGATCGTTC AGTGTTTTGC CCCTTTGATC ACTTGGGAAA	9540
	AGTTTGCGTT CAAATTCATA CGTATCAAGT GCTGCACCTT TAATCACACC ATTGTCTAAT	9600
	GCGTCTAATA ACGCCTTAGT ATCTACTAAA GAACCTCTCG CACAATTGAC AAATACTGCG	9660
20	CCCTTTTTTAA AATGTTTTAA TAATTCAGCA TTAAATAGAT AATGATTATA TTTCGTTGCA	9720
	GGTACATGTA ATGTCACGAT ATCAGCACCT TCAACCGCTT CCTCAATCGT ATCTTTGTAA	9780
	TCGACATACG TTGCAATTTT AGCATTAGGA AACGGTCGTA TGCGACCACA TCACTTTGAT	9840
25	AACCATTGGC AAATATATCG GCTACTACAC GGCCAATTGCG ACCTGTACCA ATAACAGCTA	9900
	CTTTTAAATC TTTAATGGAT TTCGATAAAA TAGTAGGTTT CCATCTAAAA TCATGCTCCC	9960
30	GCACTTTCGT TTGAATTTGA TTAAATGAC GAACCACATT AATAGCCTGG TTCACAGCAA	10020
	ACTCCGCAAT TGAATTCGGA GAGTATGACG GCACATTTGA CACAATAAAG TTATACTTGT	10080
	TTGCTAACTC CAAATCATAT GTATCAAATC CAGCACTACG TTGTGCGATT TGTTTAATAC	10140
35	CTAGTTCATT TAATCGTTTA TAAACATGCT CTGATAATGG TATTTGTTGT GATAGCGATA	10200
	AGCCATCATA ACCAGCGACA CCTTCAACAT TGTCATCAGT TAATGCTTCT TTAGTAATAT	10260
	CTACCTCAAC ATGATGTTTC TCTGCCCACG CCTTGATATA AGGCATATCT TCATCACGTA	10320
40	CATCATGAT TTTAATTTTT GTCATTTTAA CATCACCTT AACTTTATTA TTCATATAAA	10380
	TATGCTAGTT CTGTTAATCT TATTGCAGCT TCGTCTAATT TCTGGTCATC TAACGCCAAT	10440
45	GAAATTCTCA CATAACGATT ACCATTCTCT CCAAATGGTT TCCCTGGAGC AACAAGTATT	10500
	GACTTCTCTT GCACTAAAAA TTGCTCAAAT TGCTCGCTGT CATAACCAGG CGGTGTTTCC	10560
	AACCATACAT ATATGCCACC TTTAGCATGA ACAAATGGCA AATCAGCTTT TGCAAGCATG	10620
50	GCTTCGAATC GGTACAGACG TGTTTTAAAT ACATTGCTTT GTTCTTCTAA AAAATCATCA	10680
	TAATGATTCA AAGCATATAT TGCGGCATCT TGTAATGCAC CAAACATCCC AGCATTGTG	10740
55	TGCGTTTGGT ACTTTTTCAA AGCTTGAATC ATATCTTTAT TACCAACTGC AAAACCGACT	10800

	CCATTTTCCG AAGCAAGTAT ACTAGGATTT TTAGCGTCGA AACCGAAAGC ACCATAAGCA	10920
	AAATCATGCA CGATTTTAGT GTCTGTACCT TTAAATTTAG CTATCGCTTC ATCAAAACT	10980
5	TCTTTCGTAG CTGTCGATCC AGTTGGATTA TTTGGATACG TTAAATAAAT GAGTTTTGTT	11040
	TTATCTATTA TTTGTGAATC AACTTTGGAC CAATCTGGCA AATAATGTGG CGGTTCTAAA	11100
10	TTAAGCGGGA CTGGCTTGCC ATCAGCTAAA AGTACACCTG CTAAATAATC CGTGTAGCCT	11160
	GGATCAGGTA GTAATACATA GTCTCCTGGA TTGATAACAC ATGTTGGTAC TGCCACTAAT	11220
	CCATTTTTTG TACCATATAA AATGCATACT TCATCTTCTT TATCTAACGT CACATTATAT	11280
15	TGTCTTTGAT AAAAATCTAC AATAGCTTGC TTGAACGCTT CTTTACCATG AAAAGCACCA	11340
	TATTTTTGAT TTTCAGGAAT AGTTAGTGCT TTTTGAAAAT GATCAATAAT ACCTTGTGGC	11400
	GTGGGCCCCAT CAGGGATTCC AACTGCCATA TTAATTAATG GCAATGGTCC ATGTTTCGATT	11460
20	TTACGTCCCA TCGTTTTCCC GAAATAACTA TCAGGGATAT TTGCTAATTT GTTAGAGATC	11520
	ATCAAATTCC TCCTCTATCA TTAAACATAG CCTGGGCGAC TATCATAATC CTAACAACCT	11580
	GTATCACTCT CATTTAGATG GTTACAATGA CATCGCCATT CACCGTTATG TTCAACAGAA	11640
25	CTTATGACAC ACGTTGTATT GAATGAATTT ATTTTCATTT TAGGTAGGTA TAATATTATT	11700
	GTCAATATTA GGAATTTTCA GATTAATATG CACTCAATCG TTATGATTTA ACTGTCATGC	11760
30	ATATCCGCAT GCGCAACCAG TTAGATATGC TTATATAAAG TATAACGCCC ATCAAGGTAC	11820
	GTATTCAAAC GTGAACCTTA ACAGGCGTCA TTCATTGTTA AATAAAACTT CTTAAGCACA	11880
	TACTTATTTT ACTATGCCTT TTACGTTCCC CTTATACTTT TCTCACATCT TTCTCTTAGA	11940
35	CTACTCCCTT ATACGCCCCG CTCAATATCT TTAATCATTT CATCTACAGT TATTTTCGCA	12000
	CTCGTTAAGA CAATAGGAAC GCCTGCACCT GGATGCGTAC TTGCACCTGC AAAATATAAA	12060
	TCTTTATAAT CTCGCGATAC ATTTTGTGGA CGATAATAAT TACTTTGCGC TAAAGTTGGC	12120
40	ATTAAACCGA ATGCCGAACC AAATTTTCGCA TGATACGTTT GCTCAAATC ATTTGGCGTA	12180
	AAGATTGTTT CTGAAACAAT ATGCGATTTT ATATCTTCAA ATACTTCAAT CGTTGCTAAT	12240
45	TTACGATAAA TAATTTCTTT TATTTGTTGC GTCAAAGCTT CATCTGACCA ATCGATTCCG	12300
	CTACCTGTTT TAAGTTCCGG CGTCGGCATT AGCACATAAA TACCAGTTTT GCCTTCTGGC	12360
	GCAAGTGATT TATCAGCGAC CGCTGGTACA TACACATAAA TAGAAGGATC ATATGATAAA	12420
50	CGTCCCTCAA ATATTTCTTC AATATTGCCT CTAAAGTCAT CTGAAAAAAT AACATTATGA	12480
	AGTCTCACTT GATCTGTCAC ATCAATATCT ATACCGATAT ACATTAAAAA TGCTGAACAA	12540
55	GAGTAATCTA AGTCTGCAAT TTTATGTGGT GGATACTTTT TAATAGGTGC AAAATCTGGC	12600

	ATGTCACCAT TCACTTTTAT CGCATCGGCC CGTTTGAATT TAGGATCAAT AATAATTTGC	12720
	TCAATTTTCAG CATTTAGTTC AATATTAACG CCTAAGTCTT TATTTAATTG CGCTAGCCCT	12780
5	TGAGCCATGC CATACTACC GCCTTTAATA AAATGCACAC CAAACATCAT TTCAATCATA	12840
	GGAATAATTG AATATAGTGA CGGGCCTCGT TTTGGATCAA TTCCTATGTA TAACGTTTGA	12900
10	AACGCTAAAA GCTTTTGTAT CTTTTCGTTA TCAATATAAT GTTCAATTAG CTGATCTGCA	12960
	TGATTTAACG TTTTAACTT AGCACCTTGC ACAAGTGACG TCATATTATA AAAGTCACTC	13020
	GGTTTGCAT ACGTTCCTTC TAAGAAATAG CGACGTGCAA TTTCATATTT TTTATAAACA	13080
15	TCCGTTAAAA AGGACATAAA ACCATGCGTT GAACCAGGTT CTATACTTTC TAGCATTGTC	13140
	TGTAATTCAG CTAAATCTGT AGGCACCGTT ATACGATCAT CGTGGTCAAA ATACACATCG	13200
	TAAATATAAC GTAATTGTCT CAATTCAATA TAATCTTCAT AATTTTTACC ACACGCTGTA	13260
20	AAAACATCTT TATAAACATC TGGCATCATG ACAATTGTGG GACCCATATC AAATGTAAAG	13320
	CCGTCTTTCT TTAATTGATT CATA CGCCCG CCTACATTAT TATTTTTTTC AAATATCGTC	13380
	ACTTCATGAC CTGAGAAGC AATACGGGCT GCCGCTGCTA ATCCTGTGAC ACCTGCACCA	13440
25	ATTACTGCAA TCCTCATTAT TCAACCACCT ATATTCTATG ATATTTACTA TTTATTTTAT	13500
	GAAACAACCT TGCCTTTTTC CTCTTATCCA CAAAAACACG TTCATGTAAT GTATAGTTAG	13560
30	CCTGTCTCAC TTCGTCCAGT ATTTCAATAT ATATACGTGC TGCTAATTCT ATGATTGGTT	13620
	GTGCTTCAAT ACTAAATACT TTGATTTGAT CCATAACATC TTGAAAATCT TTTTCTGCGA	13680
	TAGCTGCATA ATATTCCCAT AAGTCAATAT AATGATTATT AACACCATT TGGTACACTT	13740
35	CAGCAATATC AACTTCATAT TGCTTTAATC GTTGCTTACT AAAATATATC CGTTCATTGT	13800
	CAAATCTTC ACCGACATCT CTTAATATAT TAAAGGGATC CTCTAGAGTC GACCTG	13856

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10088 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

50	ATATATAAAT ATAGATTAAG TATATAGATT AATCAACTTT TTTGGAAGAG CAAATCACGC	60
	AATCAACAAA TAATATAAGA AGTTTTTGCG ATAGTTTAA AATAGCTGTA ATAGAATACT	120
	AAATGTGACA AACTTAGAAC TAATATCAAG TGTGATGTT TTGAATATAA AAATGCTAAT	180

	ATAATTGGTT AATATATGAG TAATTAGAAA ATAGACAAAG GATGACGATT TATGTATATC	300
	AATATGAAAAG ATTATGGGTT AACAGGCATA AACAAAAC TAAGATACTCG AGCAATACAA	360
5	CGTGC GTTAA ATCGTGGAAG ATGTAAACCA ACGACAGTTT ATATACCGAA AGGGACGTAT	420
	GATATTTGCA AACCATTAA C GATATATGGC AATACAACAC TTTTGTTAGA TAATGAACT	480
	ATTTTACGCC GATGTCATT C TGGTCCTTTA TTAAAAATG GTCGTCGCTT TGGTTTTTat	540
10	CGTGGTTATA ATGGACACAG TCATATTCAT ATTAAAGGCG GCAAGTTTGA TATGAATGGT	600
	GTATCGTATC CTTATAACAA TACAGCTATG TGCATTGGGC ATGCTGAAGA TATTCAATTA	660
15	ATAGGTGTGA CCATTAAGAA TG TAGTGAGT GGT CATGCAA TTGATGCTTG TGGGATTAA C	720
	GGACTCTATA TTAAAAGCTG TTCATTTGAA GGATTCATAG ACTATAGTGG CGAACcTTTT	780
	ATTCTGAAGC AATACAATTA GACATTCAAG TACCTGGTGC TTTTCCAAA TTCGGAACgA	840
20	CAGATGGTAC GATAACGAAA AATGTCATTA TCGAAGATTG TTATTTTGA CCTTCAGAAT	900
	TGCCCGAAAT GGAAGTTGG AATCGTGCTA TTGGCTCACA TGCAAGTAGA CATAATCGAT	960
	ACTATGAGAA TATTCATATT AGAAATAATA TATTTGAAGA TATACAAGGT TATGCATTAA	1020
25	CTCCCTTGaA GTATAAGAT GCTTTCATTA TTAATAATAA GTTTATTAA C TGTGaGGGTG	1080
	GCATTAGATA TTTAGGAGTT AGAGATGGTA AAAATGCAGC AGATGTGaTG ACAGGaAAAG	1140
30	ACTTAGGTT CCAAGCAGGC ATAAATATGA ATATAATTGG AAATGAATTT AAAGGATCAA	1200
	TGTCTAAAGA TCGGATACAT GTACGTAATT ATAATAATGT TAAACATAAA GATGTATTAA	1260
	TCGTG TGGAA TACATTCAAT AATTCGACTC AATCAATTCA TTTAGAAGAT ATTGATACAG	1320
35	TGTTTTTAAG TCCTGTTGAA GCGGGTATTC AAGTTACTAC AATCAATGTA GATGAAATAA	1380
	AAAAGTAAAA AGTTTCGCAT GACATTAGGA TTAAGAATAG TAGATAATTT TTGAAAGCGC	1440
	ATTGATAAAA CGGTATAAAT ATGCTATAAT AAACCCAATT ATCTGATAAA AGGGGTATTT	1500
40	TGACGGTAAT GATAATACAA GATAGACAAC TTTCTATACT CTAATATAGT GAGTTGAAGT	1560
	AGCTTGTCAT AATCATCATG AGGGGGAAAT TTATGGCTTA TTTCAATCAA CATCAATCAA	1620
45	TGATATCGAA AAGGTATTTA ACATTCCTTT CAAAATCAA GAAAAAGAAA CCGTTTAGTG	1680
	CGGGACAACT TATTGGACTA ATATTAGGTC CATTACTTTT CCTATTAA C TTATTATTCT	1740
	TTCATCCACA AGACTTACCT TGGAAAGGCG TCTATGTTTT AGCGATTACT TTATGGATTG	1800
50	CGACTTGGTG GATTACTGAA GCAATTCCTA TTGCAGCAAC GAGCTTATTA CCAATTGTGT	1860
	TATTACCATT AGGTCATATA CTTACACCAG AACAAGTATC ATCCGAATAT GGCAATGATA	1920
55	TTATCTTTTT GTTTT TAGGT GGATTATTT TGGCAATTGC AATGGAAAGA TGGAATTTAC	1980

	TTGGATTTCAT GGTGGCAACA GGATTCTTAT CTATGTTTGT ATCGAACACT GCAGCTGTAA	2100
	TGATTATGAT TCCGATTGGT TTAGCAATTA TTAAGGAAGC ACATGATTTA CAAGAAGCCA	2160
5	ATACGAATCA AACAAGTATT CAAAAGTTTG AAAAATCTCT AGTTTTAGCA ATTGGCTATG	2220
	CAGGTACGAT TGGTGGCTTG GGTACATTAA TCGGAACCCC GCCATTAATT ATTTTAAAAG	2280
10	GACAATACAT GCAACATTTT GGACATGAAA TTAGTTTTGC TAAATGGATG ATTGTAGGGA	2340
	TTCCAACGGT CATTGTTTTG TTAGGTATTA CTTGGCTCTA TTTAAGATAT GTTGCCTTTA	2400
	GACATGATTT GAAATATTTa CCTGGTGGTC AGACGTTAAT TAAACAAAAG TTAGACGAGC	2460
15	TTGGCAAAAT GAAGTATGAA GAAAAGGTAG TACAACTAT CTTTGTACTT GCTAGCTTAT	2520
	TATGGATTAC AAGAGAGTTT CTTCTGAAAA AATGGGAAGT TACGTCATCT GTTGCAGATG	2580
	GTACGATTGC TATTTTTATA TCAATATTAT TATTTATTAT TCCAGCTAAA AATACTGAAA	2640
20	AACATCGCCG TATCATTGAC TGGGAAGTTG CAAAAGAGCT CCCTTGGGGT GTATTAATTT	2700
	TATTTGGTGG CGGTTTAGCA TTAGCGAAAG GTATTTCTGA AAGTGGTTTA GCAAAATGGT	2760
	TAGGCGAACA GTTGAAATCA TTAAATGGTG TTAGTCCGAT TCTTATTGTA ATTGTCATAA	2820
25	CAATCTTTGT CTTATTTTTA ACTGAAGTGA CATCTAATAC TGCAACTGCA ACGATGATTT	2880
	TACCGATTTT AGCAACGTTG TCTGTTGCTG TTGGAGTGCA TCCATTACTA CTTATGGCAC	2940
30	CTGCAGCTAT GCGGGCTAAC TGTGCATACA TGTTACCAGT AGGGACACCA CCGAATGCAA	3000
	TTATCTTTGG TTCTGGTAAA ATATCTATCA AACAAATGGC ATCAGTAGGA TTCTGGGTAA	3060
	ACTTAATCAG TGCAATAATT ATTATTTTAG TCGTGTATTA TGTAATGCCT ATAGTTTTAG	3120
35	GTATTGATAT AAATCAACCA CTGCCATTGA AATAGTAATT GCAGATTAGA ACGAAAAATA	3180
	AAAGGTTACA TTAGCAATTG CTTGGACGAG TGOTAACGAA ACGTATACCG CAGCATCGTG	3240
	TAAEAACAAT ACAAACAAAA GAAAGTCAAC CAAGGATGGA TTCCTATTTT AATCCTTGGT	3300
40	TGACTCTTTA TTTTATTTAA ATTGTAGAAC CTAGAAAATA AAGTTTAATT AAAAGCACCA	3360
	ATCATTTCTA CTTTGAAATC TAAGGTTTCT AAAATAGCAA TGACTTTCTT TATATCGGTT	3420
	GTAATTGCAG AATCAGCCTG AACGAAAAAT CGATACATAC CTAATTGTGT TTTTAAAGGA	3480
45	CGAGACTCAA TCCAGGATAA ATTAATATTA AACAAAGCAA ATGTATTAAG CACACTTGCT	3540
	AACAACCCAG GTTTATCATG CATTGGTGTA ATTAAAAACA TCAATGATGT CGCATTTTGA	3600
50	TCAAATGCT GCTGATTTTT TATAACTAAA AAACGTGTCA CGTTATGTGG ATAGTCTTCA	3660
	ATATGTGTAT CAATAGGTGT AAAACCATAA GctTCGCCAC TACCTAAAGG TGCAATTGCT	3720
	GCAACGCCAT TTTCAATTTT AGTCAAACCT TGAATTGTAC TGTCGACATA ATCATAGTCA	3780

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TTTTAAATAT CAGAAATGGA ATCTGTTCCA TTACCATATA ATGCAAAGTT AATATCTAAA 3900
 CGTATTTTAC CGTGTGCAAA GACATCTTGC TGTGCAAGTG CATCTGCCAC AATGTTGATT 3960
 5 GTTCCTTCTA TAGAATTTTC AATAGGGACA ACACCAATCG ATGTGTCATC ATCTGCAACT 4020
 GCCTTGATGA CTTCAAATAA ATTTGACTTT GGTGAAAAG TTGCTTCATT TTCAGAAAAA 4080
 10 TACTGACGAC AAGCCAAATA TGAAAATGTA CCTTTAGGGC CTAAATAATA TAATTGCATA 4140
 TGCTACACCT CTACTAACTT AATGATGGAA AGGGCACTGG TTAGCATTTG ATTCTTTCTT 4200
 TTTATAGAAA AAGTTTGGAT CTTTACTGT ATTGTCATAT CCGTGATGAT AATTTGACGT 4260
 15 CAATGTTGGA GATAATGGCG GTGCTAGCCA AGACCATTTT CCGGTAACCTT GACGACCTTG 4320
 TTGTGCTTCG TTACGTTTGA ATAGTTCGAA TTGCTTTGCA GCGGTCAAAT GATCGACAAT 4380
 TGATACGCCCT TCTTTTTTAA AGGAATGATA CACAGCATAG TTCAATTCAA CAAGTGCTCG 4440
 20 ATCTTTATTA AATGAATTAT TTTTAAGTGT ATCAAATTCA AACGCATCTG CAACTTTTTTC 4500
 TAGTAAATTG TAACGGTAAT CATCAATAAA GTTACGTACG CCAATTTTCA TTACCATATA 4560
 CCAACCGTTA AAGGGTGCAG TTGGATATAC AATGCCACCG ATTTTAAAGT CCATATTGGA 4620
 25 AATGATAGGG ACTGCATACC ATTTTAAGTT CAATTTTCTT AATTTTGGAT AATGATTATG 4680
 TTCAATAGGT ACTTCTTTAA TTAATGAAGT AGGATATTCTG TAAAATTTAA CTGACTCATT 4740
 30 AGGTAATTGG TAAATCAGTG GTAACACGTC AAAATTAGTA CCTTTTCCTT TCCAACCTAA 4800
 GTGATTTGCT AAGCGTGTA CTTCTTTTTC AGCAGGATCA CCACAATTGT CATAGCCAGC 4860
 ATAGCGAATT AATTGATTGT TGAAAATTTT AGGTCCATCC TTTGGAGCAT ATATAGTAAT 4920
 35 ATACGGCTTT AATTTACCTT CATTTGTAGC CTGTGTAATA TGATAAGTAA TTGATGATAA 4980
 GAACGATGCT TCGTCAGTAA CATCTCTTGC ATCAATGACA TTTAACGAAT CCCAAAATAA 5040
 ACGACCAATG CAACGATTTG AATTACGCCA AGCCATTTTA GCACCATAAA TAAGTTCTTC 5100
 40 TTCTGTATGT GTATATGTCC CAGTTTCTTT TATTTCTAGT TCAATGTCAT GTAAACGTTT 5160
 ATTGATAATT TGCCTTTCAT AATGACACTC TTTATACATG TTTTCTATGA AAGCTTGAGC 5220
 CTCTTTAAAT AACATTAAAC ACACCTCGCT TTATATTATA GTCTACATTA TTAAAATACT 5280
 45 CTTAAAAATT ATGTATATGT CATTAAATTG TTGGTTGATT TTAATTAAAA GTATGGAAAT 5340
 TAAGGGGCTC TTATGTATAT AAAAAAATGA ATTATGATAA AATGTAAGAA AATATTTAGG 5400
 50 TCGATTGGAG AGATACAAGT GTACCAATTA GAAGACGACA GTTTAATGTT ACATAATGAC 5460
 TTATATCAAA TAAATATGGC TGAAAGTTAT TGGAATGATA ATATTCATGA AAAAATGGCT 5520
 GTATTTGATT TGTATTTTAG AAAAAATGCCA TTTAATAGTG GCTATGCTGT TTTTAATGGT 5580

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	TTAAAGTCTA TTGGCTACAA GGATGATTTT TTATCATATT TAAAAGATTT AAAATTCACA	5700
	GGCAGCATCC GTTCGATGCA AGAAGGCGAA TTATGCTTTG GTAACGAACC ATTGTTACGC	5760
5	GTAGAAGCAC CATTGATTCA AGCGCAATTA ATAGAAACAA TTTTATTAAA CATTGTAAAT	5820
	TTCCATACAT TAATTACAAC AAAGGCTAGC AGAATTCGTC AAATTGCATC AAATGATAAA	5880
10	TTAATGGAGT TTGGTACACG TCGTGCGCAA GAAATTGATG CAGCATTGTG GGGCGCTAGA	5940
	GCTGCTTACA TCGGGGGCTT TGATTCTACA AGTAATGTTA GGGCGGGGAA ATTATTTGGT	6000
	ATACCTGTGT CTGGTACACA TGCACATGCA TTTGTCCAAA CTTATGGAGA CGAATATGTT	6060
15	GCCTTCAAAA AATATGCTGA AAGACATAAA AATTGTGTGT TCCTAGTAGA TACATTCCAT	6120
	ACTTTAAAAT CTGGCGTGCC AAATGCAATA AAAGTTGCAA AAGAATTAGG TGACAAAATT	6180
	AACTTTGTAG GTATTCGATT AGATTCTGGA GATATCGCTT ATTTATCTAA AGAGGCAAGA	6240
20	CGTATGCTTG ATGAAGCAGG ATTTACTGAA ACTAAAATTA TCGCGTCTAA TGATTTGGAT	6300
	GAAGAAACGA TTACGAGTTT GAAAGCACAA GGTGCAAAAG TAGATTCTTG GGGCGTTGGT	6360
25	ACAAAGCTGA TTACAGGATA CGATCAACCA GCATTAGGTG CAGTATATAA ACTTGTAGCT	6420
	ATTGAAAATG AAGATGGTTC ATATAGTGAT CGTATTAAAT TATCAAATAA CGCTGAAAAG	6480
	GTTACGACGC CAGGTAAGAA AAATGTATAT CGCATTATAA ACAAGAAAAC AGGTAAGGCA	6540
30	GAAGGCGATT ATATTACTTT GGAAAATGAA AATCCATACG ATGAACAACC TTTAAAATTA	6600
	TTCCATCCAG TGCATACTTA TAAAATGAAA TTTATAAAAT CTTTCGAAGC CATTGATTTG	6660
	CATCATAATA TTTATGAAAA TGGTAAATTA GTATATCAAA TGCCAACAGA AGATGAATCA	6720
35	CGTGAATATT TAGCACTAGG ATTACAATCT ATTTGGGATG AAAATAAGCG TTTCTGAAT	6780
	CCACAAGAAT ATCCAGTCGA TTTAAGCAAG GCATGTTGGG ATAATAAACA TAAACGTATT	6840
	TTTGAAGTTG CGGAACACGT TAAGGAGATG GAAGAAGATA ATGAGTAAAT TACAAGACGT	6900
40	TATTGTACAA GAAATGAAAG TGAAAAAGCG TATCGATAGT GCTGAAGAAA TTATGGAATT	6960
	AAAGCAATTT ATAAAAAATT ATGTACAATC ACATTCATTT ATAAAATCTT TAGTGTTAGG	7020
45	TATTTCAGGA GGACAGGATT CTACATTAGT TGGAAAACTA GTACAAATGT CTGTTAACGA	7080
	ATTACGTGAA GAAGGCATTG ATTGTACGTT TATTGCAGTT AAATTACCTT ATGGAGTTCA	7140
	AAAAGATGCT GATGAAGTTG AGCAAGCTTT GCGATTCATT GAACCAGATG AAATAGTAAC	7200
50	AGTCAATATT AAGCCTGCAG TTGATCAAAG TGTGCAATCA TTAAGAAG CCGGTATTGT	7260
	TCTTACAGAT TTCAAAAAG GAAATGAAAA AGCGCGTGAA CGTATGAAAG TACAATTTTC	7320
55	AATTGCTTCA AACCGACAAG GTATTGTAGT AGGAACAGAT CATTCAGCTG AAAATATAAC	7380

	TAAACGACAA	GGTCGTCAAT	TATTAGCGTA	TCTTGGTGCG	CCAAAGGAAT	TATATGAAAA	7500
	AACGCCAACT	GCTGATTTAG	AAGATGATAA	ACCACAGCTT	CCAGATGAAG	ATGCATTAGG	7560
5	TGTAACCTTAT	GAGGCGATTG	ATAATTATTT	AGAAGGTAAG	CCAGTTACGC	CAGAAGAACA	7620
	AAAAGTAATT	GAAAATCATT	ATATACGAAA	TGCACACAAA	CGTGAACCTG	CATATACAAG	7680
10	ATACACGTGG	CCAAAATCCT	AATTTAATTT	TTTCTTCTAA	CGTGTGACTT	AAATTAAATA	7740
	TGAGTTAGAA	TTAATAACAT	TAAACCACAT	TCAGCTAGAC	TACTTCAGTG	TATAAATTGA	7800
	AAGTGTATGA	ACTAAAGTAA	GTATGTTTCAT	TTGAGAATAA	ATTTTTATTT	ATGACAAATT	7860
15	CGCTATTTAT	TTATGAGAGT	TTTCGTACTA	TATTATATTA	ATATGCATTC	ATTAAGGTTA	7920
	GGTTGAAGCA	GTTTGGTATT	TAAAGTGTA	TTGAAAGAGA	GTGGGGCGCC	TTATGTCATT	7980
	CGTAACAGAA	AATCCATGGT	TAATGGTACT	AACTATATTT	ATCAITTAACG	TTTGTTATGT	8040
20	AACGTTTTTA	ACGATGCGAA	CAATTTTAAC	GTTGAAAGGT	TATCGTTATA	TTGCTGCATC	8100
	AGTTAGTTTT	TTAGAAGTAT	TAGTTTATAT	CGTTGGTTTA	GGTTTGGTTA	TGTCTAATTT	8160
	AGACCATATT	CAAAATATTA	TTGCCTACGC	ATTTGGTTTT	TCAATAGGTA	TCATTGTTGG	8220
25	TATGAAAATA	GAAGAAAAAC	TGGCATTAGG	TTATACAGTT	GTAAATGTAA	CTTCAGCAGA	8280
	ATATGAGTTA	GATTTACCGA	ATGAACCTCG	AAATTTAGGA	TATGGCGTTA	CGCACTATGC	8340
30	TGCGTTTGGT	AGAGATGGTA	GTCGTATGGT	GATGCAAATT	TTAACACCAA	GAAAATATGA	8400
	ACGTAAATTG	ATGGATACGA	TAAAAAATTT	AGATCCGAAA	GCATTTATCA	TTGCGTATGA	8460
	ACCTCGAAAC	ATACATGGTG	GATTCTGGAC	TAAAGGCATT	CGTCGTAGAA	AGCTTAAAGA	8520
35	TTATGAACCA	GAAGAACTGG	AAaGTGTAGT	AGaACATGAA	aTTCmAAGTA	AaTGAGAAaTG	8580
	AAmCAATtGC	TGATTGTTTG	TCACGAATGA	AatGCAAGGG	TATATGCCGG	TAAAACGTAT	8640
	TGAAAAACCC	GTGTTTCAAG	AGCAAAAAGA	TGGCACGGTT	GAAGTATCAC	ATCAAGAAAT	8700
40	CGTTTTTGTA	GGTAAGAAAA	TCCAATAACA	TAATCCAATT	TAAATAAAGA	CTATTTGAAG	8760
	AGGAAAGGCT	ATTCAAAGTT	TGAGTAATTT	TACTTTGAAT	AGCCTATTTG	TTTATACATG	8820
	CAAGATGCTC	GATCCATATT	GTATGAGAAA	CCCCCAGCAA	GCTATATAAA	GCATATGCTG	8880
45	GGGGTTCTTA	ATATTTTAAA	AATTATTGTT	AGATTATATA	TATCGTCGCT	TTTTCTAAAA	8940
	CAATCTCATC	GCATGAAATT	TTTTCTTCCT	AGAGACCTTT	AATAAGATTA	ATAGTTTACT	9000
50	TAATCATATC	TAGATAGTCT	TATGACTTAT	GCTTAATGAA	AGTCATTCTA	GGAGAAGTTC	9060
	CCAAAGCTTC	TGTGTTCATA	ATTGTTAGTA	GTATTTTATT	ATCATTGTTG	ATAAATATTT	9120
	CAATAACAAT	TGAGCTATTA	TTTTTATTAT	ATAATGTGAG	TTGTTTGTGT	TCTGTATTTA	9180

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CATTAAATC TTGAGGATGC CATTCTCCCT CAATAATATT AAGATAATAC TTAGCCTCTG 9300
 AATTACATTT GAATTTATCA AATACTAAATA ATTCAATTTG TTCCATAATA TTATTTACCT 9360
 5 TTCTAAAATA CAAATTTTAA TAACCATAAA TAGATGAATA CCATCGATAA TGGTCGCCAT 9420
 TGGATACTGG AATAACATTG TTTTGTAGCAT CTTGAGTCAT AAAACCATTA TCCCATGGAT 9480
 10 TCCATATAAT TATAACCTCT TGTCCATTAT CTAATTTAGC GTTCCCAACA ACTGCCATGG 9540
 CATGCCCTGC GTGCATACCA TTTCTTGATT CTAATCTACT ACCTAAAACA GCAATTCCTT 9600
 TATTATTTTT AGTAAGATTG TCAACTTCAT TATATGTAGT CATTCTATTA AGAAGTTGTG 9660
 15 GACTTCTTCC CTGAGTTTGT CCAAAATAAA TCATCTCTCT TGGCGTTAAA CCAGTAAATT 9720
 GGAATCGTTG TCCTTGTAAG TTTGGGTGTA AAAATCTCAT CACAGCTTCT GCATGATATT 9780
 TGTTAGTATT ATAAGTCGCA TTTAGTAATT CAGACATCGT ATAGCCTGCA CACCAACCAT 9840
 20 TGTTACCTTG AGTTTCTCTT ATCTTGAAAT TCTCAAGTTT ATTTATATAT TGsTCGTTGT 9900
 AAGTATAATT ATTACTTTTA AATTGACTAG TTGGCATAGT GACAGAAGCT TTTTGCTTTA 9960
 GTTGCCTTAC ATTATTGCCA GTAGGTATAC TCTCAGTCTT TnTnAACTnT nTATCTTCTA 10020
 25 GACGTGGTGT TTTTAGTACT AGTTTAGCTT TATGATTTTG AGTACCACAT AGTAACCTTT 10080
 TGAGTTGT 10088

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7563 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CGGAAACGnA CCCnATGCGT ATGCTTGACG TGCCAAAATT AAATACGAAG TTCATAGCTT 60
 TGAGGTACCA GAAGAACATT TATCTGGTCA AGAAGTCGCA GnACTCATAA AAGCAAATGT 120
 TAAAACAGTA TTTAAAACGC TTGTTCTAGA AAATACAAAA CATGAACATT TTGTATTTGT 180
 45 TATCCCAGTA AGTGAAACTT TAGATATGAA AAAGGCAGCT GCTTTGGTTG GAGAGAAGAA 240
 ATTGCAGCTT ATGCCTTTAG ATAATTTGAA AAATGTAACG GGATACATTC GTGGTGGGTG 300
 50 TTCGCCTGTT GGTATGAAAA CATTGTTTCC AACAGTCGTT GACAAATCGT GTGAAAATTA 360
 TAGTCATATC AGTGTGAGTG GTGGGCTTCG AACAAATGCAA ATCACAATAG CTGTTGAGGA 420
 TTTGATTACA ATAATAAAG GCAAAATTGG AGCAGTTATC CATGAATGAT TAATAACAAC 480

	TGCCCACTC	CTTTTGGATT	GAATTAGCAT	TTTACGATCA	TAAACAGTCA	TTATAATTGA	600
	GTATTTGAAC	ATAAAAATGT	AATTTTATCG	TAACAATTG	AGTGTGTTG	ATTGTTTTTG	660
5	GTAATTTATG	ATTGAAAAGT	GAAAGCGTAC	TCATTATAAT	ACAAAGTGAG	ATGGGGTGAT	720
	GATGATAATT	ACTGAAAAA	GACACGAGTT	AATATTAGAA	GAACTTTCGC	ACAAAGATTT	780
10	TTTGACTTTA	CAAGAATTAA	TAGATCGAAC	TGGTTGCAGT	GCTTCAACAA	TACGATGAGA	840
	TTTATCTAAA	CTACAACAAT	TAGGGAAATT	GCAACGTGTG	CATGGTGGTG	CAATGTTAAA	900
	AGAAAATCGT	ATGGTTGAGG	CGAATTTAAC	TGAAAAATTA	GCAACGAATC	TTGATGAAAA	960
15	GAAAATGATT	GCTAAAATAG	CAGCTAATCA	AATCAACGAT	AATGAATGCT	TATTTATCGA	1020
	TGCTGGTTCA	TCTACATTGG	AGCTAATTAA	ATATATTCAA	GCGAAAGATA	TCATTGTGGT	1080
	AACCAATGGT	TTAACACATG	TAGAAGCTTT	ACTTAAAAA	GGTATTAAAA	CAATTATGCT	1140
20	AGGTGGTCAA	GTTAAAGAAA	ATACACTTGC	TACGATTGGT	TCTAGTGCTA	TGGAGATATT	1200
	AAGACGATAT	TGTTTCGATA	AAGCTTTTAT	CGGGATGAAT	GGATTAGATA	TTGAACTTGG	1260
	ATTAACACT	CCCGATGAGC	AAGAGGCATT	AGTTAAACAA	ACAGCAATGT	CATTAGCCAA	1320
25	TCAATCATT	GTACTTATAG	ATCATTCTAA	GTTTAATAAA	GTATATTTTG	CTCGTGATACC	1380
	TTTGCTAGAA	AGTACGACAA	TCATCACATC	TGAAAAAGCA	TTAAATCAAG	AATCGTTAAA	1440
30	AGAATACCAA	CAAAAGTATC	ACTTTATAGG	AGGGACTTTA	TGATTTATAC	AGTGACTTTC	1500
	AATCCTTCAA	TTGACTATGT	CATTTTACG	AATGATTTTA	AAATTGATGG	TTTGAACAGA	1560
	GCAACAGCAA	CATATAAATT	CGCTGGGGGG	AAAGGTATTA	ATGTCTCGCG	CGTCTTAAAG	1620
35	ACATTGGATG	TTGAGTCAAC	TGCTTGGGA	TTTGCAGGTG	GATTTCTCGG	GAAATTCATT	1680
	ATAGATACAT	TAAATAACAG	TGCAATTCAA	TCGAATTTTA	TTGAAGTTGA	TGAAGATACA	1740
	CGTATTAATG	TGAAATTAAA	AACAGGACAA	GAAACAGAAA	TCAATGCACC	GGGTCCTCAT	1800
40	ATAACGTCAA	CACAATTTGA	ACAACGTGTA	CAACAAATTA	AAAATACAAC	AAGCGAAGAT	1860
	ATAGTTATTG	TTGCTGGAAG	TGTACCAAGT	AGTATTCCAA	GCGATGCGTA	TGCGCAAATT	1920
	GCACAAATTA	CAGCACAGAC	AGGTGCTAAA	TTAGTAGTCG	ACGCTGAAAA	AGAATTGGCT	1980
45	GAAAGCGTTT	TACCATATCA	TCCACTATTT	ATTAAACCTA	ATAAAGATGA	ATTAGAAGTG	2040
	ATGTTTAATA	CAACAGTGAA	CTCAGACACA	GATGTTATTA	AATATGGTCG	TTTGTAGTTT	2100
50	GATAAAGGTG	CGCAATCTGT	TATTGTCTCG	CTTGGCGGTG	ATGGTGCTAT	TTATATTGAT	2160
	AAAGAAATCA	GTATTAAAGC	AGTTAATCCA	CAAGGGAAAG	TGGTTAATAC	AGTTGGCTCT	2220
	GGTGATAGTA	CAGTTGCAGG	CATGGTGGCT	GGAATTGCTT	CAGGTTTAAC	GATTGAAAAA	2280

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	CGGGACGCTA TAGAAAAAAT AAAATCACAA GTTACGATTA GCGTACTTGA TGGGGAGTGA	2400
	AAATAATGAG AGTAACAGAG TTATTAAACAA AAGATACAAT AGCAATGGAT TTAATGGCAA	2460
5	ATGACAAAAA TGGTGTATT GATGAGTTAG TAAATCAATT AGACAAAGCA GGTAAATTAA	2520
	GTGATGTGCG GTCATTTAAG GAAGCGATT CACAATCGAGA ATCACAAAGT ACAACTGGTA	2580
10	TCGGCGAAGG TATTGCCATT CCACATGCCA AAGTGGCCGC AGTTAAGTCA CCAGCTATTG	2640
	CGTTTGGTAA ATCTAAAGCA GCGGTAGATT ATCAAAGTTT GGATATGCAA CCAGCACACT	2700
	TATTCTTTAT GATTGcAGcG CCAGAAGGTG GCGCCCAAAC ACATCTAGAT GCTTTAGCTA	2760
15	AGTTGTCTGG TATTTTAAATG GATGAAAATG TACGTGAGAA ATTATTACAT GCTTCATCAC	2820
	CTGAAGAAGT ACTAGCGATC ATAGATGAGG CTGATGATGA AGTGACAAAA GAAGAAGAGG	2880
	CAGAAGCTGA AGCACAACAA GTTGCAACTG CAGAACAATC ATCTAAACAA TCTAATGAGC	2940
20	CATATGTGTT AGCAGTAACT GCTTGTCCAA CAGGTATTGC ACACACATAT ATGGCACGTG	3000
	ATGCATTGAA AAAGCAAGCG GATAAAATGG GTATTAAAT TAAAGTAGAA ACGAATGGTT	3060
	CAAGCGGCAT TAAAAACCAT TTAAGTGAAC AAGATATTGA AAATGCAACA GGTATCATTG	3120
25	TTGCTGCTGA TGTTCATGTT GAGACGGATC GCTTCGATGG TAAAAATGTC GTAGAAGTAC	3180
	CAGTAGCAGA TGGTATTAAA CGCCCAGAAG AATTAATTAA TAAAGCATTG GATACAAGTC	3240
30	GTAAACCTTT TGTGCCCCGT GATGGTCAAA GAAAAGGTAA CTCAAATGAC AGTCAAGAAA	3300
	AATTAAGCCC AGGTAAAGCA TTCTATAAAC ACTTAATGAA CGGTGTTTCT AACATGTTGC	3360
	CACTTGTAAT ATCTGGTGGT ATTTTAATGG CAATTGTATT TTTATTTGGA GCAAATTCAT	3420
35	TTAATCCAAA AAGCTCAGAG TACAATGCGT TTGCAGAGCA GCTTTGGAAC ATTGGTAGTA	3480
	AAAGTGCATT CGCGTTAATC ATTCCAATTT TATCTGGATT CATTGCACGT AGTATTGCGG	3540
	ATAAACCTGG TTTCGCTTCA GGTCTTGTAG GTGGTATGTT AGCAATTTCA GGTGGTTTCA	3600
40	GATTTATTGG TGGTATTATT GCAGGTTTCT TAGCAGGTTA CTTAACACAA GGTGTTAAAG	3660
	CCATGACACG TAAGTTACCA CAAGCATTAG AGGGATTAAA GCCAACATTA ATTTATCCAC	3720
	TATTAACAGT GACGGCTACA GGCTTATTGA TGATTTATGC CTTAATCCA CCAGCATCTT	3780
45	GGTTAAATCA TTTGTTATTA GATGGATTAA ACAATTTATC AGGTTCTAAT ATTGTATTAT	3840
	TAGGTTTAGT TATTGGCGCT ATGATGGCGA TTGATATGGG CGGTCCATT CACAAAGCGG	3900
50	CATATGTTTT TGCAACAGGT GCGTTGATTG AAGGTAATGC AGCACCATT ACAGCTGCAA	3960
	TGATTGGTGG TATGATTCCA CCGTTAGCAA TTGCGACAGC GATGTTAATT TTTAGACGTA	4020
55	AATTTACAAA AGAACAACGT GGTTCATTA TCCCTAACTA TGTGATGGGT ATGTCATTTA	4080

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TGATTGGTTC AGGTATAGGT GCGCAATTG CTTTAGGCTT AGGTTACGA ATTACTGCGC 4200
 CACATGGTGG TATTATTGTA ATTGTTGGTA CTGATGGTGC ACACTTACTT CAAACTCTTA 4260
 TTGCACTTCT AGTTGGCACA TTAGTTTCAG CATTAAATTA CGGTTTAATC AAACCAAAGT 4320
 TAACTGAAAC AGAAATCGAA GCTTCAAAAT CAATGGACGA GTAGTTTTAA TGATGTAAAA 4380
 TGATTGTTAG CAAAGAGCTT CATATTAAGT TGTATGTTCA ATGAATATAT GTTAGTTTTA 4440
 TATATCGTGT TAACGGTAGC TTATACAAAG CTGTAAAAAC ACTTTCTATT AATTCAGTTT 4500
 TTATGAATTG ATATGAAAGT GTTTTTATTT TTAGATAAAT GAATGAAGAA ATAGACACCA 4560
 CAAATGTATA GACTTTTTTA ATATTTTGCA AAAAGTTATG CCAAACGAAG CAGATATAGT 4620
 AAAATATGAG TGTCTTAAAG TGAAAATTTA TAAATAAAGA AGGGTTTATA CGTGTCAGAA 4680
 TTAATTATAT ATAACGGCAA AGTTTATACT GAAGATGGCA AAATCGATAA TGGTTACATT 4740
 CATGTGAAAG ATGGACAGAT TGTTGCAATT GGAGAAGTGG ATGATAAAGC AGCAATTGAT 4800
 AATGATACGA CAAATAAAAT TCAAGTGATT GATGCTAAAG GTCATCATGT ATTACCAGGT 4860
 TTTATTGATA TACATATTCA TGGTGGTTAT GGTCAAGATG CAATGGATGG GTCATACGAT 4920
 GGCTTAAAT ATCTATCCGA AAATTTGTTG TCTGAAGGGA CGACATCATA CTTGGCCACT 4980
 ACAATGACGC AATCGACTGA TAAATAGAT AATGCACTTA CAAATATTGC TAAATATGAA 5040
 GCGGAGCAAG ATGTTCAACAA TGCAGCGGAA ATTGTAGGTA TACATTTAGA AGGACCATTT 5100
 ATATCTGAAA ATAAAGTTGG TGCTCAACAT CCGCAATACG TTGTACGCCC ATTTATCGAT 5160
 AAAATTAAAC ATTTTCAAGA GACTGCTAAC GGATTAATAA AGATTATGAC GTTTGCACCT 5220
 GAAATTGAAG GTGCAAAAAGA AGCGCTTGAA ACGTATAAAG ATGACATTAT TTTTCAATT 5280
 GGTCATACAG TAGCAACATA CGAAGAAGCA GTTGAAGCTG TTGAGCGAGG AGCTAAACAT 5340
 GTCACGCATT TATATAATGC AGCGACGCCA TTCCAACATA GAGAACCAGG TGTTTTTGGA 5400
 GCAGCATGGT TGAATGATGC TCTACATACC GAAATGATTG TTGATGGCAC TCATTCTCAT 5460
 CCGGCATCGG TTGCAATTGC TTACCGTATG AAAGGTAATG AACGTTTTTA TTTAATTACC 5520
 GATGCAATGC GTGCAAAAGG TATGCCTGAA GGAGAATATG ATTTGGGTGG ACAAAAAGTA 5580
 ACTGTTCAAT CGCAACAAGC ACGTCTTGCA AATGGTGCGC TTGCTGGTAG TATTTTAAAA 5640
 ATGAATCATG GGTACGTAA CTTAATATCA TTTACAGGTG ATACATTAGA TCATTTATGG 5700
 CGAGTAACAA GTTTAAATCA AGCCATTGCA TTAGGTATCG ATGATAGAAA AGGTAGTATT 5760
 AAAGTAAATA AGGATGCAGA TCTTGTTATT CTAGATGATG ATATGAATGT AAAATCTACA 5820
 ATAAACAAG GCAAGGTTCA CACATTTAGC TAATAAATAA TCATAATTAA ATGTATGCAA 5880

	TTTTCTGGGG GTGTCTAAAT GCGAAGGCGA TAACATGTAG TTGTAATTTA AGTCATAGTG	6000
	ATAAATTTGA ATGCGTGTTA CCCATGAGTG ACACATATAA CATGGAGGTG AATCCCTAGA	6060
5	AATAGGGAAT TAATTGAAA CTTCGACCAT AATTAGTTTG ATTATATTTA TTCTATTAAT	6120
	TGCATTAACC ACTGTATTTG TTGGTTCAGA ATTTGCATTA GTAAAAATTA GAGCAACAAG	6180
10	AATTGAACAG CTAGCAGATG AAGGAAATAA ACCTGCTAAA ATAGTAAAAA AGATGATTGC	6240
	TAATCTAGAT TATTATCTTT CTGCTTGTC A GTTAGGTATA ACAGTAACAT CTTTAGGGTT	6300
	AGGTTGGCTT GGTGAACCAA CGTTTGAAAA GCTATTACAC CCAATATTTG AAGCAATCAA	6360
15	TTTACCAACT GCATTAACGA CGACGATTTT GTTTGCAGTG TCATTTATAA TCGTTACGTA	6420
	TTTGCATGTA GTACTTGGTG AATTAGCGCC TAAATCTATA GCTATTCAAC ATACTGAAAA	6480
	GCTTGCTTTA GTATATGCAA GACCATTGTT CTATTTCGGT AACATTATGA AACCATTGAT	6540
20	TTGGCTGATG AATGGTCTG CACGTGTTAT TATTAGAATG TTTGGTGTAA ATCCTGATGC	6600
	CCAACTGAT GCAATGTCAG AAGAAGAAAT CAAAATTATT ATTAACAATA GTTATAATGG	6660
	TGGAGAAATC AACCAAATG AATTGGCATA TATGCAAAAT ATCTTTTCAT TCGATGAAAG	6720
25	ACATGCAAAA GATATAATGG TACCTAGAAC TCAAATGATT AACTAAATG AACCTTTTAA	6780
	TGTAGACGAA TTAGTAGAAA CAATAAAGA ACATCAATTT ACGCGTTATC CAATTACTGA	6840
30	TGATGGTGAT AAAGACCACA TTAAAGGATT TATTAACGTC AAAGAATTTT TAACTGAATA	6900
	CGCTTCTGGA AAAACGATTA AAATAGCAAA CTATATaCAT GAGTTGCCAA TGATTTTCAGA	6960
	GACAACACGT ATCAGTGATG CATTAAATTAG AATGCAACGT GAACATGTAC ATATGAGTCT	7020
35	TATTATAGAT GAATATGGTG GAACGGCAGG TATTTTAACG ATGGAAGATA TTTTAGAAGA	7080
	AATCGTTGGA GAAATTCGTG ATGAATTTGA TGATGATGAA GTGAATGATA TCGTTAAAAT	7140
	TGATBATAAG ACATTCCAAG TAAATGGCAG AGTACTATTG GATGATTTAA CTGAAGAGTT	7200
40	CGGTATAGAA TTTGATGACT CTGAGGATAT TGATACGATA GGTGGATGGT TACAATCTCG	7260
	TAATACCAAT TTACAAAAAG ATGATTACGT GGATACAACT TATGATCGCT GGGTTGTTTC	7320
	AGAAATCGAT AACCACCAAA TTATTTGGGT GATATTAAAC TATGAATTTA ATGAAGCGAG	7380
45	ACCTACTATC GGACAGTCTG ATGAAGATGA AAAATCAGAA TAGATATTAA TATATAAACC	7440
	AATAAGAAT GATTTAATTC ATTTTGGTT GGTATTTTTT TTACTAAAA TTAAnGAAAA	7500
50	GTGAAAATAG TATTGGAAC CAATATCTTT AATGATTTAA TGAATAAnTT TTATTGAAAG	7560
	CGA	7563

(2) INFORMATION FOR SEQ ID NO: 34:

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(A) LENGTH: 3492 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

10	TTATATCAAC TTCATGGCGG AACCATTGAT GACCCATTAG ACGAAACAAT AAGCGCATT	60
	SATGAATTGA AACAGAAGG AATTATACGT GCTTACGGTA TTTCTTCTAT TCGCCCAAAT	120
	GTAATTGATT ATTATTATAA ACATAGTCAA ATCGAAACGA TAATGTCTCA ATTCAATTTG	180
15	ATTGATAATC GTCCAGAATC ATTATTAGAT GCAATTCACA ACAATGATGT TAAAGTATTG	240
	GCAAGAGGAC CTGTGTCTAA AGGATTATTA ACTTCAAACA GTGTTAATGT GCTCGACAAT	300
	AAATTTAAAG ATGGTATTTT TGATTATTCT CATGATGAAT TGGGTGAAAC AATAGCCTCT	360
20	ATTAAAGAAA TTGAAAGTAA TTTATCTGCA TTGACATTTA GTTATTTAAC ATCACATGAC	420
	GTGCTTGGTT CCATCATTGT AGGTGCAAGT AGCGTCGACC AATTAAAAGA AAATATTGAA	480
25	AACTATCATA CTAAAGTTAG TTTAGATCAG ATTAAACAG CAAGAGCTCG TGTAAGGAT	540
	TTGGAATATA CCAATCATT AGTGTAGAAG TCATTTTCAG TAATAAAAAC AGCAGCATGA	600
	GGCGTTTCAT TATAAAAATG CCTTACTGCT GTTGTTTATG TACAATTCGC TATAATTTAT	660
30	GATTATGATT ACTCACTTAT GATAGAAAT AAAGCGTTGT CCTCACGCAT CAGTATTTAG	720
	TAATTTCGCC TTGCGGCATT GCCTTAAGCA AACTTCTGCC ACTTCATCTC TTAATAATTT	780
	TATTAAAACA TCTTTCTATA TTTCACTTCG CATGTTGATT CATCATTATT AGTTATTATT	840
35	TGTACACCCA GCACATTTCC TTGCAACACA AGTAGTTTGA ATTTTTCACA AGTATAATAT	900
	AATGTACCGT CTGAAATTTG GTCTACAGAA ATATCGCTA AAATATCCAG CACTGTAAAT	960
	TCTFCAAATA CTGATAGTTG TTCCGCATAT CGTACACAAA GTCTTACCAC ACTCTCCGAT	1020
40	TGACAGTTCA TTGCCATCCC ACCTATTTAT GCTTTATTTT TAAATAATTT AGGGAAACAT	1080
	CGTTCAAAA ATCTAGGCGC AATTTGATAC ATTTTCAACG CATGaTGCAT CCATTTAGGC	1140
45	CGATTAAATTT CCAATTGTTT TGTTTAAATG CCATAAATGA TATCTTCTGC AAGCTGATTA	1200
	GCAATCAAGCA TAATTTCCCC CATCTTTTTA GCATACTTCA TTGATGGGTC GGCTTTTTGA	1260
	TGAAAAGGTG TATCAATCGG GCCAACATTA ACTGTCATGA TATGTAAGTT TGGTGA CTCT	1320
50	AGTCTTAAAG CATTCATTAA TGCATAAAAC CCTGCTTTTC ATGCCCCATA ATGTGCAGCA	1380
	TTTGCTTG TGGAATATGC AGCTTGACTT GAAATACCTA CAATATGTGC GTTAGATGTT	1440
	AAATATGGTC TCAACACAGT ATATAAAACA TTAAACTAA TTAAATTAAG CTGATACGTT	1500

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	TAAATGAATC CATCGAATGA TGTATTGTCT TCAAATTGCA GTGCCTGTAT CGACTTCAAA	1620
	TCATTTAAGT CACAAGGAAT AACATTATA GTTTTCCCA ATTCTGTTC AAAGATTCTA	1680
5	GTTGCTTTAT CAACATCACG CACCAACAAC GTTACATGCA CTTTATTTTC TAGTAACTTT	1740
	CGGACAATCG ATAAACCTAA ACCACTCGTA CCACCAGTCA CTATAAAATG TTGTCCTTTC	1800
10	ATCAATTAAC CTTCTTTTTC AATTATATAG AATGCAATTT ATCAACTTTA CATAATTGAG	1860
	ACAAGTTGAT TATCTTTCCT AATATATATA CAATAATAAG AAAATATAAC ATACAAATCA	1920
	AAAATAAAG GGATGTGACG TTAATGTAAC TCGTATTTTA TGGAGCTGGT AATATGGCAC	1980
15	AAGCTATATT TACAGGATT ATTAAGTCA GCAACTTAGA TGCCAATGAT ATATATTTAA	2040
	CAAAATAATC TAATGAACAA GCTTTAAAG CATTGCTGA AAAACTAGGT GTTAACTATA	2100
	GTTATGATGA TGCGACATTA TTAAGAGATG CAGATATGT ATTTTATAGT ACCAAACCAC	2160
20	ATGACTTTGA TGCTCTAGCA ACACGCATCA AACCACATAT TACAAAAGWC AATTGCTTCA	2220
	TTTCAATTAT GGCAGGTATT CCGATTGATT ATATTAAACA ACAATTAGAA TGCCAAAATC	2280
	CaGTTGCTAG AATTATGCCA AACACAAATG CGCAAGTTGG ACACTCTGTT ACTGGCATT	2340
25	GTTTTTCAAA CACTTTGAC CCTAAATCTA AAGATGAAAT TAACGATTTA GTTAAAGCAT	2400
	TTGGTTCTGT AATTGAAGTA TCAGAAGATC ATTTACATCA AGTAACAGCT ATCACCGGAA	2460
	GCGGCCAGC ATTTTATAT CATGTATTCG AGCAATATGT TAAAGCTGGT aCsAAACTTG	2520
30	GTCTAGAAAA AGAACAAGTT GAAGAATCTA TACGCAACCT TATTATAGGT ACAAGTAAGA	2580
	TGATTGAACG TTCAGATTG AGCATGGCTC AATTAAGAAA AAATATTACC TCTAAAGGTG	2640
35	GTACGACACA AGCTGGCCTT GATACATTGT CACAATATGA TTTAGTATCT ATTTTCGAAG	2700
	ATTGTCTAAA CGCTGCCGTC GACCGTAGTA TTGAACTTTC TAATATAGAA GACCAATAAA	2760
	AACAACCCG CCAACACATG TATGCATCAT CGCAAGCACT GTGTTTGACG GGTATTTTTT	2820
40	ATAATTTATT GTTATTTGGC AAGCATTGTT TATTACTTTG TCATTAGATT TTAAACTAT	2880
	CAAAATCTTT TACAAAATTA AAATTAGGTG TATCTTCATT TTGTATCAAT GTTTGATAAA	2940
	TTTCATTTAT ATCTTCTGTA TTATAGCGAT TGCTCAAATG TGTAATCAAC GTACGTTTAA	3000
45	CATTGGCTTC TTTTATCAAT GCAAATACGT CTTCAATATG GCTATGATGA TAATTGTTGG	3060
	CTAAATGCTT TTCACCATCT ATATAGGTG CTTCATGTAC CATCACATCA GCATCTCTAG	3120
	AAATCACACG TTCATTAGAA CATGGTTTTG TATCACCAAA AATTGCTACA ACTGGACCCT	3180
50	GTTTGGACTC ACCTCTAAAA TCTTTTGATT GATAAACTTG ACCATTATGT TCAAATGTAT	3240
	CATGAGATTT TACTTCTTGA TATTAGGAC CTGGTTCAAG ACCAATGTTT TTTAACGCTT	3300

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CATGATTAAG TAAATGCGCC TCTACAGTAA AACCATCCAT GATGATATGT CAGATGATCA 3420
 TCGATTTCAA TATATGtAAT TGGATAGTTT AAATGTGACT CTGATAAAATT CATAGACATT 3480
 5 TCCACATATG CT 3492

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1973 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATCTAGCGGT ACAAGCGTCT TGGAGGCTAG TATGTTGAAC ATTGTAAACC CTGAAGATCA 60
 20 CTTGCTTGTC ATTGTTTCAG GTGCCTTTGG TAACCGATTT AAACAAATTG CACAACTTA 120
 TTACAAAAT GTGCATATTT ATGACGTAAC ATGGGGAGAA GCTGTAGATG TCAAAGATTT 180
 CATCAATTTT CTTTCAACTT TAAATGTTGA AGTTAAAGCA GTATTTAGTC AATATTGCGA 240
 25 AACATCTACG ACAGTGCTAC ACCCTATTCA CGAGTTAGGA AATGCCATTA ATCAATTTAA 300
 TAGTAATATT TATTTTGTAG TTGACGGCGT AAGTtGCATT GGTGCTGTTG ATGTTGACAT 360
 TAACAAAGAT AAAATTGATG TACTTGTtTC TGGTAGTCAA AAAGCAATTA TGTTACCTCC 420
 30 AGGATTAGCT TTTGTAGCTT ATAGCCACCG TGCAAAAGAA CATTTCAAAG AAGTAACTAC 480
 GCCAAAATTT TATCTAGACT TAAATAAATA CATTTCTGTC CAAGCTGACA ATTCTACACC 540
 GTTCACACCA AATGTGTCTT TATTAGAGG TGTAATGCA TACGTTGAAA CCGTAAAAGC 600
 35 AGAAGGTTTC AATCACGTAA TAGCACGACA CTATGCAATT AGAAATGCAT TAAGAAGCGC 660
 CTTAAAGCA TTAGATTTAA CTTTATTAGT CAATGATAAA GATGCATCTC CAACGGTTAC 720
 40 AGCATTCAAA CCTAATACAA ATGATGAAGT GAAAATAATC mAAGATGAAC TTAAAAATnG 780
 CTTTAAATA ACAATTGcng GTGGTCAAGG CCATCTTAAA GGTCAAATTT TnAGAATTGG 840
 TCATATGGGG AAAATTAGTC CTTTCGATAT TTTATCGGTA GTATCTGCTT TAGAAATTAT 900
 45 TTTAACTGAA CACCGTAAAG TTAActATAT CGGTAAAGGT ATATCAAAT ATATGGAGGT 960
 TATTCATGAA GCAATTTAAT GTACTCGTTG CAGATCCCAT ATCAAAGAT GGTATCAAAG 1020
 CATTATTAGA TCACGAACAA TTCAATGTAG ATATTCAAAC TGGCTTGTC GAAGAAGCAT 1080
 50 TAATCAAAT TATACCTTCA TACCATGCTT TAATCGTTCG TAGTCAAAct ACGGTTACTG 1140
 AAAATATCAT AAATGCTGCT GATTCTTTAA AAGTAATCGC ACGCGCCGGT GTTGGTGTAG 1200

GTAATACGAT TTCAGCTACT GAACATACAC TGGCAATGTT ATTATCAATG GCACGAAATA 1320
 TTCCGCAAGC ACACCAATCA CTTACAAATA AAGAATGGAA TCGAAATGCA TTTAAAGGTA 1380
 5 CTGAGCTTTA TCATAAAACA TTAGGTGTCA TTGGTGCTGG TAGAATTGGT TTAGGTGTTG 1440
 CTAAACGTGC GCAAAGTTTC GGAATGAAAA TACTAGCTTT TGACCCTTAC TTAACGGATG 1500
 10 AAAAAGCAAA ATCTTTAAGC ATTACGAAGG CAACAGTTGA TGAGATTGCC CAACATTCTG 1560
 ATTTGCTTAC ATTACATACA CCACTAACAC CTAAAACAAA AGGCTTAATT AATGCTGTCT 1620
 TTTTGGCCAA AGCAAAACCT AGTTTGCAAA TAATCAATGT GGCACGTGGT GGTATTATTG 1680
 15 ATGAAAAGGC GCTAATAAAA GCATTAGACG AAGGACAAAT TAGTCGGGCA GCTATCGATG 1740
 TGTTTGAACA TGAACCTGCA ACTGACTCGC CTCTTGTTGC ACATGATAAA ATTATTGTTA 1800
 CACCTCATTT GGGTGCTTCA ACAGTCGAAG CTCAAGAAAA AGTGGCAATT TCTGTTTCAA 1860
 20 ATGAAATCAT CGAAATTTTA ATTGATGGTA CTGTAACGCA TGCAgTGAAT GCACCTAAAA 1920
 TGGACTTAAG CAATATAGAT GATACTGTAA AATCATTAT CATTTAAGC CAA 1973

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7620 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GGTGTTCAG ATGTCACTGG TTGATTTTAA ATTGTAGACG GGTATTTTGG GCTTTCGCCA 60
 35 TATTTATTTG CCGGCTTACT GTCAAAGCAT AGGAATACTA TCATAACAAT TGTTAGGCCT 120
 AAATGAACAA AATAAAGAAG TACTAACAAA ATATTAAGAC CCATCGGCAT TAATGTAAAA 180
 40 TCACTGTCAT AATAACTATC GATAATCTGT AATACTATAT AAAATATAAT ACTGAATACT 240
 GTCATAATCA TTGGAAATAA CATTGTTCTT GATATATCGT GAAATCTTCG AACGCACAAC 300
 GCTAAATTTG GAATAAACGT TGCCAAACTA TAGACAAAAG TATACACAGA TGTAAGGATA 360
 45 ATCATCAATA TACTCATAAC TATTAATGTT TCGTTATCCG CCGCTATAGA AATAAAGAAT 420
 AGAAATAGGT TTATTATTAG CACACACACA GCTGGAACCA TAAGTATCAA ATGCCATAGT 480
 GCCATATACC AATATTCAT ACGTCTTGAT CTCCCCTTAA AATTACATA ATTTTCCAA 540
 50 AATAAACGA ATGATTTTAT AAAACCTACT TGAGGTAATT GTTCCATTGT AATCTCCCTT 600
 TCGTTAATCA TATTTATATT TTTAATTATT GTTACCGTTA TAATTTACAA GATTCATTAT 660

	GTAAATGAA AACCCGCTAC AAGTACACAT CTATATGGAG ACTCATTGGA AAGTCAACGC	780
	TTCGTTAACT ATACTAAAA TATGTCATAC TGCAATGTTT ACGTTTAAAA GAGTCTCAAT	840
5	CTATGCAAAAT AAAATATTCC ATAACAAAGT ATATACTTTA CATTITTTATA ATTCTTAACA	900
	ATACTATTTT ATCAAACATT TACCACAATA AAAATATCTT TTTCAITTTT ATTTAAATTA	960
10	ATCATATAAT TGCGAGGAGA ATATTATGGA TTTGTTAAT AATGATACAA GACAAATTGC	1020
	TAAAACTTA TTAGGTGTCA AAGTGATTTA TCAGGATACC ACTCAAACGT ATACAGGCTA	1080
	CATCGTGGA ACGGAAGCTT ACTTAGGTTT GAATGATCGT GCGGCTCATG GCTATGGCGG	1140
15	TAAATAACA CCTAAAGTCA CGTCATTATA TAAACGTGGT GGTACAATT ATGCACATGT	1200
	CATGCATACG CATTITACTCA TTAATTTTGT AACAAATCT GAAGGTATAC CTGAAGGCGT	1260
	ACTTATCCGC GCAATTGAAC CAGAAGAAGG TTTATCCGCT ATGTTCCGTA ACAGAGGTAA	1320
20	GAAAGGCTAC GAGGTAACGA ATGGCCCAGG AAAATGGACT AAGGCATTTA ACATTCCACG	1380
	GGCTATCGAT GCGGCTACGT TAAATGACTG TAGATTGTCT ATTGATACTA AGAATCGTAA	1440
	ATATCTAAA GATATTATTG CTAGTCCACG AATCGGTATT CCAAATAAAG GTGATTGGAC	1500
25	ACATAAATCT TTACGTTACA CAGTGAAAGG TAATCCATTT GTGTCTCGCA TCGGTAAATC	1560
	AGATTGTATG TTTCCCGAAG ATACTTGGA ATAAATGCCA TCTTTCATTG ATTACTATCA	1620
	TGAAATGAA ATCTATCTCC TTATAAGTCA ATCAATCGTG CCGTCAACAT GCGGATGGGT	1680
30	TGATTGTTTT TCTTTGTATC CATCATATTT TTTGATTGAT CTCCTCTTAT TGAACITGTT	1740
	CTTAATTATA AAATATAACA ATAGAATTAT TTATAATTAT TAAATTTAGA TGCATTAAATA	1800
35	TTATTGATAT TATTTTCAAA AACTAGAAAT ATTGATTTGT TGCATGTATA ATGTTAAAAAG	1860
	CGCCCTTTTA TAACGCITAC ATATAAAAGC TTATTTAGGG AGAGGGATAT TCAACAAGGG	1920
	GGATTGAAA ATGATAGAAC TTAATGCAAT TACAACATTA TGTTTAGCTT GTATCCTTTA	1980
40	TTTACTTGGT AAGGCTATCG TTAATCACGT TAATTTTTTA AAACGTATTT GTATACCAGC	2040
	ACCAGTGATT GCGGCTTAA TCTTTGCTAT TTTAGTTGCG GCTTTGGATT CATTTGGCAT	2100
	GGTTAAGATT AAATTAGATG CTTCAITCAT TCAAGATTC TTCATGTTAG CATTCTTTAC	2160
45	GACAATCGGT CTGGTGCAT CATTGAAATT ATTTAAATTA GGTGGCAAAG TCTTGCTATT	2220
	ATACTTTATG TTTTGTGCTA TCATTCAGT CATTCAAAC ATAGTTGGTG TATCACTAGC	2280
	AAAAGTATTA AATATTAAAC CTTTGTTAGG ATTAACAGCA GGTTCATGT CTATGGAAGG	2340
50	CGGTCATGGT AATGCTGCTG CTTATGGTAA GACAATTCAA GATTTAGGTA TTGATTGGGC	2400
	ACTGACAGCG GCTCTTGCA CTGCAACTTT AGGTCTTGTA TTTGGAGGGC TTATCGGTGG	2460

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	ATTTAAAGAT TATAGCCAAG TAGCATATAA CGAACATTTA CATAGTAAAT TTAATGCCAC	2580
	TGAAGTATTC TTCATTCAAT TTACAATCGT TGTATTCTGT ATGGCAGTTG GAAGTTATTT	2640
5	CAGTCATTG TTTACAGCTC AAACAGGGAT TAATGTTCCA ATTTACGTTG GCTCATTATT	2700
	TGTAGCTGTT ATTGTCCGAA ATATCTCTGA AAGTTTTAAT TTTAATATTG TAGATTTAAA	2760
10	AATTACTAAT CAAATTGGCG ATGTCGCATT AGGTATTTTC TTATCTCTTG CGCTAATGAG	2820
	CATTCAATTA ATCGAAATTT ATAAACTTGC TATACCTCTT ATTATTATCG TTTTAGTTCA	2880
	AGTTGTCGTT ATGATTTTAT TTGCTGTTTT AATTTTATTT AGAGGTTTAG GAAAAGATT	2940
15	TGATGCTGCA GTAATGGTAG GTGGTTTTAT CGGTCATGGG CTTGGTGCAc GCCAAATGCC	3000
	ATGGCAAATT TAGATGTTAT TACTAAAAA TATGGAACT CACCTAAAGC ATATTTAGTT	3060
	GTACCTATTG TTGGTGCACT CTTAATCGAT TTAATTGGTG TTATAGTCAT TATGGGATTC	3120
20	ATACAATGGT TTAGTTAAAC ACCAACTCA TAAATAAAG AGGAGGCCTT CGCCTCCTcT	3180
	TTTATTTATC CTCGATGTAT ATTCAAGTTA CGTTGTTCTA TCCATGACAA TATTTCCGGA	3240
	CTAAATACGA TTTGTTTTTG TGTAAAGTCG TCAATATTTT TAGCATCTAA CATCGTCATT	3300
25	ATTGATTTCA TGTGTTCAAT AAATGATTCT ACATAAGCTA CTGTATGTGC AATGCCATTA	3360
	TTTTCAACTT GATTTAAAAA CGGACGTGAC ATACCAGTTG CCTTTCACC AAGTGCTAAA	3420
	CTTTTAATTG CATCGAGTGG TGTACGTAAA CCACCACTCG CGAAAACTGA AATTTCGCTT	3480
30	TGATAAGCCG TTGTTTCAAG TAATGACTCA ACTGTAGACT GTCCCCATGA TGATAAGTAA	3540
	TCCATATCTT TATTTCACG ACGTTCATTT TCAATATCTA CAAAGTTAGT ACCACCTTGT	3600
35	CCACTAACAT CGACATACTT GACGCCTATT TGTTGTAAGT CATGCATTAA TTCTTTGCTC	3660
	ATACCAAATC CAACTTCTTT TATAATGACT GGAACAGACA CTCGTGATAC AATCGACGCT	3720
	ATATTATCTA ACCAAGTCAC AAATTCACGA TTCCCTTCAG GCATAACTAA TTCTTGAGGA	3780
40	GAATTAACAT GGATTGTAA CGCTTGCGCC TCAAGTAATT CAACTGCTTC CAAAGCCTTT	3840
	TCTACTGGTA CGTCCGCACC AACATTGCTA AAAATCATGC CTTCAGGATT CATTTTTCGC	3900
	GCAATCGTAA ACGTCTCAGC CATGCGTGGA TTTCTCAATG CCGCATGTGT TGATCCAACT	3960
45	GCCATCGCTA AGCCAGTTTC TCTTGCAACT ACAGCTAGCT TTTCAATTGAT GTTTTTCGTC	4020
	CACTCGCTAC CACCCGTCAT TGCATTAATA TAAACCGGAT ATGCCATCGT TAAGTCAGGC	4080
50	GTCTGTGATG TCAAATCGAT ATCATTTACA TTAATTGATG GGATAGAATG ATGCACAAAA	4140
	CGCATCTTAT CAAAATCTGA ATGCATTGCG TCAGATTGGG CCATTGCTAT TTCAACATGT	4200
55	TCATTTTTTC TCTGTTCTCT TTGAAAATCA CTCATGATTA AACCTACCTT TTCGTCATTT	4260

	ATTACAGCTA AGCAAATATA ATATCCATAA TGTAATGTGTA ATGCCGGCAT ATTTACAAAG	4380
5	TTCATACCAT AAATCCCAGC TATGAATGTT AACGGTGAAA ATATAACTGA TACTAATGTC	4440
	AGTACTTGCA TAATACTATT CATTCTAAAT GACGTGTATG ACTCAAATTT TTCTCGTATT	4500
	TCGTTTGTCA TTTCTTGAGC AGTACGAATG ATATTACGTT GCTTAATCAA GTGGTCATCG	4560
10	ATATGTTGAA TGTATAGCGA ATGTTTATTA TCTATAATCA AATCACCATT TTGTTTCATT	4620
	GTATCAATTA GCTCTTGCAT AGGAAACAGT ACACGTTTTA CTTTAATCAA ATCCGAACGT	4680
	AACTTAAAGA CACTATCCAT GACCATTTTA TTAAAGCGAT CATCTACATG GCGGTCTTCA	4740
15	AAATGATAAA CACTATCTTC AAGTGCATAT ACAAAGTTGA AATATTTATC AACCATCATA	4800
	TCTAAATTA ATATGACGAC ATCTGCACAA TCTAATTCTG CATCTAATGT ATTATATAC	4860
	TTATAGACTA CTTTATTTAA TGATTCCAAC GTTTGATGAT GATATGTTAC TAATACATTG	4920
20	TCTTGTATAA AAATATTTAG TGCTATTGGT GAATAGTTTG ACCCCATAAT ACTATGGAAT	4980
	ACTAAGTATT GATAATCTTT ATAAGATTTA TATTTAGCTC GTGGCATACC GTTAATTGCA	5040
25	TCATCCACTT CTAATCATT AAAATTAAAA TGTGCTTTAA ACCATTCAAT TTCTTGTTCA	5100
	TTCGGTTTCAT CAAAATCATA CCAAACAATA GTCGCATCTT TTGGTATCTC TTGATATCA	5160
	TCAACTACTT TAAACGGTTC ATATGTAGTT TGATACCGTA TCTTTAAAGC CATCGATACT	5220
30	CCCCCTAAAT AACGAATTCT CTATTATTTT ATCATGAATT AAATAACGTG TATGTCTTAA	5280
	TTTATTTTAG TATGATAGTC ACTAAGGAGA TGTTTATTAT CAAACAACCT TTTACACATA	5340
	CTCAAACCGT AACATCTGAA TTCATTGACC ATAACAATCA TATGCATGAT GCAAATTATA	5400
35	ATATCATTTT TAGTGACGTC GTGAATCGTT TTAATTACAG CCACGGTCTT TCTTTAAAAG	5460
	AACGCGAAAA TTTAGCATAT ACGCTATTTA CACTAGAAGA ACATACGACA TACCTCTCAG	5520
	AATFGTCTCT TGGCGATGTA TTTACTGTTA CTTTATATAT TTATGATTAC GATTATAAGC	5580
40	GGTTGCATTT ATTTTAAACA TTAACATAAG AAGATGGTAC ACTAGCATCA ACAAATGAAG	5640
	TAATGATGAT GGAATTAAT CAGCACACAC GTCGTTCTGA TGCTTTTCCT GAATCATTTT	5700
	CAACACAAAT AGCACACTAT TATAAAAATC AATCAACTAT CACTTGGCCT GAACAATTAG	5760
45	GACATAAAAT AGCAATTCCA CACAAAGGAG CATTAAAATG ACAGATGCAT TACAACAAAA	5820
	GATTCATATC GAATTACTAG ATTTATTAGA TGATGTTAAG TTTGAATTAA CAGAATTAAA	5880
50	TGCACAAAAA GGGTTATACA TTAACGGACC AGCAAATCAG CTACTTAAGC GTGGCGTGCA	5940
	TATGGCTTAT GTTCAAGGAC AAAAGCAAGC CATCGATAAT ATTATGACTA TTGTGGAACA	6000
55	ACAGCTTGAA AGATCAACAT TTCCTAGAAC ATTATGATAA ATTTCAAAT GAGGTTGCTC	6060

5 ATAATTTTTT AGATCAATTT TATCAAATTA AAGGGCAATA CTTTATCATC ACACATATCA 6180
 ATACACTTAT TGGTGATTTT CACTCAGAAG CTCATTAACA ATTAGTCTAT ATAACCCTTG 6240
 CTATATTTTC AAAAACAAAA CCCAATTACG TTTTCATGTC AAATATCATC TTGCATGAAA 6300
 TCGTAACTGG GTCATTTATA TGTTATTAGT TATTTTGTGT TACATCCTCA TCTATCGATT 6360
 10 TGGCAATTG TTTAATAGCT TTATGTGATT GTCTAATTGG ATAAATTGGA AAATCATGTA 6420
 CCATCTTAGG ATAATCATAA AACTCAATGT ATTGATGATG TTGCAACATC ATTTGTTCAA 6480
 ATAGCTTCAT ATCAGGATGT GTCATTTTAC GTCCACCACC AAACATATAA ACTGGTGGCA 6540
 15 ATCCTTCTAT TGTGCCATTA ATTGGCGATA TGCGCTTATC TGTTAATGGT AGGCCATTCTG 6600
 CCCATTTTTT CATAATCTCA TTGACACCAA ACTGACTTAG aACCGCATCT TGTTTCGATTA 6660
 AGGCGTCCGA AATATCTTTA TTAGATAGTG TTGCATCTAA AATTGGTGAG ATTAAATACA 6720
 20 ATTTATTCCG TAATGGCTGT TGATTAKCTA AAAGAGATTG TACAAAGGAT AATGCCAGTG 6780
 CACCACCTGA ACCATCACCC ATGACTACGA CATTTTGTAT TCCTACTTCA GATACTAATT 6840
 GATCATAAAC ACGTGTATC GCTTGnAAA GTATCGTcaA TATGnAAACT CTGGTGTCTT 6900
 25 TGGATAGATA GGCAGTACAA CCTCATATAA TGtACTTAAA GTGATTTTAT CCCAACAATC 6960
 TCCAATGGAA CGGTGATGGT TGTAAGTCAT TGAATCCACC GTGAATATAT AAAATTTTCT 7020
 TATCAATTTG ATGTCTGAAA TTAAAGCGAA AGACTTGCAT ATCATCTAAT GACAATTTTT 7080
 30 CTAAATTTGC TTTAACATTT AATGTTGAAG GCTGCTTATG TTTTTTTCTA TTTTCAATTT 7140
 CTCTTTTATA AAAAAATCTT TCAACATCTT GATCATTTTT AAACATAATC GAGCGATTGT 7200
 GAAGCAAATA TTTATTGACA ACGCTATTCA TAACACGGTT TCTAATCAAT GTCTTAACCT 7260
 35 ACCTTTTATAT ATTTTATGTA TCCAATGATk GTCTATCCCC TACATTCTTT GCCAAAAAAA 7320
 GTATATAATG TAGAAGATAT TTTCTTTTTC ACTTTCAAAT TTAAGACTAC AATTGAACAG 7380
 40 TGATTTTTCA TCATTATAAC AGACAAC TAGTATTGAT AAGTAAAGAA AAGAACTTTA 7440
 TACGGAGGTA CCTTGCATGA CAAATCCAAA TCAACGATTA GAACCATTG ATGAGACATT 7500
 TCAACAACCG AATATTCATC GTGGTAAGCG ATATGGTAAG AAAAAACGTT CATTGGTAAG 7560
 45 CATGATTATT CAAATCATTG TTGTWATATT AACCACCATC GCTGGAATAC AGCATGGTGG 7620

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9834 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

	GTCATTACCG amTTTCtTAG AaTCATTTAA AGATGATAAA TATACAAACG TTGGTAATTT	60
5	AAAAGAAGTG AATTTTGATA AAATTGCTGC GACGAAACCC GAAGTAATCT TTATCTCTGG	120
	ACGTACAGCT AATCAAAAGA ATTTAGATGA ATTCAAAAAA GCTGCACCTA AAGCGAAAAAT	180
	TGTTTATGTT GGTGCAGATG AAAAGAACTT AATTGGTTCA ATGAAACAAA ACACTGAAAA	240
10	TATCGGAAAA ATTTACGATA AAGAAGATAA AGCTAAAGAA TTAAATAAAG ATTTAGATAA	300
	CAAAATTGCT TCAATGAAAG ATAAAACGAA AAACCTTCAAT AAAACTGTTA TGTATTTACT	360
	AGTTAACGAA GGTGAATTAT CAACATTTGG ACCTAAAGGT CGTTTTGGTG GATTAGTTTA	420
15	CGATACATTA GGATTCAATG CAGTTGATAA AAAAGTAAGT AATAGCAATC ATGGACAAAA	480
	TGTTTCTAAC GAATATGTTA ATAAAGAAAA TCCAGATGTT ATTTTAGCGA TGGATAGAGG	540
20	TCAAGCGATA AGTGGTAAAT CAACTGCGAA ACAAGCATT AATAATCCTG TATTAAAAAA	600
	TGTTAAAGCA ATTAAAGAAG ACAAAGTATA TAATTTAGAT CCTAAATTAT GGTACTTTGC	660
	AGCTGGATCA ACTACAATA CAATTAAACA AATTGAGGAA CTTGATAAAG TTGTAAAATA	720
25	ATTTTAAAG AGGGGAACAA TGGTTAAAGG TCTTAATCAT TGCTCCCCTC TTTTCTTTAA	780
	AAAAGGAAAT CTGGGACGTC AATCAATGTC CTAGACTCTA AAATGTTCTG TTGTCAGTCG	840
	TTGGTTGAAT GAACATGTAC TTGTAACAAG TTCATTTCAA TACTAGTGGG CTCCAAACAT	900
30	AGAGAAATTT GATTTTCAAT TTCTACTGAC AATGCAAGTT GGCGGGGCC AAACATAGAG	960
	AATTCAAAA AGGAATTCTA CAGAAGTGGT GCTTTATCAT GTCTGACCCA CTCCCTATAA	1020
35	TGTTTGAAT ATGTTGTTTA AATTCAAAA TAAATATGAT AGTGATATTT ACAGCGATTG	1080
	TTAAACCGAG ATTGGCAATT TGGACAACGC TCTACCATCA TATATTCATT GATTGTTAAT	1140
	TCGTGTTTGC ATACACCGCA TAAGATTGCT TTTTCGTTAA ATGAAGGCTC AGACCAACGC	1200
40	TTAATGGCGT GCTTTTCAA CTCATTATGG CACTTATAGC ATGGATAGTA TTTATTACAA	1260
	CATTAAATTA TAATAGCAAT AATATCTTCT TCGGTAAAAT AATGGCGACA scgTGTTTCA	1320
	GTATCGATTA ATGAACCATA AACTTTAGGC ATAGACAAAG CTCCTTAACT TACGATTCCT	1380
45	TTGGATGTTT ACCAATAATG CGAACTTCAC GATTTAATTC AATGCCAAAT TTTTCTTTGA	1440
	CGGTCTTTTG TACATAATGA ATAAGGTTTT CATAATCTGT AGCAGTTCCA TTGTCTACAT	1500
	TTACCATAAA ACCAGCGTGT TTGGTTGAAA CTTCAACGCC GCCAATACGG TGACCTTGCA	1560
50	AATTAGAATC TTGTATCAAT TTACCTGCAA AATGACCAGG CGGTCTTTGG AATACACTAC	1620
	CACATGAAGG ATACTCTAAA GGTTGTTTAG ATTCTCTACG TTCTGTAAAA TCATCCATTT	1680

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	AGTGTTCCTTT TTGAATAATG CTATTACGAT AATCTAACTC TAATTCTTTT GTTGTAAGTT	1800
	TAATTAACGA GCCTTGTTTCG TTTACGCAAA GCGCATAGTC TATACAATCT TTAACCTTCGC	1860
5	CACCATAAGC GCCAGCATTG ATATACACTG CACCACCAAT TGAACCTGGA ATACCACATG	1920
	CAAAATCAAG GCCAGTAAGT GCGTAATCAC GAGCAACACG TGAGACATCA ATAATTGCAG	1980
	CGCCGCTACC GGCTATTATC GCATCATCAG ATACTTCGAT ATGATCTAGT GATAATAAAC	2040
10	TAATTACAAT ACCGCGAATA CCACCTTCAC GGATAATAAT ATTTGAGCCA TTTCTTAAAT	2100
	ATGTAACAGG AATCTCATTT TGaTAGGCAT ATTTAACAAC TGCTTGACT TCTTCATTTT	2160
	TAGTAGGGGT AATGTAAAG TCGGCATTAC CACCTGTTTT AGTATAAGTG TATCGTTTTA	2220
15	AAGGTTCATC AACTTTAATT TTTTCATTTG GGATAAGTTG TTGTAAAGCT TGATAGATGT	2280
	CTTTATTTAT CACTTCTCAG TACATCCTTT CTCATGTCTT TAATATCATA TAGTATTATA	2340
20	CCAATTTTAA AATTCATTTG CGAAAATTGA AAAGAAAGTA TTAGAATTAG TATAATTATA	2400
	AAATACGGCA TTATTGTCGT TATAAGTATT TTTTACATAG TTTTTCAAAG TATTGTTGCT	2460
	TTTGCATCTC ATATTGTCTA ATTGTTAAGC TATGTTGCAA TATTTGGTGT TTTTTTGTAT	2520
25	TGAATTGCAA AGCAATATCA TCATTAGTTG ATAAGAGGTA ATCAAGTGCA AGATAAGATT	2580
	CAAAATGTTTG GGTATTCAAT TGAATGATAT GTAGACGCAC CTGTTGTTTT AGTTCATGAA	2640
	AATTGTTAAA CTTCGCCATC ATAACCTTCT TAGTATATTT ATGATGCAAA CGATAAAACC	2700
30	CTACATAATT TAAGCGTTTT TCATCTAAGG ATGTAATATC ATGCAAATTT TCTACACCTA	2760
	CTAAAATATC TAAAATTGGC TCTGTTGAAT ATTTAAAATG atGctACCGC CAATATGTTT	2820
	TGTATATTTT ACTGGGCTGT CTAAGAGGTT GAATAATAAT GATTCAATTT CAGTGTATTG	2880
35	TGATTGAAAA CAATTAGTTA AATCACTATT AATGAATGGT TGAACATTTG AATACATGAT	2940
	AAAGTcCTTT GATATTGAAA ATTAATTTAA TCACGATAAA GTCTGGAATA CTATAACATA	3000
40	ATTCATTTTC ATAATAACA TGTTTTTGTA TAATGAATCT GTTAAGGAGT GCAATCATGA	3060
	AAAAAATTGT TATTATCGCT GTTTTAGCGA TTTTATTTGT AGTAATAAGT GCTTGTGGTA	3120
	ATAAAGAAAA AGAGGCACAA CATCAATTTA CTAAGCAATT TAAAGATGTT GAGCAAAAAC	3180
45	AAAAAGAATT ACAACATGTC ATGGATAATA TACATTTGAA AGAAATTGAT CATCTAAGTA	3240
	AAACTGATAC AACTGATAAA AATAGTAAAG AATTTAAGGC ACTACAAGAA GATGTTAAAA	3300
	ACCATCTCAT ACCTAAATTT GAAGCATATT ATAAGTCAGC AAAAAATTTG CCTGATGATA	3360
50	CAATGAAAGT TAAGAAATTA AAAAAAGAAT ATATGACGCT TGCAAATGAG AAGAAGGATG	3420
	CGATATATCA ATTAACAAAA TTCATAGGTT TATGTAATCA ATCTATCAAG TATAACGAAG	3480

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	AATTAGCTGA TAATAAAAGT GAAGCAACTA ATCTTACGAC AAAATTAGAA CATAATAATA	3600
	AAGCGTTAAG AGATACTGCG AAGAAGAACC TAGATGATAG TAAAGAAAAT GAAGTAAAAG	3660
5	GCGCGATTAA AAATCACATT ATGCCAATGA TTGAAAAGCA AATTACCGAT ATTAACCAAA	3720
	CTAATATTAG TGATAAGCAT GTTAATAATG CAAGGAAAAA CGCAATAGAA ATGTATTACA	3780
	GTCTGCAGAA CTATTATAAT ACACGTATTG AAACAATAAA GGTTAGTGAG AAGTTATCAm	3840
10	AAGTCGATGT AGATAAGTTG CCGAAAAAGG GTATAGATAT AACTCACGGC GATAAAGCCT	3900
	TTGAAAAAAA GCTTGAAAAA TTAGAAGAAA AATAACTATA ATCATTTTTC AAAGTTAAAA	3960
	ATTTTGAATT TATGGTTAAC ATGTCAACTT ACTATGTGTA TAATGGTAAA CATTGATATT	4020
15	AACTATATGT ATAAAAATGT CACGCAGATG CTATTTAAAT GTGATAAATA TTTTtagagg	4080
	TGAATAGAGT GGCTATAAAG CTAAGTTCAA TTGACCAATT TGAACAGGTT ATTGAGGAAA	4140
20	ATAAATATGT TTTTGTATTA AAACATAGTG AACTTGTCC AATATCGGCA AATGCGTACG	4200
	ATCAATTTAA TAAATTTTAA TATGAACGCG ATATGGACGG TTATTATTG ATTGTCCAAC	4260
	AAGAACGCGA TTTGTCAGAT TATATTGCTA AAAAAACGAA CGTTAAACAT GAATCACCTC	4320
25	AAGCATTTTA TTTTGTAAAT GGTGAAATGG TTTGGAATCG AGACCACGGT GATATCAATG	4380
	TGTCGTCAAT AGCACAAGCA GAAGAATAAT GAACTATAG GGTGGAACA TTTTGCCTTA	4440
	CACTAGTAGA CGTGAATAGC ACAACTTAAA TTCGTGTGAA TCAGAGTAGT TTGGCTATAA	4500
30	TGATGTTCTG ACCTTTTATT TTATGTCACC TTTAGAAGCA GTTAAGTTAG TACTTTTTTA	4560
	CAAACATATG TATAATATAT TCGAGTATTT TTATTGAAAa tATTTTGGAA AACGACGAAT	4620
	CCAATAAGAA AATTTAAACA TGATTTGTAA GTTAGTTTAA TAGGAAATAT ATGCTAAACC	4680
35	AAAAGAAGCA TATTGTTATT TACTGGAATA ATTAATAATC ATGTCATGTT AAATGTTAGC	4740
	ATATAATCAC GAGATAAAAT CTAAAATTTA AGATTAATCT TTTATGAATA AAAAACGTAT	4800
40	CACAACAAAT AATAAAGTAA GGTGGTCAAG GTTATGAAAG TATTAGTAGC CATGGATGAG	4860
	TTTCATGGAA TTATTTCAAG TTATCAAGCT AATAGATATG TTGAAGAGGC AGTTGCAAGC	4920
	CAAATTGAAA CTGCAGATGT AGTTCAAGTA CCATTGTTTA ATGGAAGACA TGAATTATTA	4980
45	GATTCTGTAT TTTTATGGcm ATCTGGGcaA AAGTATCGTA TACCAGTACA TGATGCAGAT	5040
	ATGAATGAAG TTGAAGGTGT TTACGGACAA ACTGATACAG GGATGACCGT TATCGAGGGG	5100
	AATTTATTTT TAAAGGTAA AAAACCAATT GTTGAACGAA CAAGTTATGG TTTAGGAGAA	5160
50	ATGATTAAAC ATGCATTAGA TAACGACGCA AAACATGTTG TAATTTCACT AGGTGGGATT	5220
	GATAGTTTTG ATGCTGGTGC AGGTATGTTA CAAGCATTAG GTGCTCAATT CTATGATGAC	5280

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	GATATGTCGA ACTTACACCC TAAATGGAA ACAGCAAGAA TTCAAGTAAT GTCGGATTTT	5400
	TCAAGTCGAT TATATGGTAA GCAAAGTGAA ATCATGCAAA CTTATGATGC GCATCAGTTG	5460
5	AATCATAATC AAGCAGCAGA AATCGATAAT TTAATTTGGT ATTTTAGTGA GTTATTTAAA	5520
	AGTGAATTGA AAATTGCAAT TGGTCCAGTT GAACGTGGTG GTGCTGGTGG TGGAATTGCA	5580
	GCAGTCTTGA ATGGACTGTA TCAAGCTGAA ATATTAACCA GTCATGCATT AGTAGACCAA	5640
10	CTAACACATT TAGAAAATTT AGTTGAACAA GCGGATTTAA TTATTTTGGG AGAAGGATTA	5700
	AATGAAAATG ATCAGTTGCT AGAAACGACA ACATTGCGTA TTGCAGAACT TTGTCATAAA	5760
	CATCAAAAGG TTGCCATTGC AATTTGTGCA ACTGCTGAAA AGTTTGATTT ATTGAATCA	5820
15	CAAGGGGTTA CAGCAATGTT TAATACATTT ATCGATATGC CAGAACTTA TACTGACTTT	5880
	AAAATGGGTT ACAAATTAGG CATTATACGG TTCAGTCTTT AAAACTGTTG AAAACACATT	5940
20	TTAATGTTGA GGTTTAGTAA AGAAGGACTA AATTGGTGAT GCTGTCATGA TGGTTAATAA	6000
	CATTATGAT GGTTAGCAAA ACGAATTAGA AGATCGAAAG TATACGTAAA AAATATGAAA	6060
	AATCACGCTA TCATTGCACT GAATGTTAGC GTGATTTTAA TATATTAATT AAGCCTGAGT	6120
25	TGAACTAGTA TATAATCGTT GGTTTTTAGT GATTTTCAGC GATATCTTCT ACAATTCCAA	6180
	TGATTACTTG TACTGCTTTT TCCaTAACAT CAATGGATGC aTATTCATAT GGGCCGTGGA	6240
	AGTTACCGCA ACCTGTAAAG ATGTTTGGAG TTGGTAACCC CATAAATGAC AATTGTGAAC	6300
30	CATCTGTACC ACCGCGAATA GGTTCACTGT TTGCTGGAAT ATCTAATTTG GCAAAGACAC	6360
	GTTTAGGTAT ATCAATAATA TGAGGCAATG GTAATATTTT TTCTGCCATA TTGAAATATT	6420
	GATCCGATAT ATCAACTTTA ACTGGATAAT TTTCAAAATG GGCATTGATA TCGTCACGTA	6480
35	TTTCTAAAAT ACGTTTCTTA CGCAATTGCA ATTGTTTTTT ATCATGATCA CGAATAATGT	6540
	ATTGCAAAGT TGCTTTTTCA ACAGTTCCTT CAAAGTTCAT TAAGTGATAA AAGCCTTCGT	6600
40	ATCCTTCTGT TCGTCCGGA ACTTCACTAT CAGGTAGCAA ACTATCGAAT TGTTACCTA	6660
	AACGTATTGC GTTTACCATT GCATTTTTAG CTGAACCAGG ATGAACATTT ACACCGTGCC	6720
	ATGTAATAAC CGCTTCAGCA GCGTTAAAGC TTTCATATTG TAATTCTCCA TATTGACTAC	6780
45	CATCCATAGT ATAAGCAAAA TCAGCATTGA AGCGGTCAAC ATCAAATTTA TGTGGACCAC	6840
	GACCGATTTT TCGTCTGGT GTAAATCCAA TCGGAATGGT ACCATGTTTA ATTTCTGGAT	6900
	GTTCTTGTA ATAACAAATA GCTTCCATAA TTTCCACAAT ACCCGCTTTA TCGTCTGCAC	6960
50	CTAGTAACGA TGTACCATCA GTTACCATTA ATGTATGACC AACTAAACTG TTAAGTTCTG	7020
	GAAATACTTT AGGATCTAAG ACACGTTTAG TATTGCCTAG TTTGTATGGC TTACCATCAT	7080

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	GCGCCAAAAA	TCCAACGTGTT	GGGACGTCGA	CATCGATGTT	ACTTTCTAAT	GTAGCAAATA	7200
	AGTAGCCATT	TTCATCTAAA	TCAGTTGGCA	ATCCTAATTG	TTGTAATTCT	TTTTCTAATA	7260
5	AATGTAACAA	ATCCCATTGC	TTTTCAGTTG	AAGGTGTTGT	TGTAGATTTT	GGATCAGATT	7320
	GCGTATCAAT	TGTCGTATAT	CTTGTTAATC	TATCTATCAA	TTGGTTCTTC	ATTATATTCTG	7380
	ACCCCTTAAA	CTCTATTATT	CATGTTGTAA	GATTTTTTAT	ATGTCTTACC	TTTGATTTTA	7440
10	CCATACAGTT	GTTTGATACG	TGTGTATAGG	TAATATAGAA	TTTCAGAAAC	TAATATACCG	7500
	AAAGCAATCG	CACCTGAAAT	CAGTGTACTT	CTAAAAATGT	ATTTACAGCA	CTTGTATAAT	7560
	CATTGATAC	TAAAAAACGA	GTCGCTTGAT	AAGCTGCACC	ACCAGGTACT	AATGGTATAA	7620
15	TGCCTGGCAC	TATGAATATA	ATTACCGGTC	GTTTATATCT	GCGACTCATA	GTATGACTCA	7680
	TTAAGCCTAA	AATTAAGCTT	CCCAAAAATG	AAGCGCCAAC	TTTTCCAAAC	TCTAAATCTA	7740
20	CCGTAAATTG	GTAAATCGTC	CATGCAATGG	CACCCACAAA	TCCACATGCT	ACTAAGAGGC	7800
	GTTTGGGTGC	ATTGAAAATG	ATAGAGAAAA	GTACTGTTGA	TATAAAGCTG	ATTGTAAAT	7860
	GAAATAAATA	AAATAGCATG	CTTTAACAGT	CCTTCCTTAA	ATGATTAATA	AAACGATTGC	7920
25	GACACCAGCA	CCGATTGCGA	ATGCTGTTAA	TGCAGCTTCA	ACACCGCGAG	ACATACCTGC	7980
	AAGTAATTCA	CCCGCTAATA	AATCTCGAAT	GGCATTGGTA	ATTAATATAC	CAGGGACAAG	8040
	TGGCATGACA	CTGGCTATAG	TAATGATATC	TTGATTGGTT	GCAATGCCTA	ATTTAGTAAA	8100
30	TGTGGCTGCA	ATGGATATGA	CCACAGCGGC	TGCAACAAAC	TCTGAGAAAA	ATTTAATTTG	8160
	TATATAGCGT	TGCACAAAGC	TGAATGTTAA	AAATGCGGAT	CCGCCAGCAA	TGACTGCAAT	8220
	CCAACAATCT	GATGCGACAC	CACCAAACAT	AAATAGGAAG	AAGCCACATG	CAATGGCAGC	8280
35	TGCAAAAGAAA	TTCGTTAAAA	AAGAATATTG	TAATGATGCA	TGCTGTAAAT	GAATAAATTC	8340
	AGATTAGCT	TCATCAATTG	TGAGTTCTTT	ATTTGATATT	TTACGTGAAA	GACTATTTCGT	8400
40	TAAAGCGATT	TTCTCTAAAT	CTGTTGTACG	CTCTTGTTACA	CGAATTAATC	TTGTACTTGT	8460
	TCGATCGTTT	AATGAAAAAA	TAATTGCAGT	TGAACTGACA	AAACTATATG	TATTATGAAG	8520
	ACCATAACTA	TGTGCGATAC	GGTTCATTGT	ATCTTCAACT	CGATATGTTT	CAGCACCTGA	8580
45	TTCaAGTAAA	ATTCTACCTG	CAATTAATAC	AACATCAATC	ACTTTGTTTT	CATCTATAAT	8640
	TGTGATTGAA	TCTGGCATAT	CAATTCACCT	CCAATGATAT	GTGTTATTTA	TTGAACAAT	8700
	TGaAGTTTAC	AACCTGTTGT	TACAACTTTC	AATAGTGAGA	CTTTGTGTTA	GTATGATGAA	8760
50	CTTGTATGGT	TCAAATTTAA	ATAAGAAAAA	CTGTTAATCT	TTGCTATTAT	ACTATGATTT	8820
	AATAATAGCA	AAGGATTAAC	AGTTTTGTCTG	TTGTTATAAA	TTGATAATAG	GGTTAAACAT	8880

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TTTACGCTGT GATTTTGGAT CGTCATCTGT TAAATAACCA ACACCGATAG AACTGACAA 9000
 TTTAATAACT TCTTTGTTTG GTAAATGGAA TGATGATTTT TCAACACCCG AACGAATATT 9060
 5 TTCAGCTAAT TTAACACTTT GATCAAGTGA ATAATTGTGA ATGACAAC TG AGAACTCTTC 9120
 GCCACCATTT CTAAAAATTT TAAATTGATT CGGCACATAG TTTTAAAGTA ATTGAGACAT 9180
 TTGTTTTAAT ACAGCATCAC CTGATTTGTG TGAGTAGGTA TCATTGACAT CTTTAAATCC 9240
 10 ATCGATATCG ATTAATAATA ATGCGATACT TTGATGTTCT TTTTCAGCTT TTCGTGAAAT 9300
 TTCATTTAAA TGTCTATCAA ATTCTTTTAC ATTACCTAAG CCTGTTAAGT AATCATATTT 9360
 ATCTTCGTTT TCATAACGAT TTACGAGTGA GAAGAAATGC CAAATATCGA CAAATGTTAT 9420
 15 CGCTGAAGCT AAAGTGATAA TTAATGAAAT TGGTATTAAA ATGATAACTT CCGATAGTGT 9480
 GTAAATAGGA CTCACTAACG CGACACCAA TAAATGATT ATTGTAACAA CATTAAGTAT 9540
 20 TAATAATGAT AGCACATCAT TTGTTTTTAA AAATGGTCCA ATAGCACTTG TTAGTGCAGC 9600
 AATAACAATC AACGTAACAC CGTACATAAT CGAGTTGTTA AATACTACAA TTTCAACAAT 9660
 TGCTACAATT ACTGTGGCAG ATAATGTATA GACCATATTT GTAAATCTAC CTAAAAACAA 9720
 25 TAAAGGAACG AATGTTAAGT GAATTAAATA ATCTTCACGA TAAGGGATAG GGTAGACAGA 9780
 TAATAATAAT GATACGATTG TCATTAAAAC AGTGACATAA GCCTTAGAAA AAAC 9834

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23439 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

TCTCAATCAG ATGAAAAATT GCATATCGTA GGTTTTACAG AAAGTGCAA ATATAATGCG 60
 40 TCATCAGTCA TTTTCACGAA TGACGCTACC ATTGCCAAGA TCAATCCTAG ATTGACTGGA 120
 GATAAAATTA ATGCAGTTGT TGTACGTGAT ACAAATTGGA AAGACAAAAA ATTAAACCAA 180
 45 GAGCTTGAAG CGGTAAGTAT TAATGACTTT ATTGAAATT TACCAGGTTA TAAACCACAG 240
 AACTTAACAT TAACTTTTAT GATTTCAATC TTATTTGTCA TTTTCAGCTAC AGTTATAGGC 300
 ATTTTCCTAT ATGTCATGAC ATTACAAAAG ACGAGTTTAT TTGGCATATT AAAAGCTCAA 360
 50 GGATTTACGA ATGGCTATTT GCGGAATGTG GTAATTTTCG AGACGGTCAT ATTAGCACTA 420
 TTTGGTACGG CATTGGCTT ACTGTTAACA GCGGTTACAG GTGCATTTTT ACCTGATGCA 480

	TCTGTATTAG GAAGTTTATT CTCCATTTTA ACAATTAGAA AAATAGATCC GTTAAAGGCG	600
	ATTGGGTAGG AGGTGTAGCA AATGTTGAAA TTTGAAAATG TAACAAAGTC ATTTAAAGAT	660
5	GGGAATCGTA ACATTGAAGC GGTAAAGAT ACAAATTTTG AGATAAATAA AGGTGATATT	720
	ATAGCATTGG TTGGACCTTC TGGCTCTGGT AAAAGTACAT TTCTAACTAT GGCAGGTGCT	780
	TTACAAACAC CGACATCTGG GCACATTTTA ATCAATAACC AAGATATTAC GACAATGAAG	840
10	CAAAAAGCAT TGGCAAAAGT TAGAATGTCT GAAATAGGTT TTATTTTACA AGCTACAAAC	900
	CTTGTACCAT TTTTAACGGT AAAGCAACAA TTTACATTAT TGAAAAAGAA AAATAAGAAT	960
	GTTATGTCTA ATGAAGACTA TCAGCAACTT ATGTCACAAT TAGGTCTAAC TTCATTGCTT	1020
15	AATAAGTTAC CTTCAGAAAT TTCAGGTGGT CAGAAACAAC GTGTGGCGAT AgCaAAGCGT	1080
	TATATACGAA TCCGTCGATT ATTTTAGCGG ATGAACCTAC CGCGGCGTTA GATACTGAAA	1140
20	ATGCGATTGA AGTCATTAAA ATTCTACGTG ATCAAGCCAA ACAAAGAAAG AAAGCATGTA	1200
	TTATTGTTAC ACATGATGAA CGACTTAAAG CATATTGTGA TCGTTCATAT CATATGAAAG	1260
	ATGGCGTCCT TAATCTTGAA AATGAAACAG TAGAATAGTT TTATTAAGCC GGTACATCAT	1320
25	GTGCCGGTAT TTTTATGTTT ATGTATTATT TGAATAAACT TTCACATTCA ATTAATAATA	1380
	ATTATTATCG AAAATCAGAA ATATTCCGTG AAATATAATA TTTTTTGTAG TAAAATGGCC	1440
	TCTAAGTATT CAATATTTAA ATATGGGGAT TGAATATAAA ATTATCGTAA TGGGGGTCAA	1500
30	TGGTTATGGA TTTATTGATA GGTACTTTAT TTTTATTTT GGTCTTAGTG ATTTTACAT	1560
	TATTTACATA TAAAGCGCCT AATGGTATGC GTGCCATGGG AGCATTAGCT AATGCAGCAA	1620
	TCGCAACATT TTTAGTGGA GCAITTTAATA AATATGTTGG TGGCGAAGTA TTCGGTATTA	1680
35	AATTTTTAGA AGAGCTAGGA GACGCTGCGG GAGGTCTAGG TGGTGTGCT GCGCTGGAT	1740
	TAACAGCATT AGCTATCGGT GTGTCACCAG TATATGCATT AGTTATAGCA GCCGCGTGCG	1800
	GTGGTATGGA TTTATTACCA GGTTCCTTTG CGGGTTATAT GATTGGATAT GTGATGAAAT	1860
40	ATACAGAGAA ATATGTGCCG GATGGTGTG ACTTAATTGG ATCGATTGTC ATCTTAGCGC	1920
	CATTAGCTCG TCTTATTGCA GTATTATTAA CGCCAGTAGT GAATAGTACA TTGATTGCAA	1980
45	TTGGTGATAT TATCCAAAGT AGTACGAATA CGAATCCAAT TATCATGGGT ATCATTTTAG	2040
	GTGGTATTAT TACGGTTGTC GGCACAGCGC CATTGAGTTC AATGGCATTG ACAGCATTAT	2100
	TAGGTTTAAC GGGTGTACCT ATGGCTATTG GTGCCATGGC AGCATTTAGT TCGGCATTTA	2160
50	TGAATGGGAC GCTATTCCAT CGCTTAAAAT TAGGTGATCG TAAGTCTACG ATTGCAGTAA	2220
	GTATTGAACC TTTATCACAA GCAGATATTG TATCAGCCAA TCCAATTCCA ATCTATATTA	2280

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	ATGCGACAGG TACAGCTACA CCGATTGCAG GATTTTTAGT TATGTTTGA TTTAATCATC	2400
	CGACGACAAT TGTGATTAT GGTGTAGTAA TGGCGATTGT AGGTGCGCTT GCAGGTTATC	2460
5	TTGGTTCAAT TGTATTTAAA AAATATCCAA TTGTTACTAA GCAAGACATG ATTAATCGAG	2520
	GTGCAGTAGA CGCATAGCAT CATCATATTG AATAGTAAAA ACAAATAAAA CATAGTAACG	2580
	TGATTCAGTC GATGTAACAG TCGATAATGA GTCACGTTTT TTTATAGAAA AATACAAGAC	2640
10	ATAAAAAATGT CATAATTTAT TGTGACAAAA TATCATACTG TATAAACATT TATCATTTTC	2700
	TCAAGTACCT TTTACACGAT GGAATGAACT TACTTTTTAC GAAATTATGC GTATTTTATA	2760
	AACAAATATC ATTGATATAA CGGTAAATGT AAGCGTTTAC AACAGAAATA ACAGCATGCT	2820
15	ACGATATTTT TGTAAATTCA CTGATTCAAG TATTTTAAAGT CAATATGAGG AGGGATGTTA	2880
	TGAGCGATTC TGAGAAAGAA ATTTTAAAAA GAATTAAAGA TAATCCGTTT ATTTCAACAC	2940
20	GTGAACTTGC TGAGGCAATT GGATTATCTA GACCCAGCGT AGCAAACATT ATTTCAAGAT	3000
	TAATACAAAA GGAATATGTT ATGGGAAAGG CATATGTTTT AAATGAAGAT TATCCTATTG	3060
	TTTGTATTGG CGCAGCGAAT GTAGATCGTA AGTTTTATGT GCATAAAAAT TTAGTTGCAG	3120
25	AAACATCAAA TCCTGTAACG TCAACACGCT CTATTGGTGG CGTAGCAAGA AATATTGCTG	3180
	AGAACTTAGG TAGGCTTGGC GAAACGGTCG CTTTTTTATC TGCTAGTGGA CAAGATAGTG	3240
	AATGGGAAAT GATTAAACGA TTGTCCACAC CATTATGAA TTTGGATCAT GTTCAACAAT	3300
30	TTGAAAATGC GAGTACAGGT TCATATACAG CTTTAATTAG TAAAGAAGGC GACATGACAT	3360
	ATGGCTTcGC AGATATGGAA GTGTTTGACT ACATTACGCC TGAATTTTTA ATTAAGCGTT	3420
	CACACTTATT GAAAAAGGCT AAGTGCATTA TTGTAGATT GAATTTAGGC AAAGAGGCAT	3480
35	TAAACTTCTT ATGTGCCTAT ACCACGAAAC ATCAAATCAA ATTAGTTATC ACCACGGTTT	3540
	CTTCCCCAAA AATGAAAAAT ATGCCTGATT CATTACATGC TATTGATTGG ATTATCACGA	3600
	ATAAAGATGA AACAGAAACA TACTTAAATT TAAAAATAGA ATCTACTGAT GATTTAAAAA	3660
40	TAGCTGCTAA ACGCTGGAAT GATTAGGTG TAAAAATGT TATTGTGACA AATGGCGTGA	3720
	AAGAATCAT TTATCGAAGT GGTGAGGAAG AAATCATTAA GTCAGTTATG CCATCAAATA	3780
45	GTGTGAAAGA TGTTACAGGT GCAGGCGATT CATTCTGTGC TGCAGTAGTG TATAGCTGGT	3840
	TAAATGGGAT GTCTACTGAA GATATATTAA TTGCTGGTAT GGTTAACGCA AAGAAAACGA	3900
	TAGAAACGAA ATATACAGTT AGGCAAAACC TAGATCAACA GCAACTTTAT CACGATATGG	3960
50	AGGATTATAA AAATGGCAAA TTTACAAAAG TATATTGAGT ATTCTCGAGA AGTTCAGCAA	4020
	GCACGGGAGA ACAATCAACC GATTGTAGCA TTAGAATCAA CAATTATTTT GCATGGTATG	4080

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	GCCATTCCAG CAACCATAGC CATTATAGAT GGCAAAATTA AAATTGGTTT AGAAAGCGAA	4200
	GATTTAGAAA TACTGGCAAC TAGTAAAGAC GTTGCTAAAG TATCTAGAAG GGATTTAGCA	4260
5	GAAGTTATTG CGATGAAGTG TGTGGTGCT ACTACTGTAG CGACGACGAT GATATGTGCT	4320
	GCAATGGCTG GTATTCAATT TTTGTTACA GGAGGTATTG GGGGCGTCCA TAAAGGTGCA	4380
	GAACATACGA TGGACATTTT AGCAGACTTA GAAGAACTGT CTAAAACAAA TGTCCTGTT	4440
10	ATCTGTGCAG GTGCCAAATC AATTTTAGAC TTACCTAAGA CGATGGAGTA TTTAGAAACA	4500
	AAAGGCGTTC CAGTTATTGG ATATCAAACG AATGAATTGC CAGCATTCTT CACTCGCGAA	4560
	AGCGGTGTTA AGTTAACAAG TTCGGTTGAA ACGCCAGAAC GACTTGCTGA CATTCAATTA	4620
15	ACAAAACAGC AGTTAAATCT TGAAGGTGGC ATTGTTGTTG CTAATCCAAT TCCATATGAG	4680
	CATGCCTTAT CAAAAGCATA TATTGAGGCA ATCATAAATG AAGCTGTTGT TGAAGCGGAA	4740
	AATCAAGGTA TTAAAGGTAA GGACGCCACA CCGTTCTTGT TAGGGAATAA TGTAGAAAAA	4800
20	ACGAATGGTA AAAGTTTAGC AGCAAATATA AAAGTTGTTG AAAACAATGC GGCCTTGGGT	4860
	GCTAAATTTG CTGTCGCTGT TAATAAATTA TTGTAGGTGA TGATACATGA ATATTTTATT	4920
25	CGCTATCACA GGGATAGCAT TTGCACTATT TGTTCGTTTT TTATTCAGTT TTGATCGTAA	4980
	AAAAATAGAC TTCAAAAAGA CGTTAATAAT GATATTTATT CAAGTGTGTA TCGTGTATT	5040
	TATGATGAAC ACAACGATTG GTTTGACAAT TTTAACTGCA CTAGGTTTAT TTTTGAAGG	5100
30	GCTAATAAAT ATTAGTAAAG CAGGCATAAA TTTTGTTTTT GGAGATATAC AAAATAAAAA	5160
	TGGCTTTACG TTCTTTTTAA ACGTATTACT GCCATTAGTT TTTATTTCTG TATTAATAGG	5220
	CATCTTTAAT TATATTAAGG TATTACCATT TATTATCAAA TATGTAGGTA TCGCTATTAA	5280
35	TAAATAAAT AGAATGGGGC GCTTAGAAAG TTATTTTGCT ATTTCAACAG CAATGTTTGG	5340
	GCAACCAGAA GTATATTTAA CAATAAAGA TATTATTCCA AGATTATCTA GAGCGAAATT	5400
	ATATACAATT GCGACGTCTG GTATGAGTGC TGTTAGTATG GCAATGCTAG GTTCATATAT	5460
40	GCAGATGATT GAACCCAAGT TCGTAGTTAC AGCAGTAATG TTAAATATTT TTAGTGCGCT	5520
	TATCATCGCC AGTGTAAATCA ATCCCTATAA ATCTGATGAT ACTGATGTTG AAATTGATAA	5580
45	CTTAACGAAA TCCACAGAAA CTAAAACATT GAATGGAAAA ACAGGAAAAC CTAAGAAAGT	5640
	TGCCTTTTTC CAAATGATTG GTGATAGTGC GATGGATGGG TTAAATTCG CTGTTGTAGT	5700
	AGCCGTAATG TTGTTAGCAT TTATTTTATT AATGGAAGCA ATTAATATCA TGTTTGGTAG	5760
50	TGTTGGTTTG AACTTTAAAC AGCTTATTGG CTATGTGTTT GCACCAATCG CATTCTTAAT	5820
	GGGATTCCA TGGAGCGAAC TGTTCCAGCT GGCTCTTTAA TGGCGACTAA ATTAATTACA	5880

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	CAAGGTATCA TTTCAGTTTA CTTAGTAAGc TTCGCTAATT TTGGTACGGT TGGTATCATC	6000
	GTAGGTTCAA TTAAAGGCAT TAGTGATAAA CAAGGAGAAA AAGTTGCATC CTTTGCAATG	6060
5	AGGTTGCTAC TTGGTTCAAC TCTAGCTTCA ATCATTTCAG GATCAATCAT TGGCTTAGTA	6120
	TTGTAAATGA ATCGAAGTAC CTAAATTAAA TTCATGGCAA AGCTAAACCC CGTCACCAAG	6180
	TTGGCGCAAC AGCGcATgca TAACTTAGTG ACGGGGTTTT ATCATAACAA TCTACTTTTT	6240
10	CGTAGCCGTT TTTGAAATGT ATGTTGATGG TTTATCTTTT TCAAAAATTG TTAATCCCGT	6300
	TATATCTTTT TTATGTTTTG AAGGGACAAT GAAGCTAAGT ATATAAGCAA AGACAAAAGC	6360
15	AACTGTAAAT GAAATGGTAG ATACATAGAA AGGTGAGTTA CCTTTGCCAA CACCATTATA	6420
	GACATAAGCA AAGATGATAC CCAATATTAA TCCACAAATA ACACCGAATG TATTCGTACG	6480
	TTTAGTGAAA ATACCAACTG CAAATACACC AGCCAATGGA ACGCCGAATA ATCCAGTCAC	6540
20	AAACAAGAAT AAATCCCATTA AGTCATTTGA ATTAGAAGCA ATTAAGTATA GTGACATTCC	6600
	AAAACCGAAA ATACCTGCAA TGATAATAAT GAAACGTGCA AAGTTAACTT CGTGTCGCTC	6660
	GCTACCTTTT CCGAAGAAGC GTTGCTTAAT GTCGATTGAA ATACAAGCAG ATATAGAATT	6720
25	TAAACTAGAT GAAATGGTAG ACTGTGCAGC GCGGAAAATG GCTGCAATAA GTAATCCTGC	6780
	TACAAATGGT GGCATCTCAG TCAAAATGAA ATATGGCACT ACAGATGATG TATTGAAGCC	6840
	TTTTGGTAAA ACAGCTTCAT GTGTATAAAA TGAATACAGC ATTGTACCCA TACCATAAAA	6900
30	TAAGGGTGCT GAAATTAAAG CTAGGATACC ATTTGTCCAT AACGATTTAT TTGTTTCTTT	6960
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	GTGTTGTATT TGGAAATTGG AATTGGTTAT ACTACACCAC AATTGTGTAA GCATCCTTTT	21060
	CAGCGTATGA CACGTAAAAA TGAAAATGCC CTTTATATGA CGATGAATAA AAAGGCATAT	21120
25	CGCATTCCGA ATTCAATTCA AGAACGTACC ATACATTTAA CTGAGGATAT CTCAACATTG	21180
	ATTACAGCAG CACTCCGGAA CGACAGCACA ACGAAAAATA ACAACATTGG AGAGACAGAA	21240
	GATGTACTTA ATAGAACCGA TTAGAAATGG AGAATATATT ACTGATGGTG CGATTGCACT	21300
30	CGCTATGCAA GTTTATGTTA ACCAGCATAT CTTTTTAGAT GAAGATATTT TATTCCCTTA	21360
	TTATTGTGAT CCAAAAGTGG AAATTGGACG TTTTCAAAAT ACTGCTATAG AAGTGAATCA	21420
	AGATTATATA GATAAACACA GTATTCAAGT AGTTCGCCGA GATACTGGTG GTGGCGCTGT	21480
35	GTATGTTGAT AAAGGTGCCG TTAATATGTG TTGTATTTTA GAACAAGACA CTTCAATTTA	21540
	TGGTGATTTT CAACGATTTT ATCAACCAGC TATAAAGGCG TTGCATACAT TAGGTGCAAC	21600
	AGATGTGGTA CAAAGCGGTA GAAATGATTT AACATTGAAT GGTAAAAAAG TGTCAGGCGC	21660
40	CGCAATGACA TTAATGAATA ATCGTATTTA TGGCGGTTAT TCGCTATTAC TTGATGTTAA	21720
	TTATGAAGCA ATGGATAAAG TGTTAAAGCC TAATCGCAA AAGATTGCAT CGAAAGGGAT	21780
45	TAAATCTGTG CGCGCACGTG TTGGTCATCT TAGAGAAGCA CTGGATGAAA AGTATCGTGA	21840
	TATAACCATT GAAGAATTTA AAAATTTAAT GGTGACGCAG ATTTTGGGAA TCGATGACAT	21900
	TAAAGAGGCG AAACGATATG AATTAACGGA TGCAGATTGG GAAGCGATTG ATGAATTAGC	21960
50	TGATAAAAAG TATAAAAATT GGGATTGGAA TTATGGCAAG TCACCCAAAT ATGAATACAA	22020
	TCGAAGTGAA AGATTATCTT CAGGTACGGT AGACATAACA ATTTCTGTTG AACAAAATCG	22080

AGAAGCATT A CAAGGAACAA AAATGACAAG AGAAGATT A ACGCATCAGT TAAAGCAATT 22200
 AGACATCGTT TATTATTTTG GCAATGTTAC GGTAGAAGCA TTAGTGGATA TGATTTTAAG 22260
 5 TTAATATTGT TATTTTATGT ATGCTGAATC ATTGGAAGTG TTTGCTTGCT CTTGAAAAGG 22320
 TGACAATAGT GTTTGGTGAA GGTGAACAT ATGAGTGGAA ATTATTGCCT TTAAC TATTC 22380
 10 AAAGTATGAT ATATATATGG TTTTGTTC TAAATGATTG GGTATTTGAA AATAGATGAG 22440
 TTTAATATTT TAAGGAATAT AATGATGTTT ACTTTTATAA TTCATATAGA ATATTAAGCA 22500
 ATATAAGTCT GTTGATATAT ACAAATATA ATGACTGCTA TAATGAGTAA TCAATAGACA 22560
 15 CAAAGAGGAG ATTATGTGAT GAATAATAAA GTATTAGTAA CCGGTGGTAC AGGGTTTGTT 22620
 GGCATGCGAA TTATTCACG ATTATTAGAA CAAGGTTATG ACGTACAAAC GACGATACGT 22680
 GATTTAAGTA AAGCTGATAA AGTAATTAAA ACRATGCAAG ACAATGGCAT TTCCACAGAG 22740
 20 CGATTAAATGT TTGTCGAAGC GGATTATCA CAAGATGAAC ATTGGGATGA AGCAATGAAA 22800
 GATTGCAAGT ATGCTTGAG TGTAGCATCT CCGGTGTTT TCGGTAAAAC AGACGATGCA 22860
 GAAGTGATGG CGAaCTGcAA TTGAAGGTAT ACAACGTATT TTAAGAGCTG CAGAACATGC 22920
 25 GGGTGTTAAA CGTGTGGTAA TGA CTGCAAA CTTTGTGCA GTTGGTTTTA GTAATAAAGA 22980
 TAAAAATTCA ATCACAATG AAAGTCATTG GACAAATGAA GATGAACCAG GCTTATCAGT 23040
 ATATGAAAAA TCAAAATTGT TAGCTGAAAA GGCAGCGTGG GATTTTGTG AGAATGAAAA 23100
 30 TACAACAGTA GAATTTGCCA CAATCAATCC AGTTGCAATT TTTGGGCCAT CATTAGATGC 23160
 ACACGTTTCA GGAAGCTTTC ATTTATTAGA AAATTATTG AATGGTTCAA TGAAACGTGT 23220
 ACCGCAAATT CCGTTAAATG TTGTTGATGT GAGAGACGTA GCTGAACTGC ACATTTTGGC 23280
 35 AATGACAAAT GAACAAGCTA ATGGCAAGCG ATTTATTGCG ACGGCTGATG GACmaATTWA 23340
 tTTGTTGGGA ATTGcCAAAt TAATTAAAGA AAAGGGCCTG GAAATAGCTC CAAAAGTTCC 23400
 TACTAAAAAA TTACCCAGCT TTATTTTGAG CnAnGnGCC 23439
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(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4522 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CCCTTTGAGA GTATATCATC TAGTCAAATT ATGCCTGTCA TTAGAGCGAC TAGCTTTGAT 60

	TATTATGCAG	TCGATTTAGG	GAAATCATAT	CGTCTAATTG	ACGAAAGCAT	GTTAGAGGAT	180
	TTGAAGTTAA	CTGAACAACA	AATAAGAGAA	ATGTCTCTGT	TTAATGTTAG	AAAATTGTCA	240
5	AATTCATATA	CGACTGATGA	AGTAAAAGGT	AATATTTTTT	ATTTTATTAA	CTCAAATGAC	300
	GGGTATGATG	CAAGTAGGAT	ACTAAATACT	GCATTTTTAA	ATGAAATTGA	GGCACAATGT	360
	CAAGGCGAAA	TGCTCGTAGC	AGTGCCACAC	CAAGATGTGT	TAATTATTGC	AGATATACGC	420
10	AATAAAACAG	GATATGATGT	GATGGCACAT	TTAACAATGG	AATTTTTTCAC	TAAAGGTCTA	480
	GTTCCAATTA	CATCATTATC	CTTTGGATAT	AAACAGGGTC	ATCTTGAACC	GATATTTATT	540
	TTAGGTAAAA	ATAATAAACA	AAAAAGAGAT	CCAAACGTGA	TTCAGCGTTT	AGAAGCAAAT	600
15	CGTCGTAAAT	TTAATAAAGA	TAAATAGAAA	TAATTGGATA	AGGAGTTTTG	TCATAATGAA	660
	TTTATTTTAC	AATCCTAAAT	ATGTAGGAGA	TGTCGCATTT	TTACAAATTG	AACCAGTTGA	720
20	AGGTGAATTA	AAC TACAATA	AAAAAGGTAA	TGTTGTTGAA	ATTACTAATG	AAGGTAATGT	780
	TGTAGGTTAT	AATATTTTTG	AAATTTCAAA	AGATATAACA	ATTGAAGAAA	AAGGTCATAT	840
	TAAATTAACT	GATGAAC TTG	TAAATGTATT	CCAAAAGCGT	ATTT CAGAAG	CTGGTTTTGA	900
25	TTATAAATTA	AATGCTGATC	TATCACC GAA	ATTTGTAGTT	GGCTACGTTG	AAACTAAAGA	960
	CAAACATCCT	GATGCAGATA	AATTAAGTGT	ACTAAATGTA	AACGTTGGAA	ATGACACATT	1020
	ACAAATTGTA	TGTGGCGCGC	CTAACGTTGA	AGCTGGACAG	AAAGTTGTTG	TTGCTAAAGT	1080
30	AGGTGCAGTG	ATGCCTAGCG	GTATGGTAAT	TAAAGATGCT	GAATTACGTG	GTGTTGCCTC	1140
	AAGCGGTATG	ATTTGTTCAA	TGAAAGAATT	GAATTTACCT	AATGCACCTG	AAGAAAAAGG	1200
	TATTATGGTA	TTAAATGACA	GCTATGAAAT	TGGACAAGCA	TT TTTGAAT	AATTAAGGAA	1260
35	GGTAGTGAAA	ATATGAGCTG	GTTTGATAAA	TTATTCGGCG	AAGATAATGA	TTCAAATGAT	1320
	GACTTGATT C	ATAGAAAGAA	AAAAAGACGT	CAAGAATCAC	AAAATATAGA	TrACGATCAT	1380
	GACTCATTAC	TGCCTCAAAA	TAATGATATT	TATAGTCGTC	CGAGGGGAAA	ATTCCGTTTT	1440
40	CCTATGAGCG	TAGCTTATGA	AAATGAAAAT	GTTGAACAAT	CTGCAGATAC	TATTT CAGAT	1500
	GAAAAAGAAC	AATACCATCG	AGACTATCGC	AAACAAAGCC	ACGATTCTCG	TTCACAAAAA	1560
45	CGACATCGCC	G TAGAAGAAA	TCAAACA ACT	GAAGAACAAA	ATTATAGTGA	ACAACGTGGG	1620
	AATTCTAAAA	TATCACAGCA	AAGTATAAAA	TATAAAGATC	ATT CACATTA	CCATACGAAT	1680
	AAGCCAGGTA	CATATGTTTC	TGCAATTAAT	GGTATTGAGA	AGGAAACGCA	CAAGCCAAAA	1740
50	ACACATAATA	TGTATTCTAA	TAATACAAAT	CATCGTGCTA	AAGATTCAAC	TCCAGATTAT	1800
	CACAAAGAAA	GTTTCAAGAC	TT CAGAGGTA	CCGTCAGCTA	TTTTTGGCAC	AATGAAACCT	1860

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	AAACAAAAAT ATGATAAATA TGTAGCTAAG ACGCAAACGT CTCAAATATA ACAATTAGAA	1980
	CAAGAAAAAC AAAATGATAG TGTTGTCAAA CAAGGAACTG CATCTAAATC ATCTGATGAA	2040
5	AATGTATCAT CAACAACAAA ATCAATGCCT AATTATTCAA AAGTTGATAA TACTATCAAA	2100
	ATTGAAAATA TTTATGCTTC ACAAATTGTT GAAGAAATTA GACGTGAACG AGAACGTAAA	2160
	GTGCTTCAAA AGCGTCGATT TAAAAAAGCG TTGCAACAAA AGCGTGAAGA ACATAAAAAAC	2220
10	GAAGAGCAAG ATGCAATACA ACGTGCAATT GATGAAATGT ATGCTAAACA AGcGGAACgC	2280
	TATGTTGGTG ATAGTTCATT AAATGATGAT AGTGACTTAA CAGATAATAG TACAGATGCT	2340
	AGTCAGCTTC ATACAAATGG CATAGAGAAT GAAACTGTAT CAAATGATGA AAATAAACAA	2400
15	GCGTCAATAC AAAATGAAGA CACTAATGAC ACTCATGTAG ATGAAAGTCC ATACAATTAT	2460
	GAGGAAGTTA GTTTGAaTCA AGTATCGACA ACAAACAAT TGTCAGATGA TGAAGTTACG	2520
	GTTCGAATG TAACGTCTCA ACATCAATCA GCACTACAAC ATAACGTTGA AGTAAATGAT	2580
20	AAAGATGAAC TAAAAAATCA ATCCAGATTA ATTGCTGATT CAGAAGAAGA TGGAGCAACG	2640
	aATAAAGAAG AATATTCAGk AAGTCAAATC GATGATGCAG AATTTTATGA ATTAAATGAT	2700
25	ACAGAAGTAG ATGAGGATAC TACTTCAAAT ATCGAAGATA ATACCAATAG AAACGCGTCT	2760
	GAAATGCATG TAGACGCTCC TAAACGCAA GAGTACGCAG TAACTGAATC TCAAGTAAAT	2820
	AATATCGATA AAACGGTTGA TAATGAAATT GAATTAGCAC CGCGTCATAA AAAAGATGAC	2880
30	CAACAAACT TAAGTGTCAA CTCATTGAAA ACGAATGATG TGAATGATAA TCATGTTGTG	2940
	GAAGATTCAA GCATGAATGA AATAGAAAAG AATAACGCAG AAATTACAGA AAATGTGCAA	3000
	AACGAAGCAG CTGAAAGTGA ACAAATGTC GAAGAGAAAA CTATTGAAAA CGTAAATCCA	3060
35	AAGAAACAGA CTGAAAAGGT TTCAACTTTA AGTAAAAGAC CATTTAATGT TGTGATGACG	3120
	CCATCTGATA AAAAGCGTAT GATGGATCGT AAAAGCATT CAAAAGTCAA TGTGCCTGAA	3180
	TTAAAGCCTG TACAAAGTAA GCAAGCTGTG AGTGAAAGAA TGCCTGCGAG TCAAGCCACA	3240
40	CCATCATCAA GATCTGATTC ACAAGAGTCA AATACAAATG CATATAAAC AAATAATATG	3300
	ACATCAAACA ATGTTGaGAA CAATCAACTT ATTGGTCATG CAGAAACAGA AAATGATTAT	3360
	CAAAATGCAC AACAATATTC AGAGCAGAAA CCTTCTGTTG aTTCAACTCA AACGGAAATA	3420
45	TTTGAAGAAA GTCAAGATGA TAATCAATTG GAAAATGAGC AAGTTGATCA ATCAACTTCG	3480
	TCTTCAGTTT CAGAAGTAAG CGACATAACT GAAGAAAGCG AAGAAACAAC ACATCCAAAC	3540
50	AATACTAGTG GACAACAAGA TAATGATGAT CAACAAAAAG ATTTACAGTC ATCATTTTCA	3600
	AATAAAAATG AAGATACAGC TAATGAAAAT AGACCTCGGA CGAACCAACA AGATGTTGCA	3660

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CCAAGTGT TT CATTACTAGA AGAACCACAA GTTATTGAGT CGGACGAGGA CTGGATTACA 3780
 GATAAAAAGA AAGAACTGAA TGACGCATTA TTTTACTTTA ATGTACCTGC AGAAGTACAA 3840
 5 GATGTAAGT AAGGTCCAAG TGTTACAAGA TTTGAATTAT CAGTTGAAAA AGGTGTTAAA 3900
 GTTTCAGAA TTACGGCATT ACAAGATGAC ATTAAAATGG CATTGGCAGC GAAAGATATT 3960
 CGTATAGAAG CGCCTATTCC AGGAACTAGT CGTGTGGTA TTGAAGTTCC GAACCAAAAT 4020
 10 CCAACGACAG TCAACTTACG TTCTATTATT GAATCTCCaA GTTTTAAAA TGCTGAATCT 4080
 AAATTAACAG TTGCGATGGG GTATAGAATT AATAATGAAC CATTACTTAT GGATATTGCT 4140
 AAAACGCCAC ACGCACTAAT TGCAGGTGCA ACTGGATCAG GGAAATCAGT TTGTATCAAT 4200
 15 AGTATTTTGA TGTCTTTACT ATATAAAAAT CATCCTGAGG AATTAAGATT ATTACTTATC 4260
 GATCCAAAAA TGGTTGAATT AGCTCCTTAT AATGGTTTGC CACATTTAGT TGCACCGGTA 4320
 ATTACAGATG TCAAAGCAGC TACACAGAGT TTAAATGGG CCGTAGAAGA AATGGAACGA 4380
 20 CGTTATAAGT TATTTGCACA TTACCCATGT ACGTAnTATA ACAGCATTTA ACnAAAAAGC 4440
 CCCATATGAT GAAAGAATGn CAAAAATTGT CATTGTaATT GATGAGTTGG CTGATTTAAT 4500
 25 GATGATGGTC CGCAAGAAGT TG 4522

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

TCAAGTTTAC GGATACGTAT ATATTTTGCA TGACATTTAG TGCAATAATA TTCATAATTT 60
 GCCCGTTGTT GATAGCTTTC AATGCTGTTA CAAAATCTAG GCGCTCCAAC CTGTTGGCTC 120
 40 AATCGTTTAA AATCTTGATC TTTATGTTGA TAACCTTTAC CAGCAATATG CAAGTGATAA 180
 TGACACAATT CGTGCAGTAT AATTTTACA ACAGCATCTT CTCCATAATG CTCATATTGT 240
 TTTGGATTAA TTTCAATATC ATGGGACTTT AAAAGATAAC GTCCGCCTGT TGTACGTAAC 300
 45 CTTTATTAA AATATGCACA ATGTCGAAAC GTACGTCCAA ATTTTCTTC CGAAAGATTC 360
 TCAACCATTG GCTGAAGTTT GTCATTATTC ATGTGGATCA ATCATCGTTA ATGATACTTT 420
 50 GTCTTTATTT TTGTCAATAC TGTAATCCA AACGTCAACG ATATCACCAA CACTGACAAT 480
 ATCCATTGGA TTTTACGA ACTTCTTAGA AAGTTTCGAA ACATGGACAA GTCCATCTTG 540

TTTCATTCTT TCTTGTAAT CTTCAATTGA TAGCACATCG GATTTAAGGA TTGGTGTTTC 660
 AAACCTCGTCC CTGGATCTC GATTAGGTGC GTTCAAGGAT TTAATAATAT CCTCTAATGT 720
 5 AGGTACACCG ACTTGTAATT CAATCGCCAG T 751

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1076 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

TCTCCAGCTT TAACTTGATC TGGCACTTTA ACAATTGTCT GATCCATACA TACGCGACCA 60
 20 ATAACTTCGC ATTGATGACC ATTTACATTT ACAAAGCTAC CTTCGATTAT GCGTAAATGG 120
 CCATCTGCAT ATCCAATAGG TAACAATGCT ATTGTAGTTG GGTCAGTAGC TGTATAAGTT 180
 GCACCATAAC TTACAGACTC ACCCGCTTGT AGCGTCTTTG TTTGAACTAC ATTAGCAATT 240
 25 AATTGCACAC TTGGTTTAAG GTGTACTTTA ACTTTTGTCT GTACATACTC TGATGGATAA 300
 TATCCATAAA GGGAAATTCC TGGTCTTATT GCATTACAGA ATTGGCAATC CATTAAATAGA 360
 GAGCCTGCTG AGTTCTGACA ATGTATATAT TCAGGTTTAA TTGCTTCATT GACCATATCT 420
 30 TTAAAACGTT GATATTGTTT AGTTGTCATA TCTCCTGGTT CGTCAGCACA GGCAAAGTGT 480
 GTAAACACGC CTTCAAATAC AAGTTGCTCA TATTGTTGAA TGATTTCAAT CACTTCTTGA 540
 TACGTTTTAG TATCTTTAAT ACCTAAACGT CCCATTCTCTG TATCTAATTT AATGTGCAAC 600
 35 CATAACTTTT TCTCTTGCTC ACCAGAAATG TTTTAAATTG CTTCTTTCAA CCACTGTTTA 660
 GACGGAACCG TTAAGGCAAC TCGGTGTTGT ATCGCTTTAT CAATATCTTT AGCTGGTAAC 720
 ACACCTAAGA CTAAATTTT AGCAGTAATC CCATGCATTC TAAGTTCTAT CGCTTCATCT 780
 40 AACGTTGCTA CAGCAAAAAA TGTGGCGCCA TTTTCATTA AATGACGTGC TACTTTAACA 840
 CTACCTAGTC CATAGGCATT GGCTTTAACG ACAGCCATCA CTGTTTTATT TGGATGCAAT 900
 45 GTACTGAATA CTTTGAAATT TGATGCAACA GCGTTTAAAT CTACATTCAT ATACGCAGAT 960
 CTATAATATT TATCCGACAT ATTACTTCCT CCTGTAATTC CCACACGTTT TAAACTAGA 1020
 TCTTAATTAT CATTGTATAA CAAATTTAAA ATGCTGACTT TTCTAAAACA ACTTGG 1076

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2930 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

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TGACCACAAT	GCCCAATACA	ACCATCCCAT	GGTAAAGCCA	AGAGATGAGT	CAATAAAGCG	60
TGTTGAATAA	GAGCTGAATG	AACCTGATAC	TGGATAAAAT	GTTGCCAACT	CTCCAATTGA	120
TGACATTAAG	AAATATAGCA	TGACACCAAT	AACAAGATAA	GCGAGTATAG	CGCCTCCAGG	180
ACCAGCTTGA	GAAATGATAT	TACCAGTAGC	TACAAATAGA	CCAGTCCCAA	TTGCACCACC	240
TATAGCAATC	ATGGAAATGT	GTCTTGAGTT	AAGACTACGG	TTCATTTTAT	TATCTTCCAT	300
ATTTAGTCTC	CCATCTATTT	AAATATACCC	ATTATTGTAA	GCTTTTTAAG	TGTACTATTC	360
AATAACTATT	TAGTACTGTA	AAGCGAAAAA	ATTAAAATTT	TCTGATTTTT	TAATCATCTT	420
GAGCATGTTT	AATTGTAATT	TTGATGGGGT	TAAATTATAA	TATGTATTAA	ATTATAATTA	480
TnATAAATTG	TGGAGGGaTG	ACTATGTCAC	AACAAGACAA	AAAGTTAACT	GGTGTTTTTG	540
GGCATCCAGT	ATCAGACCGA	GAAAATAGTA	TGACAGCAGG	GCCTAGGGGA	CCTCTTTTAA	600
TGCAAGATAT	TTACTTTTTA	GAGCAAATGT	CTCAATTGA	TAGAGAAGTA	ATACCAGAAC	660
GTCGAATGCA	TGCCAAAGGT	TCTGGTGCAT	TTGGGACATT	TACTGTAAC	AAAGATATAA	720
CAAAATATAC	GAATGCTAAA	AtATTCTCTG	AAATAGGTAA	GCAAACCGAA	ATGTTTGCCC	780
GTTTCTCTAC	TGTAGCAGGA	GAACGTGGTG	CTGCTGATGC	GGAcGTGACA	TTCGAGGATT	840
TGCGTTAAAG	TTCTACACTG	AAGAAGGGAA	CTGGGATTTA	GTAGGGAATA	ACACACCAGT	900
ATTCTTCTTT	AGAGATCCAA	AGTTATTTGT	TAGTTTAAAT	CGTGCGGTGA	AACGAGATCC	960
TAGAACAAAT	ATGAGAGATG	CACAAAATAA	CTGGGATTTC	TGGaCGGGTt	TCCAGAAGCA	1020
TTGCACCAAG	TAACGATCTT	AATGTCAGAT	AGAGGGATT	CTAAAGATTT	ACGTCATATG	1080
CATGGGTTTCG	GTTCTCACAC	ATACTCTATG	TATAATGATT	CTGGTGAACG	TGTTTGGGTT	1140
AAATTCCATT	TTAGAACGCA	ACAAGGTATT	GAAAACTTAA	CTGATGAAGA	AGCTGCTGAA	1200
ATTATAGCTA	CAGATCGTGA	TTCATCTCAA	CGCGATTTAT	TCGAAGCCAT	TGAAAAAGGT	1260
GATTATCCAA	AATGGACAAT	GTATATTCAA	GTAATGACTG	AGGAACAAGC	TAAAAACCAT	1320
AAAGATAATC	CATTTGATTT	AACAAAAGTA	TGGTATCAGC	ATGAGTATCC	TCTAATTGAA	1380
GTTGGAGAGT	TTGAATTAAA	TAGAAATCCA	GATAATTACT	TTATGGATGT	TGAACAAGCT	1440
GCGTTTGCAC	CAACTAATAT	TATTCCAGGA	TTAGATTTTT	CTCCAGACAA	AATGCTGCAA	1500
GGGCGTTTAT	TCTCATATGG	CGATGCGCAA	AGATATCGAT	TAGGAGTTAA	TCATTGGCAG	1560

GGTCAAATGC GCGTAGTTGA CAATAACCAA GGTGGAGGAA CACATTATTA TCCAAATAAC 1680
CATGGTAAAT TTGATTCTCA ACCTGAATAT AAAAGCCAC CATTCCCAAC TGATGGATAC 1740
5 GGCTATGAAT ATAATCAACG TCAAGATGAT GATAATTATT TTGAACAACC AGGTAAATTG 1800
TTTAGATTAC AATCAGAGGA CGCTAAAGAA AGAATTTTTA CAAATACAGC AAATGCAATG 1860
GAAGGCGTAA CGGATGATGT TAAACGACGT CATATTCGTC ATTGTTACAA AGCTGACCCA 1920
10 GAATATGGTA AAGGTGTTGC AAAAGCATTG GGTATTGATA TAAATTCTAT TGATCTTGAA 1980
ACTGAAAATG ATGAAACATA CGAAAACCTT GAAAAATAAA TTTGATATGT AGTTTCTATA 2040
TTGCGTAGTT GAGCAGTTTA TGATATCATA ATAAATCGTA AAGATTCCTA ACAAGAGAGG 2100
15 GTGTTTAAACG TGCGCGTAAA CGTAACATTA GCATGCACAG AATGTGGCGA TCGTAACTAT 2160
ATCACTACTA AAAATAAACG TAATAATCCT GAGCGTATTG AAATGAAAAA ATATTGCCCA 2220
AGATTAAACA AATATACGTT ACATCGTGAA ACTAAGTAAT TCTTATCATT CAAATACGAC 2280
20 GATTTGAAAA TAAAGCGGGC TTACCTATTA TATTGGGGAG CTCGCTTTTT TATGAAATTT 2340
TTGTGAAGAG TGATTAATGG ATTGAGTTTC ATCGGTAGAA CAATATATGA TTATATTAGT 2400
TGTTACTTTA TTAaaaTTTG AGAATATTTA TAGAAGGAAA TAGATTACTG ATTTTATAAA 2460
25 GTCACTTTGT TAGCGAATGC TTGAAAGAGT ATTTAATATA GTAGAATTTA AAATTTCAAA 2520
GCGGAATTTA ATAAGTACGA AGTAGTTCTG GGTATGTTTT ATAAATGTTC GATAATACAC 2580
30 TTTAATCTTA AATATGATGG TTTAGAAAAT GATTTAACAA AGAAATGAaa CTTTACTGTT 2640
GAATTATGTG AGGATTGTGT TATTATATAA ATCGTAATAA TTACGATTTG ATAAAAAGTG 2700
AGGTAACAT ATATGGCTAA GAAATCTAAA ATAGCAAAAG AGAGAAAAAG AGAAGAGTTA 2760
35 GTAAATAAAT ATTACGAATT ACGTAAAGAG TTAAGACAA AAGGTGATTA CGAAGCGTTA 2820
AGAAATTTAC CAAGAGATTC ATCACCTACA CGTTTAACTA GAAGATGTAA AGTAACTGGA 2880
AGACCTAGAG GTGTATTACG TAAATTTGAA ATGTCTCGTA TTGCGTTTAG 2930

40 (2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3606 base pairs
(B) TYPE: nucleic acid
45 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

50 CTTCTTGCCA TGGCTCTCTT TATTTAAAAA TGCTTCCAAC TTGTCCATTT GATTGTTTCT 60

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	TTATAAAAAA CTAATTTTAC AAATGCTTTT GCGTTCTTAC AAAAAATGCA TTTGACTATT	180
	ATTATAATAA GCGTATAATT GTCGCATATT ATTTTTTGTA TTTTGGCAA TAACGAAGGA	240
5	GTATTTATGA ATAAAGACAA GCAATTGCAC AACGACAAAA TCAATCTATC CCAATTAGTC	300
	TTATTAGGGT TAGGCTCTTT AATAGGATCT GGTGGCTAT TTGGTGGCTG GGAAGCATCA	360
	TCAATAGCTG GACCAGCAGC AATCATATCA TGGGTTCTTG GATTCCTAGT CATTGGAACC	420
10	ATTGCCTATA ACTACATTGA AATCGGCACA ATGTTTCCTC AATCAGGTGG CATGAGTAAC	480
	TATGCCCAGT ATACACATGG CTCATTATTA GGCTTTATG CTGCTTGGGC GAATTGGGTG	540
	TCTTTGGTGA CAATAATACC TATCGAAGCT GTGTCAGCTG TTCAATATAT GAGTTCTTGG	600
15	CCGTGGCATT GGGCGAAACC AATGAGATAT TTAATGGAAA ATGGCTCTAT TAGCACATAC	660
	GGATTGCTAG CTGTATATCT CATCATTGTT ATTTTTTCAT TATTAACTA TTGGTCCGTA	720
	AAACTTTTAA CATCATTTAC GAGTTTAATT TCTGTATTTA AATTAGGCGT ACCCATGTTA	780
20	ACCATCATCA TGTGATGCT ATCAGGATTC GACACTTCAA ATTACGGCCA TTCGGCAAGC	840
	ACATTTATGC CTTACGGAAG TGCACCGATT TTTGCTGCAA CAACAGCATC AGGGATTATT	900
	TTTTCATTCA ATTCATTCCA GACAATTATT AATATGGGT CAGAAATTAA AAATCCTGAA	960
25	AAAAATATCG CAAGAGGCAT CGCTATCTCA CTGTCAATCA GTGCAGTGTT GTACATCATT	1020
	TTACAAAGTA CGTTTATCAC TTCTATGCCT CAATCAATGT TACAACATAG TGGATGGAAT	1080
30	GGCATCAACT TCAATTCACC ATTTGCTGAT TTAGCTATCT TATTAGGAAT TAATTGGCTC	1140
	GCAATTTTAC TATACATTGA AGCTTTTGTA TCACCATTCTG GTACTGGCGT GTCATTTGTC	1200
	GCCGTTACAG GTCGAGTTTT ACGAGCAATG GAGAAAAATG GACATATCCC TAAATTTCTT	1260
35	GGGAAGATGA ATGAAAAATA TCATATCCCA CGGTAGCAA TCATCTTTAA TGCCATCATT	1320
	AGTATGATTA TGGTTACATT ATTTAGAGAT TGGGGTACGC TAGCAGCAGT TATTTCTACT	1380
	GCAACTTTAG TAGCCTATTT AACTGGCCCA ACGACAGTGA TTGCATTAAG AAAAAATGGGA	1440
40	CCAACAATGA CTCGTCCATT TAGAGCAAAA ATTTTAAAAG TAATGGCACC ATTATCATTT	1500
	GTATTAGCTT CATTAGCTAT ATATTGGGCA ATGTGGCCAA CAACGGCTGA AGTTATTTTA	1560
	ATCATTATAC TTGGATTACC AATCTACTTC TTCTATGAAT ATCGTATGAA TTGGCGTAAT	1620
45	ACAAAGAAAC AAATTGGTGG TAGCTTATGG ATTATTGTAT ATTAAATCGT GCTATCAATA	1680
	CTGTCAATTA TAGGAAGCAA AGAATTTAAA GGCTTAAATA TGATTCATA TCCATTTGAC	1740
	TTTATCGTTA TTATTATTGT GGCATTATC TTCTATTACA TCGGTACAAC GAGTTCATTT	1800
50	GAAAGCGTCT ATTTCCGTCG CGCAACACGA ATCAATACGA AGATGCGTGA GTCATAAAT	1860

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	CACACACATT AACCAACCAT TGATTTC AAC ATCTTGGTTG GTTTTTTATT TTGAAAATCG	1980
	GTTATAAATA ACTAACATAA CAAGATGATG ATCAGGCTGG GACATAAATC AATGTTCTAT	2040
5	GCTCTACGAA GTTATATTGG CAGTAGTTGA CTGAACGAAA ATGCGCTTGT AACAAAGCTTT	2100
	TTTCGATTCT AGTCAGGGGC CCCAACACAG AGAATTTCTGA AAAGAAATTC TACAGGCAAT	2160
	GCAAGTTGGG GTGGGACGAC GATAAAGAAA TACTTTTTCT ATAGAAATTA GTATYtCTTA	2220
10	TGCATGAGTT TTA CT CATGT ATTCATATTT TTAAGTACAC ATTAGCTGTG GCTAATGTAT	2280
	AAGAACCACT ACATAATAAA TCATTTGTGG CTCTTTATCA TTTCTGTCCC ACTCCCCTAG	2340
	AAGTACATCA TATAATGCTG AAAATGGTTT GAGTTAAAAC AGATATCAAG CTCGTCTGAT	2400
15	TCAGTCACAA AATTGTCTTG TTATACTTGT CACCTATCAT CTATAGACCG TGGTATGATT	2460
	AAATTGGGGA TGATAAAGGA GGTTAATAAA TATGAAGATT AATACTACAG GTGGTCAAAT	2520
	TCATGGTATT ACACAAGATG GTTTAGATAT CTTCTTAGGC ATTCCTTATG CAGAACCACC	2580
20	AGTTCATGAC AATCGCTTTA AACATTCTAC GTTAAAAACA CAATGGTCAG AGCCAATTGA	2640
	TGCAACTGAA ATACAACCCA TCCCACCGCA ACCAGACAAC AAATTAGAAG ATTTTTTCTC	2700
	CTCACAATCT ACAACTTTTA CTGAACATGA AGACTGTTTA TATCTAAATA TTTGGAAACA	2760
25	ACATAATGAT CAGACGAAGA AACCTGTCAT CATTTATTTT TATGGTGGTA GTTTTGAAAA	2820
	TGGTCATGGT ACAGCCGAAC TCTATCAACC GGCACATTTA GTACAAAATA ACGACATTAT	2880
30	CGTTATTACA TGCAATTATC GTTTAGGCGC ATTAGGATAT TTAGACTGGT CATATTTTAA	2940
	TAAAGATTTT CATTCCAATA ATGGCCTTTC AGATCAAATC AATGTCATAA AATGGGTGCA	3000
	TCAATTTATT GAATCCTTCG GTGGCGACGC TAATAACATT ACTTTAATGG GTCAGTCTGC	3060
35	AGGCAGTATG AGCATTTTGA CTTTACTTAA AATACCTGAC ATTGAGCCAT ACTTCCATAA	3120
	AGTCGTTCTA CTAAGTGGCG CACTACGATT AGACACCCTT GAGAGTGCAC GCAATAAAGC	3180
	ACAACATTTT CAAAAAATGA TGCTCGATTA TTTAGATACA GATGATGTTA CATCATTATC	3240
40	GACAAATGAT ATTCTTATGC TGATGGCGAA GcTAAAACAA TCTCGAGGAC CTTCTAAAGG	3300
	GCTTGATTTA ATATATGCGC CTATTAAAAC AGATTATATA CAAAATAATT ATCCAACAAC	3360
	GAAACCAATT TTTGCATGTT ATACAAAAGA TGAAGGCGAT ATTTATATTA CTAGTGAACA	3420
45	GAAAAAATTA TCGCCGCAAC GCTTTATCGA CATTATGGAA TTAAATGATA TTCCTTTAAA	3480
	ATACGAAGAT GTTCAGACGG CGAAGcAACA ATCTTTAGCG ATTACACATT GTTATTTCaA	3540
	ACAGCCGATG aAGCAATTTT TACmACmACT CAATATACmA GATTCCAACC GCACCAACTA	3600
50	TGGCTT	3606

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

10	GAAATTAAAA AAGCAATTGG nACAAGATGC AACAGTGTCA TTGTTTGATG AATTTGATAA	60
	AAAATTATAC ACTTACGGCG ATAAC TGGGG TCGTGGTGA GAAGTATTAT ATCAAGCATT	120
	TGGTTTGAAA ATGCAACsAG AACAAACAAA GTTAACTGCA AAAGCAGGTT GGGCTGAAGT	180
15	GAAACAAGAA GAAATTGAAA AATATGCTGG TGATTACATT GTGAGTACAA GTGAAGGTAA	240
	ACCTACACCA GGATACGAAT CAACAAACAT GTGGaAGAAT TTGAAAGCTA CTAAAGAAGG	300
	ACATATTGTT AAAGTTGATG CTGGTACATA CTGGTACAAC GATCCTTATA CATTAGATTT	360
20	CATGCGTAAA GATTTAAAAG AAAAAATTAAT TAAAGCTGCA AAATAATTCA GCTATATAAG	420
	TTAGTGAAAT GAGAGTCTGA AACATATCAA TCTTTTGATA TTGTATTAGG CTCTTATTTT	480
	TATAGCTAGA AAGTTAGATA TTTGTATTTT TTTAAATAAT AAGTGCCGTT GTTATCGTTC	540
25	AATTTAATTA ATGATAGATT AGTATTATTA TAGCTAAAGT AGTATACCTG AGAAAATAGC	600
	TCAATGTATC TCTTTATTAA TAAGTTATAT CATAATTATT TTAGTGATA CTTTATGGAA	660
	GGGATATCAG GGAATGGCTT TCAATTAAAG AAGAGGTTTA AAAGGATTAC AACAGAATGT	720
30	TATGATTTTG TAGAAAGATA TATAACAACG TTTTATAAAA ACATAATATT GTTAATGGAA	780
	AATGAAATGT AAGGGGGATT TCGAGTGA CT AAGAAAGTTT ATTTTAACCA CGATGGTGGT	840
	GTAGATGATT TAGTATCTCT ATTTTATTAT TTACAAATGG AAAACGTTCA ATTGATAGGG	900
35	GTCAGTACAA TTGGTGCTGA TTGTTATTTA GAGCCATCTT TGAGCGCATC AGTAAAAATT	960
	ATTAATCGTT TTTCAAATGA AGATATTCAA GTTGCGCCAT CATATGAACG AGGAAAAAAT	1020
40	CCATTTCTTA AAGAATGGCG TATGCATGCC TTTTATATGG ACGCATTGCC AATTTTAAAT	1080
	GAGCCAGTCA AACATGTTGC TTCAAATGTG AGCGACAAAG AAGCCTTTGA AGACATTATT	1140
	CAAAC TTTAA AGAGACAATC AGAAAAAGTA ACATTATTAT TTACAGGCCC GCTTACAGAT	1200
45	TTAGCAAAAG CACTACAAAA AGATTCATCT ATCGTTCAGT ATATAGAAAA ATTAGTTTGG	1260
	ATGGGTGGCA CCTTTTTACC AAAAGGAAAT GTTGAAGAAC CTGAGCATGA TGGTCTGCA	1320
	GAATGGAATG CATATTGGGA TCCAGAAGCG GTTAAAATTG TTTTGTATAG CGATATAGAG	1380
50	ATTGATATGG TTGCTTTAGA AAGTACGAAT CAAGTACCGC TAACGTTAGA TGTTAGACAA	1440

	GTACCACCAT TAACACACTT TATAACAAAT TCTACTTACT TTTTATGGGA TGTTTTAACG	1560
	ACTGCTTATA TTGGTAACAA GGACTTGGTT CATTCAATTG AGAAAAAGT CGATGTAATA	1620
5	AGTTATGGAC CAAGTCAAGG TAAGACATTT GAGTGTAAG ATGGGCGCAA AATTAATGTC	1680
	ATAAATCATG TAGATAACAA CGCATTTTTT GATTATATAA CTGCACTTGC TAAAAAAGTA	1740
	AATTAACAGC TGTGTAGAAT AATTAAGGTT TTAATTTATA TAGAACAACT TATTGTAAAC	1800
10	TTTTCATTTT TTAAGTTTA CAATGGTGCT ATAATAATGG TCATGAAATA CGAAAGGAAG	1860
	TAAAAATGA CAACAAACA GTTAGTATAT ACAGCTTTAA TGACAGCGAT TATCGCTATT	1920
	TTAGGATTGG TACCGTAAT TCCACTACCA TTTTCTTCAG TACCAATTGT ACTTCAAAAC	1980
15	ATTGGTATTT TCTTAGCAGG TGCGATTTTA GGACGTAAAT ATGGCACATT AAGTGTATC	2040
	GTCTTTTTAT TATTAGTAGT TGCTGGCTTG CCATTGTTAT CAGGTGGTCG CGGTGGCATC	2100
	GGTGTATTCG CAGGTCCTTC AGCAGGGTTT TTACTATTAT ATCCAGTTGT AGCATTTCATG	2160
20	ATTGGGGCGA TTCGAGATAG ATTCATCAAT GAAATTAATT TCTGGATTTT ATTCGTTGGT	2220
	ATTTAGTTT TTGGTGTTAT AGCATTAGAT GTTATTGGTA CATTGATTAT GGGCATGATT	2280
	ATTAACATAC CATTACGAA AGCTATTTCA ATTTCATTAG CTTATTTGCC TGGTGATATA	2340
25	TTAAAGCAA TTGTAGCAAG TTTGATTGGT ACAGCTTTAC TTAATCACTC GCAGTTTCGT	2400
	CAAATTATGG GAATAAAATA ATCATATTTA AGATAGTAAA GTAATTGAAT AAGTTGCTTT	2460
	GAAATTTATA AAAGTGAAAG GAGTAGGTGT CAATGGCTAG TATAAGTATG TCAGATATAT	2520
30	ATTGTAACGG CACTATATTT GAAAATGACG ACGAGCAGTT GATTTATTTA ACGCCTCTT	2580
	TTCCACAACG ATACACAAGT AACACATGGA TATATAAAAA GACGCCTACC CAAGAGCGAT	2640
	GGCTGAAAGA CTTAGAACGT CAACATCAAT TACATACAAA TCAAGGTTCA AATCATTATG	2700
35	CGTTTAGTTT CCCGAAAAT GAACAACCTG ATAATCATTG GATGGCTATG TTAAAGATA	2760
	TGAATTTTGA ACTAGGTATT ATGGAATTGT ATGCCATAGA AAGTGATGCG CTTGCCAATT	2820
40	TGCCGCGTAA CTCTGACGTT GAAATTGCCA TCGTTGACGA GTCGCATATA GATGCCTATT	2880
	TAAAAGTTGC ATATCAGTTT AGTTTGCCAT TTGGAAGA CTATGCAGAT GCACATGAAG	2940
	AAATGGTAAG GGAACATTAT CAAAAAGATG TGATTAAACG CTTAGTAGCT TATTTAAATA	3000
45	ATGAACCTAT TGGCGTTGTA GATGTCATTG AAAGTGAAAA TTACATTGAA TTAGATGGAT	3060
	TTGGTGATT AGAACAATTT CGGCACCAAG GAATTGGATC TACAATTCAA TCGTTGATAG	3120
	GTGAATACGC CATATCAAAA AATCACAAAC CAATCATATT AGTTGCAGAT GGTGAAGATA	3180
50	CAGCAAGA TATGTATGCA AAGCAAGGTT ATGTCTATCA ATCGTTTGT TATCAAATAT	3240

	TAAGCTGGTT TCGAGTAGAA ATCAACTTAC TGCTTTTTAA ATTGTTTTGA GCTACTTATA	3360
	CTTATAAAAA TAGTGCGTTT AAATTGTTGA TTCATGTAGA ATATCGTTCA TTATGACACA	3420
5	CTATAATGAA TATGTTATG TTCAGAATCA ATGATACGTT CTGGATGACT GTATATATTA	3480
	AAGCCACCAT TTCGAATAAA TCCAACGGCC GTAATATTTA GGTCATTAGC TAAGGTTACA	3540
	GCAAGCGTTG TCGGAGCTGA TTTAGATAAA ATGACGCCAA CACCAATTTT TCGCGCTTTA	3600
10	ATTAAAAATT CTGATGAAAT ACGTCCACTA AAAATTAATA CTTTATCTCG GACAGTAATA	3660
	TGTCGCTGAA TACAAAATCC ATATAATTTA TCTAGAGCGT TATGTCTACC AATGTCTTGT	3720
15	CGATGTACAA AAAATGTCAA ACCATCGCTT ATAGCAGCAT TATGTAAGCC ACCTGTTTCT	3780
	TGGTAAATAT GACTTGCCTT TTGTAATCGA GTCATCATGT TAATAATTTG CATTGGAGTT	3840
	AAAGTGATTT TAGACATAGA TGTTTTAGCG ATAGCAGCAT CATTTTGAAA ATAAAACTCA	3900
20	CGACTCTTTC CGCAACAAGA TGCAATCATT CGTTTTGTGG AATATTGAAA GCGATCGCCT	3960
	AAATCTTTAT TAAGTTCAAC ATGGGCAAAA CCTTTACTAT CATCAATCAG TACAGATTTT	4020
	AATTCATCTC GCTTTAAAAT GGCACCTTCC GAAGCCAGAA ATCCAATGAC TAACTCCTCA	4080
25	AGGTTTGTG GACTGTCATAT AACAGTCGCA AATTCCTCAC CATTCAACCAT AATTGTAAGT	4140
	GGAAATTCTG TCACATATTG ATCTGTTGTA TTGAATAATT TTCCATCTTC ATATCTAACA	4200
	ATTGGTTGAC CTAAAGATAC ATCTTTGTTC ATTATCTAAC CCCTTTAATT AGCTTAAACT	4260
30	TTATTTTAAA GCAATTTGCT TAAAATTTTA ACATATTTGC TTAAGTTTGA AATTTGATTG	4320
	ATAAAAATTA ATAGCGAGCA ATCTGTTTGA TTAAATTTGA ATTCGAGAAT ATACATACTA	4380
	GGGCATCAAT TAATAAATAT CAATCTTATG CAAATTTGAC AATTGTTTGA ATCAATATAT	4440
35	AAACAGGCAA CGGTTCTTTT CAAATATAAT AGTAAGTGTA TAATGAAAAT GTAAATATTA	4500
	TTAAAAATGG GGGTTCCTC AATGAAATTG AAACGTTTAT TTGCTGTTGT GATTGCAATG	4560
40	CTTTTAGTAT TAGCTGGTTG CTCTAATTCT AACGATAATA ATGAAAGTAA AAAAGATGAC	4620
	GCAGACAATG GTAAGAAACA AGAGATTCAA GTTGCAGCGG CAGCAAGTTT AACAGATGTA	4680
	ACCAAGAAAT TAGCTTCAGA ATTTAAAAAA GAGCATAAAA ATGCTGATAT TAAATTTAAC	4740
45	TATGGTGGAT CAGGGGCATT AAGAAAACAA ATTGAATCAG GCGCACCTGT TGACGTATTT	4800
	ATGTCTGCAA ATACTAAAGA TGATAGTCA TTAAGAGACA AGAATAAAGC GCATGATACA	4860
	TATAAATATG CGAAAAATAG TCTAGTATTA ATTGGTGATA AAGATTCAA TTACACTTCA	4920
50	GTAAAGACT TAAAGACAA TGATAAATTA GCATTAGGTG AAGTGAAAAC TGTACCAGCA	4980
	GGAAAAATATG CGAAACAGTA TTAGATAAC AATAACTTAT TTAAAGAAGT CGAAAGTAAA	5040

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	CAAGGTTTTG TGTATAAAAC TGACTTATAT AAACAAAATA AAAAAATTGA TACTGTAAAA	5160
	GTAATTAAAG AAGTAGAACT TAAGAAGCCA ATCACATACG AAGCTGGTGC TACATCAGAT	5220
5	AGTAAATTAG CAAAAGAGTG GATGGAATTC TTAAAATCAG ATAAAGCTAA AGAAATACTA	5280
	AAAGAATACC ACTTTGCAGC ATAAGGAGTT GTAATCCATG CCTGACTTAA CACCTTTTTG	5340
	GATATCAATA CGAGTTGCTG TAATCAGTAC GATTATTGTA ACGGTTTTAG GTATTTTTAT	5400
10	ATCTAAATGG TTGTATCGTC GTAAGGGTTC GTGGGTAA GTATTGGAAA GTTTATTGAT	5460
	ATTACCTATT GTTTTGCCGC CAACGGTATT AGGTTTTATT CTATTAATCA TCTTCTCGCC	5520
	AAGAGGACCA ATCGGTCAAT TCTTTGCGAA TGTACTACAT TTACCTGTAG TGTTCACTTT	5580
15	GACAGGTGCT GTGATAGCAT CTGTCATTGT TAGTTTTCCA CTAATGTATC AACATACTGT	5640
	GCAAGGCTTC AGAGGTATAG ACACGAAAAT GATTAATACA GCTAGAACGA TGGGAGCAAG	5700
20	TGAAACGAAA ATTTTCCTCA AATTAAATTTT ACCATTAGCT AAACGCTCTA TTTTAGCAGG	5760
	TATAATGATG AGTTTTGCTC GTGCATTAGG TGAGTTTGGT GCTACATTAA TGGTTGCAGG	5820
	ATATATTCCA AATAAAACGA ATACACTACC TTTAGAAATA TACTTCTTAG TGGAACAAGG	5880
25	TAGAGAAAAT GAAGCGTGGT TATGGGTATT AGTGCTAGTC GCATTCTCTA TTGTGGTTAT	5940
	ATCTACAATT AATTTATTGA ATAAAGATAA ATATAAGGAG GTCGACTAGA TGCTTAAAT	6000
	CAATGTGAAA TATCAATTAA AGAACACTTT AATTCGCATC AATATAGATG ATACTGAACC	6060
30	AAAAATTTAT GCAGTTCGTG GTCCATCTGG CATTGGTAAA ACTACTGTTT TAAATATGAT	6120
	TGCCGGATTA CGTAAAGCAG ATGAAGCTAT TATCGAAGTG AATGGGCAAT TACTTACTGA	6180
	TACGGCAAAA AACGTGAATG TTAAAATTCA ACAACGACGT ATTGGATATC TGTTTCAAGA	6240
35	CTACCAATTG TTTCTTAATA TGACGGTCTA TAAAAATATT ACTTTTATGG CTGAACCATC	6300
	TGAACACATC GATCAATTAA TTCAAACCTT AAACATTGAT CATTGATGA AACAAATATCC	6360
40	TATGACATTG TCAGGTGGAG AGGCACAACG TGTAGCACTT GCACGTGCAC TTAGCACrAA	6420
	ACCAGATTTA ATTTTATTAG ATGAACCTTT TTCTAGTTTG GATGATACTA CAAAAGATGA	6480
	GAGTATTACA TTAGTTAAAC GTATTTTCAA CGAATGGCAA ATACCAATCA TATTTGTGAC	6540
45	ACATTCAAAC TATGAAGCAG AACAAATGGC TCATGAAATT ATTACAATTG GGTAATCATT	6600
	TATTTGCCAT TAAAGAGTTT AGAACGTATT TAAAATTGTA GAAGTGAATG CTTCTATCAG	6660
	CATTTTAATG ATGTTTTAAA CTCTTTTTTA GGGGCAGTTT TTTTGAGAGA CATTGACGCG	6720
50	CGTCATATAA TGAAAGTAAT GATAAAAAGA AAGGATAACT TAATGTGAGT CAAGAACGTT	6780
	ATTCAAGGCA AATTTTATTT AAACAAATAG GTGAAATAGG TCAAAGCAA ATAAATCAAA	6840

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	GAGCAGGCAT TGCCAAACTA ATCATTGTTG ATAGAGATTA TATTGAATTT AGTAATTTAC	6960
	AAAGACAAAC ATTGTTTACT GAAGAAGATG CTTTGAAAAT GATGCCTAAG GTGGTTGCAG	7020
5	CTAAAAAGCA TTTGCTAGCG TTACGTAGTG ATGTTGATAT TGATGATTAT ATTGCCCATG	7080
	TGGATTATTA TTTTTTGGAA ACACATGGAC AGGACGTTGA CGTTATTATT GATGCAACCG	7140
	ATAACTTTGA AACACGACAA CTGATTAATG ATTTTGCATA TAAATATCGT ATACCTTGGA	7200
10	TTTATGGTGG TGTTGTACAG AGTACATATA CAGAAGCTGC ATTTATACCT GGTAAAACAC	7260
	CTTGCTTTAA CTGTTTGGTA CCACAATTGC CAGCATTAAA TTTAACATGT GATACAGTAG	7320
	GGGTCAITCA ACCTGCCGTG ACGATGGCAA CAAGTTTACA ATTAAGAGAT GCGATGAAAG	7380
15	TATTAACGGA ACAACCAATT GACACAAAAA TAACTTATGG CGATATTTGG GAAGGTAGTC	7440
	ATTATTCATT TGGTTTCAGT AAAATGCAAC GTTCAGACTG TACAACTTGT GGAGATGTAC	7500
20	CAAGTTATCC GTATTTAAAC AAGAATGAAC AACGTTATGC AACATTGTGT GGTAGAGACA	7560
	CTGTACAGTA TGAAAATGCA TCAATTACAC ACGACATTCT TGTTCAATTT TTAACAACAC	7620
	ATCAGTTAAA TTATCGCAGT AATTCGTATA TGGTTATGTT TGAATTTAAA GGACACCGCA	7680
25	TTGTTGCTTT TAAAGGTGGA AGGTTTTTAA TACATGGCAT GACACGCACA TCAGATGCCA	7740
	CACATCTAAT GAATTTATTG TTTGGATAAA AAAAGATAAG ACAAAGGAG TGTAATATTA	7800
	TGGGCGAACA TCAAAACGTT AAATTGAATC GTACAGTTAA AGCAGCCGTA CTAACGGTAT	7860
30	CAGATACTAG AGACTTTGAT ACAGATAAAG GTGGTCAATG CGTGCGCCAA CTATTACAAG	7920
	CAGATGACGT TGAAGTGAGT GACGCACATT ATACAATTGT GAAAGATGAA AAAGTAGCCA	7980
	TCACGACGCA GGTGAAGAAG TGGTTAGAAG AAGATATTGA TGTCATCATT ACGACTGGTG	8040
35	GAACAGGTAT TGCACAACGT GATGTGACGA TTGAAGCAGT AAAACCACTT TTAAGTAAAG	8100
	AGATAGAAGG CTTTGGGGAA TTGTTTAGAT ATTTGAGTTA TGTTGAAGAT GTTGGCACGC	8160
40	GTGCATTATT GTCTCGTGCT GTAGCAGGTA CAGTTAATAA TAAATTGATA TTTTCGATTG	8220
	CAGGATCAAC AGGCGCAGTT AAATTAGCAT TAGAAAAGCT CATTAAACCA GAATTAAATC	8280
	ATCTGATTCA TGAGCTTACA AAATAATTTA TTGATTTGAT TGGCGTTGAA AATCTCCAGA	8340
45	TTTACCGCCA GACTTGCTTT CAAGGTAGGT TTCGCCAATA ATCATACCTT TATCAACTGC	8400
	TTTCGTCATG TCGTAAATGG TTAAAGCCGT TGCTGATGCA GCGGTTAAAG CTTCCATTTG	8460
	AACACCGGTT TTGCCAGTTG TAGAGACAGT TGTTTGAATG TTTAAAGTAT AAAGGGGTGC	8520
50	ATTTGTTTCA TCCCAGCTGA AGTGAACATC TATGCCAGTC AATGGTAATG GATGGCACAT	8580
	CGGAATAAGT GTTGATGTAT TTTTGGCAGC CATAATACCA GCGATTTGAG CAGTGTTCAA	8640

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	AATGCTTGAA TGAGCGACAG CAGTTCCTTTT TGTAATTTGT TTGTCTGATA CATCGACCAT	8760
	TTTGGCGTGG CCTTGTGTGAT TAATATGAGT AAACCTCAGTC ATTTTACCCC TCCTAGTGCA	8820
5	TCTAGTATAT CATGAAAAAA TAAAAGTTTT GGAGATGATT TTTAATGGTA GTAGAAAAAA	8880
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10	CGGCAATTAC GGTAGCACTT GAAAAAAGTC TAAATCATAT CTTAGCAGAA GATATTGTAG	9000
	CTACTTATGA TATACCAAGG TTTGATAAAT CACCTTATGA TGGTTTTGCA ATTGCGCAGTG	9060
	TTGATTCACA AGGGGCAAGT GGTGAGAATC GCATTGAGTT TAAAGTGATT GATCATATTG	9120
15	GTGCAGGTTT AGTTTTCTGAT AAATTAGTTG GGGATCACGA AGCGGTGCGT ATTATGACTG	9180
	GAGCACAAAT ACCTAATGGC GCAGATGCTG TTGTTATGTT TGAACAAACG ATTGAACTAG	9240
	AAGATACATT TACAATTGCT AAACCATTTT CAAAAAATGA AAATATATCT TTTAAAGGTG	9300
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	TCGCGGTCCT TGCAACATAT GGCTATGCAG AGGTTAAAGT TATTAAGCAA CCGAGTGTCG	9420
	CTGTTATTGC AACAGGAAGC GAATTATTAG ATGTTAATGA TGTATTAGAA GATGGGAAAA	9480
25	TTGTAAGTCT TAATGGCCCA ATGATTCTGT CCTTAGCAGA AAAATTAGGT CTTGAAGTTG	9540
	GTATTTACAA AACACAAAAA GATGATTTAG ATAGTGGCAT CCAAGTCGTT AAAGAAGCTA	9600
	TGGAAAAACA TGATATCGTT ATTACAACGG GCGGAGTTTC TGTGGAGAT TTGACTATT	9660
30	TACCTGAGAT TTATAAGGCT GTAAAGGCGG AAGTGTATT TAATAAAGTA GCAATGCGTC	9720
	CTGTTAGCGT AACACGGTT GCATTTGTAG ATGGaAAGTA TTTGTTTGa TTATCTGGAA	9780
	ATCCATCAGC TTGTTTTACA GGATTTGAAC TATTTGTGAA nCCAGCTGTT AAACATATGT	9840
35	GTGGCGCACT AGAAGTCTTC CCGCAAATAA TTAAAGCAAC ATTAATGGAA GATTTTACCA	9900
	AGGCAAACCC ATTCACACGA TTTATACGTG CTAAAGCAAC GTTAACAAGT GCTGGAGCTA	9960
40	CTGTAGTACC TTCAGGATTC AATAAATCAG GTGCGGTTGT AGCGATTGCA CATGCTAACT	10020
	GTATGGTCAT GTTACCAGGA GGGTCACGTG GTTTTAAAGC GGGGCATACA GTAGATATTA	10080
	TATTGACTGA ATCTGACGCT GCTGAAGAGG AACTTCCTTT ATGATTTTAC AAATTGTAGG	10140
45	TTACAAAAAG TCTGGTAAGA CAACATTGAT GAGGCATATT GTCTCTTTCT TAAAGTCACA	10200
	TGGTTATACA GTTGCTACTA TTAACATCA TGGGCATGGT AAGGAAGATA TTCAATTACA	10260
	GGATTCAGAC GTCGATCACA TGAAGCATTT TGAAGCGGG GCAGATCAAA GTATTGTACA	10320
50	AGGTTTTCAA TATCAGCAAA CTGTAACACG TGTAGATAAT CAAAATCTTA CTCAAATTAT	10380
	TGAAAAATCT GTTACAATTG ACACCAATAT CGTATTAGTT GAAGGCTTTA AAAATGCTGA	10440

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	GAATGTTTGT TATAGCATT A ATGTAAGGGA GCATGAAGAT TTTACAGCAT TTGAGCAATG	10560
	GTTATTAAAT AAAATTAAAA ATGATTGTGA TACACAATTA ACATAGAGGA TTGAAATGAA	10620
5	TGAAACAATT TGAAATCGTG ACAGAACCGA TACAAACAGA ACAATATCGT GAATTCAC TA	10680
	TAAATGAATA TCAAGGTGCA GTAGTTGTTT TTACCGGTCA TGTTCCGGAA TGGACTAAAG	10740
	GCGTCAAAAC GGAATATTTA GAATATGAAG CGTATATTCC AATGGCTGAA AAGAAATTGG	10800
10	CACAAATTGG AGATGAAATA AATGAAAAAT GGCCTGGAAC GATAACGAGT ATTGTT CATA	10860
	GAATAGGGCC ATTACAAATT TCAGATATCG CTGTATTAAT TGCGGTTTCT TCACCGCATC	10920
	GTAAAGATGC CTATCGAGCA AATGAATATG CAATTGAGCG TATAAAAGAA ATTGTTCCGA	10980
15	TTTGGA AAAA AGAAATTTGG GAAGATGGTT CAAAATGGCA AGGGCATCAA AAAGGGAATT	11040
	ATGAAGAAGC AAAGAGGGAG GAATAAGAGA GATGAAGGTA CTTTACTTCG CAGAAATTAA	11100
20	AGATATATTA CAAAAGCAC AGGAAGATAT TGTGCTTGAA CAAGCATTGA CTGTACAACA	11160
	ATTTGAAGAT TTATTGTTTG AACGTTATCC GCAAATCAAT AATAAAAAGT TTCAAGTTGC	11220
	TGTAAATGAG GAATTTGTAC AAAAATCGGA TTTCATTCAA CCTAATGATA CTGTTGCATT	11280
25	AATTCCACCG GTTAGTGGAG GTTAAGGGAG CATGAAAGCA ATAATTCTTG CAGGTGGTCA	11340
	TTCAGTGC GA TTTGGTAAGC CCAAAGCTTT TGCGGAAGTG AACGGTGAGA CCTTTTATAG	11400
	TAGAGTAATT AAGACATTAG AATCAACAAA TATGTTCAAT GAAATTATTA TTAGTACAAA	11460
30	TGCGCAATTG GCAACGCAAT TTAAATATCC AAATGTTGTT ATAGATGATG AGAATCATAA	11520
	TGATAAAGGT CCATTAGCAG GAATTTATAC AATCATGAAG CAACATCCTG AAGAAGAATT	11580
	GTTTTTTGTC GTTTCTGTTG ATACACCAAT GATTACTGGT AAAGCTGTAA GCACGTTGTA	11640
35	TCAGTTTTTA GTTTCTCATC TTATTGAAAA TCATTTAGAT GTCGCAGCTT TTAAAGAAGA	11700
	TGGACGTTTT ATTCCAACAA TTGCATTTTA TAGTCCGAAT GCATTAGGCG CTATAACTAA	11760
	AGCACTACAT TCTGATAATT ACAGTTTTTA AAATGTATAT CATGAATTAT CAACGGATTA	11820
40	TTTGATGTA AGGGATGTAG ATGCGCCCTC ATATTGGTAC AAAAATATAA ATTATCAGCA	11880
	TGATTTGGAC GCTTTAATTC AAAAATTGTA AGCTGTTAGG AGGTCCACAA ATGGTAGAAC	11940
45	AAATAAAAGA TAAACTAGGA CGTCCCATCC GTGACTTACG GTTATCTGTG ACAGATCGGT	12000
	GTAAC TTTAG GTGTGATTAT TGCATGCCTA AAGAGGTATT TGGAGATGAT TTCGTATTTT	12060
	TACCTAAAAA TGAAC TTTTA ACGTTTGATG AAATGGCTAG AATCGCTAAG GTATATGCAG	12120
50	AATTAGGTGT AAAAAAATA CGCATTACAG GTGGAGAACC ATTGATGCGA CGGGATTTAG	12180
	ATGTACTTAT AGCTAAATTA AATCAAATCG ATGGTATTGA AGATATTGGT TTGACTACAA	12240

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	ATGTCAGTTT GGATGCTATT GATGATACGC TATTTCAATC AATCAATAAT CGTAATATTA	12360
	AAGCGACTAC GATTTTAGAA CAAATTGATT ACGCGACGTC TATTGGTTTG AATGTAAAAG	12420
5	TAAATGTTGT TATACAAAAA GGTATTAACG ATGATCAAAT CATACCAATG CTTGAATATT	12480
	TTAAAGATAA ACATATAGAG ATTTCGATTTA TAGAATTTAT GGATGTTGGT AATGATAATG	12540
	GATGGGATTT CAGTAAAGTT GTAACATAAG ATGAAATGCT TACAATGATA GAGCAGCACT	12600
10	TTGAAATCGA TCCTGTAGAA CCAAAATATT TTGGGGAAGT AGCAAAATAT TATCGCCATA	12660
	AGGATAATGG TGTTC AATTT GGTTTGATTA CAAGTGTTC ACAATCATTT TGTCTACAT	12720
	GTACACGCGC AAGGCTGTCA TCAGATGGGA AGTTTTACGG ATGTTTATTT GCAACTGTCTG	12780
15	ATGGATTTAA CGTTAAAGCG TTTATTCGTT CTGGCGTGAC CGACGAAGAA TTAAAAGAAC	12840
	AATTTAAAGC TTTATGGCAA ATAAGAGATG ATCGATATTC AGATGAGAGA ACTGCTCAAA	12900
20	CAGTTGCCAA TCGTCAACGT AAAAAGATAA ACATGAATTA TATTGGTGGT TAATGTGTAG	12960
	GGACCACTAC ATATTAAATC ATTAGAGATG TTTTAATATT TCTGTCTTAC TCCCTAAAAT	13020
	ACAATATTAT TTATTAAAGT AAAAACGGTC ATATCTATGC CAGATTTAAT AGAAATGATC	13080
25	GTTTTTAAAG TTTTACAAG TTGGCGGGGC CCCAACACAG AAGCTGACAG AAAGTCAGCT	13140
	TACAATAATG TGCAAGTTGG CGGGGCCCCA ACATAGAGAA TTTCAAAAAG AAATTCTACA	13200
	GACAATGCAA GTTGGGGAAC GGGGCCCCAA CACAGAAGGT GACGAAAAGT CAGCATACAA	13260
30	TAATGTGCAA GTTGGCGGGG CCCCAACATA GAGAATTTCA AAAGAAATTC TACAGACAAT	13320
	GCAAGTTGGG GATCAACGAA ATAAATTTTA TGAGAATATC ATTTCTATCC CACTCTTAAG	13380
	AATCACTACA TAATAAATCT TTAGTGGTTC TTAAACATTG ATGTCACACT CCATGCCATT	13440
35	GAGTTGTAAT ATATCTTTTT TAGGTATAAA TGTTGTCGAA TAAACAACAA GTTGTCCAAA	13500
	AGATAATAAT CTAAACAAGA TATAGCCAGC AATTTAATAT TTGTAATAGA TAAAATGCTA	13560
	AGTTTGATAT ATAATAAATT TAAGTAATTG TATAATAATA TGAATTACAA ACATCTAAGA	13620
40	AGAAACATAG GAGGCATCAT ATTATGAGTA ATAAAGTTCA ACGTTTTATA GAAGCAGAAA	13680
	GGGAGTTAAG TCAGTTAAAG CACTGGTTAA AAACAACACA TAAGATTTCA ATTGAAGAAT	13740
45	TTGTAGTCCT TTTTAAAGTG TATGAAGCTG AAAAGATTAG CGGTAAAGAA TTGAGGGATm	13800
	CATTACATTT TGAAATGCTA TGGGATACAA GTAAATCGA TGTGATTATC CGTAAATCT	13860
	ATAAAAAAGA GCTTATTCT AAATTGCGTT CTGAAACGGA TGAAAGACAA GTATTCTATT	13920
50	TCTATAGTAC TTCTCAAAAG AAATTGTTAG ATAAATTAC TAAAGAAATA GAAGTGTTAA	13980
	GCGTTACAAA CTAAAACTT aaaaagcaTG CCAATCTCTA TTCATCATAA TTGCGTCTTG	14040

GTTCATGGCA TTTCTAGTTA CATGACGTCC ATGAATTAAG AAGTAAACAA GCATAGTAAT 14160
 GATTGCTAAA GCGGCCATAA AGCCGAAGAT TTCACTATAT GAAAACATAT GAGTAAATAA 14220
 5 CCCAAGGAAT GATGGACCGA AGCCGACACC TGCATCTAGA CCAACGTAAA AAGTAGATGT 14280
 CGCGATACCA TATTTAATCG GGGGTGAGAC TTTTATCGCA ATAGATTGCA TTGCAGATGA 14340
 TAAATTTCCA TACCCTAAAC CTAGGCAAGC ACCAGCAAGT AATATTAACC AGCTTTGATA 14400
 10 GCTTGAAATT AAGCATACAA ATGAAAGGAA AAGCATGATA AATGCTGGGT AGACAATAAT 14460
 ATTTTCATTT TTATCATCCA TCAATCTACC AGCAATAGGT CTAGTAATTA ACGATGCTAT 14520
 AGCATAGCAA ATAAAGAAAT AGCTTGCTGC AGTGACTAGG TGTCGCTCTA AAGCAAATGC 14580
 15 TTGTAAATAA GTTAGGATGG ACGCATAGGT AACGCCAATT AAAAGCATAA TTACAGCAAC 14640
 AGGAATGGCC TCTTTTGCAA TAAATTGATG AATACTAAAT CTGGGTTTAT CAATGACATT 14700
 AGTTTCAGTT TTGTTATTTG TTACTTCGAA ATCAACTTTT ATAAATAATG AGATAATGAG 14760
 20 TCCGAGTATG CCTAATATGA CACAAATAAT AACAGTAAG TCAATTGCGT ATTTTGTAAT 14820
 AAGTAACATG CCTAGAAATG GGCCAATCGC TGTACCTAAT ACTAACTTA AGGAAAATAA 14880
 ACTGATGCCT TCACTTTTTT TATTAACAGG GGTAACGTAT GCCGCAATAG TACCTGTTGC 14940
 25 AGTTGTCACA ACTGCAGTTG CGATACCGTT TATGAGACGT ACAAAGATTA AAAAAGCTAA 15000
 AGATCCATCA ATAAATAAAA GTAATTGCGT GATAATTAAG GCAATTAAAC CAATAAATAA 15060
 30 TAATCGTTTA GGTCCrATTT sATTTACAAA TTTACCTGTA GCAAATCGA 15109

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9072 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GAGAGTCAAT GGCAAGAAGA ATATAAATAT TTGAGAGCGT TAATCTTTAA TGAAACAGAA 60
 TTAGAGGAAG CGTATAAATG GATGCATCCT TGTACACGT TGAATAATAA AAATGTAGTA 120
 45 CTTATCCATG GCTTCAAAAA TTATGTTGCA CTATTATTTT ATAAAGGTGC CATTTTGGAG 180
 GATAAATATC ATAACTCAT TCAACAGACT GAAAAGGTGC AAGCAGCTCG TCAGTTACGA 240
 TTTGAAATTA TAACAGAGAT TCAAGCACGT ACCGAAGAAA TTAAATATTA TCTAGCCGAA 300
 50 GCAATTAAAG CTGAAAAAGC TGGTAAAAAA GTTGAAATGA AGAAAACAGA GGAATATGTT 360

	AAATTAACGC CAGGCAGACA ACATCAATAT ATATATCATA TTGGACAAGC TAAACGCagT	480
	GgAACCAAGAC AAAAGCGTGT TGAAAAGTAT ATTAACCAAA TACTAGAAGG TAAAGGGATG	540
5	CATGATAAGT AATTAATGAG TAAAGCATAC CGGTTATACA ACAACATACA AGATGACACG	600
	AAACAACCAA TGGCTCATGC TGTTGGTTGT TTTTTAGGT GTGTCTGTCA TGGGCAACAC	660
	TTTGACGTTG GAATTCCGTT ACAGGCTTGG GAGTAGAAAA TGTTAGCAAA AGGCAAGGGT	720
10	GTCTACAATG AATGATGAAG ATATTAAAAT ATAAGGATGA CTTTGTGAGT GCGGATGGG	780
	CGGTTGTCCG TCTGTAACAA TGGATGCGTG TGCATTATTA CAAAAATTCG ACTTTTGTAA	840
	TAATATTTCA CATTTTCGAC ACTTTTTTGC TATAAAACAA CCAATTGAGC GATAATAAAT	900
15	TCGCTTTTAA AAAATATGAG TTATCTATTT AGTTGCCAAA GATAAAATAA TAATGTTTAA	960
	TAACATCATA TAGAGTATGT TAGTTTTTAA TGTCGAATAT ACGAATGTGc AAACAAAGTA	1020
20	ATCGGTAGAA ATTCAACATA CATAGCGCCG TTTACTGTTA AGTATTCACA TTACAGATGA	1080
	AAAATATAAA ATTCTACATA ATCAAGACCA TGATGTGTAC TTGTTTAACT TATGACTCTA	1140
	TTTGTTTAAC AATTGCGATA ATGGTCTTTT TATTTTATGC GTATCATTCG TCATATTTTT	1200
25	TATGAGGAAG GAGAAATGAT TATGTTAAGT ATTAAGCATT TAACGAAAAT TTATTCTGGT	1260
	AATAAAAAGG CAGTAGATGA CATCTCTTTA GATATTCAAT CTGGGGAATT TATCGCATTT	1320
	ATTGGAACCA GTGGAAGTGG CAAAACGACT GCTTTAAGAA TGATAAACCG TATGATTGAA	1380
30	GCGACAGAAG GACAAATTGA AATTGATGGT AAAGATGTTc GGAGTATGAA TCCTGTGCGAA	1440
	TTGCGTAGAA ATATTGGCTA TGTTATTCAA CAAATTGGCT TAATGCCTCA TATGACGATT	1500
	AAAGAGAATA TTGTGTTGGT ACCCAAATTG TTGAAATGGA CTAAAGAGGA AAAGGATAAA	1560
35	CGTGCAAAGG AATTAATTAA ACTTGTGGAT TTACCGGAGT CATTTTTAGA GCGTTATCCA	1620
	GCAQAACTAT CAGGTGGGCA ACAACAACGT ATCGGTGTTG TAAGAGCACT TGCGGCCGAA	1680
	CAAGATATTA TTTTAATGGA TGAACCTTTT GGTGCATTGG ATCCTATTAC GAGAGATACG	1740
40	TTACAAGATT TAGTTAAAAC GTTACAACGA AAATTAGGCA AGACGTTTAT CTTTGTAACA	1800
	CATGATATGG ATGAAGCGAT TAAATTAGCA GACAAAATTT GTATTATGTC AGAAGGTAAG	1860
45	GTGGTGCAAT TTGATACGCC AGACAATATT TTAAGACATC CCGCAAATGA TTTTGTACGT	1920
	GATTTTATAG GACAAAATAG ACTGATTCAA GACCGTCCCA ATGACAAGAC TGTAGAAGGT	1980
	GTAATGATTA AACCAATCAC GATACAAGCA GAAGCAACAC TGAATGACGC CGTTCATATT	2040
50	ATGAGACAAA AACGTGTTGA TACTATTTTT GTAGTAGATA GTAATAACCA TTTACTAGGT	2100
	TTCTTAGACA TTGAAGATAT AAATCAGGGT ATACGTGGAC ACAAAGTTT ACGAGACACC	2160

	ATTTTAAAAA GAAACGTTAG GAATGTACCT GTCGTAGATG ATCAACAGCG TTTAGTAGGA	2280
	CTGATTACGC GTGCCAATGT TGTGTATATT GTATATGACA CGATTGGGG CGATAGTGAG	2340
5	GATACAGTGC AAACAGAACA TGTGGGGGAA GACAcTGCCT CCTCAAAAGT GCATGAGCAA	2400
	CACACTACTA ATGTCAAAGT ACGTGACATA GGAGATGATA AATCATGATT GAGTTCCTAC	2460
	ATGAACATGG TGGACAGTTG ATGTCGAAAA CACTGGAACA TTTCTATATT TCTATAGTGG	2520
10	CATTATTACT TGCCATCATT GTTGCACTAC CTATAGGCAT TTTATTATCA AAAACAAAGC	2580
	GAACTGCCAA TATTGTATTA ACTGTGGCAG GTGTCTTACA AACTATTCCA AACTAGCTG	2640
	TACTTGCTAT TATGATACCG ATTTTGGTG TTGGTAAAC GCCTGCAATT GTAGCGCTAT	2700
15	TTATTTATGT ATTATTACCT ATTTTAAATA ACACGGTACT CGGTGTTCAA AATATTGATA	2760
	GCAACATTAA AGAAGCTGGA AAAAGTATGG GAATGACACA ATTTCAATTG ATGAAGGATG	2820
20	TTGAATTGCC GTTAGCATTG CCGCTTATCA TTGGTGGCAT TCGTTTGTC TCTGTGTATG	2880
	TAATTAGTTG GGCTACACTT GCAAGTTATG TAGGTGCGGG TGGATTAGGT GATTTCATTT	2940
	TCAATGGTTT AAATTTATAT GATCCACTGA TGATTGTAAC TGCAACGGTA CTCGTTACTG	3000
25	CACTAGCATT AGGTGTTGAT GCCTTATTAG CTTTAGTTGA AAAATGGGTA GTTCCCAAAG	3060
	GCTTAAAGT ATCTGGATAA TTAGGAGGCT AAGATAATGA AGAAAATTAA ATATATACTT	3120
	GTCGTGTTTG TCTTATCGCT TACCGTATTA TCTGGATGTA GTTTGCCCGG ACTAGGTAGT	3180
30	AAGAGCACGA AAAATGATGT CAAAATTACA GCATTATCAA CAAGCGAATC GCAAATTATT	3240
	TCACATATGT TACGGTTGTT AATAGAGCAT GATACACACG GTAAGATAAA GCCAACATTA	3300
	GTAAATAATT TAGGGTCAAG TACGATTCAA CATAATGCCT TAATTAATGG GGATGCTAAT	3360
35	ATATCAGGTG TTAGATATAA TGGCACAGAT TTAACGGGAG CTTTGAAGGA AGCACCAATT	3420
	AAAAATCCTA AGAAAGCAAT GATAGCAACA CAACAAGGAT TTA AAAAGAA ATTTGATCAA	3480
	ACGTTTTTTG ATTCGTATGG TTTTGCGAAT ACGTATGCAT TCATGGTAAC GAAGGAAACC	3540
40	GCTAAAAAAT ATCATTTAGA GACAGTTTCA GATTTAGCAA AGCATAGTAA AGATTTACGT	3600
	TTAGGTATGG ATAGTTCATG GATGAATCGT AAAGGCGATG GCTATGAAGG ATTTAAAAA	3660
45	GAGTATGGTT TTGACTTTGG TACAGTGAGA CCAATGCAAA TAGGTCTAGT CTACGACGCA	3720
	TTAAACTCAG AGAAGTTAGA CGTTGCATTA GGTATTCTA CAGATGGTCG AATTGCGGCG	3780
	TATGATTTGA AAGTACTTAA AGATGATAAA CAATTTTCC CACCTTATGC TGCGAGTGCT	3840
50	GTTGCAACAA ATGAATTATT ACGGCAACAC CCAGAACTTA AAACGACGAT TAATAAGTTG	3900
	ACAGGAAAGA TTTCGACTTC AGAGATGCAA CGCTTGAATT ATGAAGCGGA TGGTAAAGGT	3960

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	AAAGGTGGTC ATAAGTAATG GAAGGTAATT TATTACAGCA ATTATTCAAT TATTATGTTA	4080
	CGAACTTTGG TTATCTATGG GATTTATTTT TCAAACACTT ATTAATGTCT GTCTATGGTG	4140
5	TGCTGTTTGC AgCTTTAATT GGTATTCCAT TGGGAATCTT GCTTGCaAGA TACACAAAAC	4200
	TTTCTGGATT TGTAATTACA ATTGCAAATA TAATTCAAAC AGTTCCAGTC ATTGCAATGT	4260
	TAGCTATTTT AATGTTAGTC ATGGGCTTAG GTTCAGAAAC AGTAGTTTTA ACAGTGTTTT	4320
10	TATATGCGTT ACTTCCAATT ATAAAAACA CTTATACTGG TATAGCTAGT GTTGATGCGA	4380
	ATATTAAGGA TGCTGGCAAA GGTATGGGAA TGACACGCAA TCAAGTGCTA CGAATGATTG	4440
	AATTACCGTT ATCTGTTTCG GTTATTATCG GTGGCATTCT TATTGCCTTG GTTGTTGCGA	4500
15	TAGGTGTTGT TGCCGTTGGA TCATTTATAG GAGCACCTAC GCTTGGTGAC ATTGTGATTC	4560
	GTGGTACAAA TGCGACGGAT GGCACAACGT TTATTTTAGC AGGTGCGATT CCGATTGCTA	4620
20	TCATTGCAAT CGTCATTGAT GTACTATTAA GATTTTTAGA AAAACGATTA GACCCAACAA	4680
	CACGACATCG TAAAAATCAA TCTAATCATC GGCCGCAAAG TATTAAATATG TAATAGTAGA	4740
	AGATGTTTAT AATTTAGCGA TTTCGTTTCA TGATTTATAA AAAATGAGGC TACTCAAGGA	4800
25	GCTCAAATAA TCTTTGAGTA GCCTTTTIAT AGGTTGTGTT TGTATGCGTT TACACTAAAA	4860
	TAGCAATTAT TATCATGAAA GTTTTGGAT AAAAAGCGTT AATTATTGTA AAAATACTAA	4920
	AAAATGAGAT GTTTTATTTA TAATTTCTG CAAATTTATG ATATTGTTTC TTAATATATC	4980
30	ATATTAAAAA TTTGTTTTTC TTAAACATAG GAGGCTTATC TAATTCATGG ACACATCAAA	5040
	ACAATTTAGA GGTGACAACC GATTGCTTTT GGGTATCGTT TTAGGGGTTA TTACCTTTTG	5100
	GCTATTCGCG CAGTCACTTG TTAATCTTGT TGTCCCATTA CAATCAACAT ATAGTAGTGA	5160
35	CGTTGGAACG ATAAATATCG CTGTTAGCTT ATCTGCCTTA TTTGCTGGTT TGTTTATCGT	5220
	AGGTGCTGGT GATGTTGCTG ATAAATTTGG TCGCGTCAAA ATTACTTATG TAGGATTGAT	5280
	ATTAAATGTT GTAGGTTTCAT TACTCATCAT CATTACACCT TTGCCAGCAT TTTTAATTAT	5340
40	AGGTAGAATA ATTCAAGGTT TGTCTGCAGC ATGTATTATG CCATCAACAC TTGCTATTAT	5400
	TAACGAATAT TATATTGGTA CAAGAAGACA ACGTGCCTTA AGCTATTGGT CTATTGGTTC	5460
45	TTGGGGTGGT AGTGGTATTT GTACGTTGTT TGGTGGCTTA ATGGCTACAT ATATAGGTTG	5520
	GCGTTCAATA TTTGTTGTTT CAATTCTATT AACATTATTA GCAATGTACT TAATCAAACA	5580
	TGCACCTGAG ACTAAAGCAG AACCAATCAA AGGTATGAAA GCAGAAGCTA AAAAGTTTGA	5640
50	CGTTATTGGT TTAGTCATTT TAGTAGTGAC GATGTTAAGT TTAAATGTAA TCATCACACA	5700
	GACGTCTCAT TTTGGTTTATG TTTCACCGTT AATTCTAGGT TTAATTGTTG TGTTTATCTG	5760

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	AATTTTAAA AATAGAGGAT ACAGTGGTGC AACTATTTC AACTTCTTAT TAAATGGTGT	5880
	AGCAGGTGGT GCACTTATCG TTATTAACAC GTATTATCAA CAACAATTAG GATTTAATTC	5940
5	TTCGCAAACG GGTATATTT CATTAACGTA TTTAATAACA GTGTGTCAA TGATTCGTGT	6000
	AGGTGAAAAG ATTTTATCTC AACATGGTCC GAAGCGCCCA CTATTACTAG GAAGTGGCTT	6060
	TACAGTGATT GGGTTAATCT TATTGTCGTT AACATTTTTC CCAGAAGTGT GGTATATCAT	6120
10	ATCTAGTATA GTTGGATATT TATTGTTTGG TACTGGTTTA GGATTATATG CTACACCATC	6180
	AACTGATACA GCAGTTGCTA GTGCGCCAGA TGATAAGTCG GGTGTTGCTT CAGGTGTGTA	6240
	TAAATGGCG TCATCATTAG GAAATGCATT TGGAGTAGCA GTATCTGGTA CGGTTTATAC	6300
15	TGTGTTAGCA GCTAATTTAA ATTTGAACTT AGGTGGTTTC ACAGGTATGA TGTTTAATGC	6360
	CTTGCTAGCA ATTGTTGCAT TTTTAGTCAT TTTACTATTA GTTCCTAAAA ATCAAACGAA	6420
20	TTTGTAAGAC TGAAATGAAA GCAAGTTATT ATGTAGGGAT TTTAAAGGAA ATTTTGTGAA	6480
	AGTAAGTTTA TCATACACAC TTAATGTTGC GTATTGACGT TTAATGTTAG GTGTGTTCTT	6540
	TTATAGACGA TAAAAGCTGT GTGCATATTA AGCGAATGAT TTTCAAATTG ACGCTAATAT	6600
25	GCGAAAGTAG TATTTTAAA ATGAACAACA ACGATGAAGA GGGGTTTATA GGATGAAAAT	6660
	TGCAATTGCT GGATCGGGTG CATTAGGTAG TGGCTTTGGT GCCAACTAT TTCAAGCAGG	6720
	ATATGATGTC ACACTTATTG ACGGATATAC ATCTCATGTT GAAGCGGTTA AGCAACATGG	6780
30	ATTAAATATA ACGATTAATG GAGAGGCATT CGAGTTAAAC ATTCCGATGT ATCATTTTAA	6840
	TGATCAACCG GACGAAAGCA TTTACGATGT TGTCTTTCTA TTTCCAAAGT CTATGCAATT	6900
	AAAAGAAGTG ATGGAAGATA TGAAGCCACA TATTGATAAT GAAACGATCG TCGTATGTAC	6960
35	GATGAATGGT CTGAAGCATG AAGAAGTCAT TGCGCAGTAT GTTGCTCAAT CACAAATTGT	7020
	CAGAGGTGTT ACGACTTGGA CGGCAGGTCT TGAAAGCCCT GGACACAGTC ATTTACTTGG	7080
	TAGTGGACCA GTTGAAATAG GTGAAGTAGT GGATGAAGGT AAAGAAAATG TTATAAAAGT	7140
40	TGCTGATTTA CTTAACGAAG CGGAATTGAA TGGTGTCATT AGTAAAGATT TATACCAATC	7200
	GATTTGAAA AAGATTTGTG TTAATGGTAC GGCAAATGCA TTAAGCACAG TGTTGGAGTG	7260
45	TAATATGGCA TCGCTGAATG AAAGTAGTTA TGCGAAGTGT TTGATTTATA AATTAACGCA	7320
	AGAAATAGTG CATGTAGCGA CGATTGATAA TGTTCAATTA AATGTTGATG AAGTATTTGA	7380
	ATATTTAGTT GATTTAAATG AAaAAGTTGG TGCGCATTAT CCATCCATGT ATCAAGATTT	7440
50	AATTGTTAAT AATAGAAAA CTGAAATTGA TTATATTAAT GCGCAGTTG CAACATTAGG	7500
	TAAACAACGT CaTATTGAAG CGCCAGTCAA TCGCTTTATT ACTGATTTAA TTCATACTAA	7560

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CAATCACGTG ATATTACGGT CATTATTAAG ATTGAAATGT AATAAATAAA GAACAGCAGT 7680
 AAGGTACTTT CAAATTGAAA TGATCTTGCT GCTGTTTTTC TTGATTGATC TTCGTCATAA 7740
 5 TTCAGATTTG TCATAGGcTA CGACATACTA TTAGTATTTA CTAGACAGTT TTTACGACGA 7800
 CACTTTGAAA AATTTTGAGG CAAATCATTT GGAAGTCTCA CGTGAATTTT GTAAACTCAT 7860
 CAAGCAAGTA ATTATATTAA AAAGACAAAT AGAGAAAAGG TGTTTATAAT GAGTAAAATT 7920
 10 TTTGTAACGT GTGCAACGGG CCTTATTGGC ATTAAATTAG TTCAAAGACT AAAAGAAGAG 7980
 GGGCATGAGG TTGCTGGTTT TACTACATCT GAGAATGGTC AACAAAAGCT AGCTGCTGTT 8040
 AATGTAAAAG CATATATTGG TGATATATTA AAAGCTGATA CTATTGATCA AGCGTTAGCA 8100
 15 GATTTTAAAC CAGAAATCAT TATCAATCAA ATTACGGATT TAAAAAATGT TGATATGGCA 8160
 GCAATACGA AAGTACGTAT TGAAGGTCTT AAAAACCTAA TTGATGCGGC GAAAAAGCAT 8220
 GACGTTAAGA AAGTAATTGC CCAAAGTATT GCCTTTATGT ATGAACCTGG CGAAGGATTA 8280
 20 GCAATGAGG AAACCTCACT TGATTTTAAAC TCAACTGGCG ATAGAAAAGT AACGGTTGAT 8340
 GGTGTGGTTG GTTTAGAAGA AGAAACGGCT CGTATGGATG AATACGTTGT TTTACGTTTT 8400
 25 GGCTGGTTAT ATGGCCCAGG TACTTGGTAC GGAAAAGATG GCATGATTTA TAATCAATTT 8460
 ATGGATGGTC AAGTGACACT TTCAGATGGC GTAACATCAT TTGTGCATCT TGATGATGCA 8520
 GTTGAAACAT CTATTCAAGC TATTCATTTT GAAAATGGTA TCTATAATGT AGCAGATGAT 8580
 30 GCACCTGTTA AAGGTTCTGA ATTTGCAGAA TGGTATAAAG AACAACTTGG TGTTGAACCA 8640
 AATATTGATA TTCAACCTGC GCAACCATTT GAACGTGGCG TAAGCAATGA GAAGTTTAA 8700
 GCGCAAGGTG GTACTCTGAT TTATCAAAC TGGAAAGATG GCATGAATCC AATTAAATAA 8760
 35 TAATTTATCC GTTTAATATA CAAAGAATAA AGACTTGGTC GAATCGTGGA TGATATATTA 8820
 TCAAACGCAC GGCTCGAACA AGTCTTTTTT ATTATGCTCT CGTTATCTTT GTATGAAGGA 8880
 ATAACAGAAT TACAATTAAT GTACTGAATA ATGCAATTAA TGTTGTGATT AGTGCTAATT 8940
 40 TAATTTCTAT TGGTAGCCAA GTCAGTACAA AAGACCAATT ATTGCTACCG AGAATGAGAT 9000
 ATGGTAATGC ATATAATATG AGCGCTAAAG CGATACATAT ACATAATGAT AACCAACTCA 9060
 45 ATACAGCAAT CC 9072

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16826 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

	GTGGAACAGC TGTAACATA TCATTTCTTT CAACATTTAT TGGGAAAATG TTAGCTACAT	60
5	TTCTATATCC GATTAATAAT GTAGTACTTT CATATATnTC TGTAAATGAA AGTGACAATA	120
	TAAAGAAGCA ATATTTGaaa ACTAATCTAA TTGCTATAGC TGGCCTATGT TTAGTCATGA	180
	TTATATGTTA TCCAATTACA ATAATTATTG TCTCTTTACT GTATAACATT GATTCAAGTT	240
10	TATATTCGAA GTTTATTATT TTAGGTAATA TAGGTGTTTT ATTCAATGCA GTGAGTATTA	300
	TGATCCAAAC TTAAATACA AAACACGCAT CAATAACATT ACAAGCGAAT TATATGACGC	360
	TTACACGAT TACATTTATA TTCATAACTA TTTTAATGAC AATTGCGTTT GGTCTAAATG	420
15	GATTCTTTTG GACAACGCTG TTCAGCAACA TTATTAAGTA TGTGATTTTA AATATTATAG	480
	GTTTAAAGTC TAAATTCATT AATAAAAAGG ACGTCGATTA GATGAGTGAA AAAAAGATTT	540
20	TGATTTTATG TCAGTATTTT TATCCGGAAT ATGTATCTTC TGCGACGTTA CCAACTCAAT	600
	TGGCGGAAGA TTTAATTGCG AATCACATTA ATGTCGATGT CATGTGTGGA TGGCCATATG	660
	AATATAGTAA TCATAAACAG GTTTCTAAAA CCGAGATGCA TCGTGGTATT CGCATTGAC	720
25	GTCTCAAGTA TTCGAGGTTT AATAACAAAA GTAAGGTTGG AAGGATCATC AATTTCTTTA	780
	GTTTATTTTC AAAATTCGTG ATTAATATAC CTAAAATGTT GAAATATGAT CAGATTCTTG	840
	TTTACTCTAA TCCACCAATC TTGCCATTAA TACCAGACGT TTTACACAGA CTGCTTAAGA	900
30	AAAAATATTC TTTGTGGTG TATGATATAG CACCTGATAA TGCGATTAAG ACAGGTGCAA	960
	CTCGTCCAGG TAGCATGATT GATAAGCTGA TGCGTTACAT TAATAGACAT GTCTACAAGA	1020
	ATGCTGAAAA TGTCATTGTC CTTGGTACGG AAATGAAAAA CTACTIONA AATCATCAAA	1080
35	TTTCTAAAAA TGCTGACAAT ATCCATGTGA TTCCTAACTG GTATGACATG CGTCAATTAC	1140
	AAGCAATCG TATCTATAAT GACACATTTA AAGCTTACCG TGAGCAATAC GACAAAATTT	1200
	TATTGTATAG CGGTAATATG GGGCAGTTAC AGGATATGGA GACACTTATC TCATTTTAA	1260
40	AATTAAATAA GGATCAGTCT CAAACGTTAA CAATACTTTG TGGTCATGGT AAGAAATTTG	1320
	CAGATGTCAA AACGGCAATA GaAGACCATC GTATTGAAAA TGTTAAAATG TTTGAGTTTT	1380
45	TAACAGGTAC AGACTATGCT GACGTATTAA AAATTGCGGA TGTATGTATT GCATCGCTGA	1440
	TTAAAGAAGG CGTCGGTTTA GCGGTGCCGA GCAAGAATTA TGGCTATCTT GCAGCTAAGA	1500
	AAGCGTTGGT ACTCATCATG GATAAGCAAT CTGATATCGT TCAACATGTT GAACAATATG	1560
50	ATGCGGGTAT CCAAATTGAT AATGGCGATG CACATGCCAT TTATAACTTC ATCAACACTC	1620
	ACTCGAGTAA GGAATTGCAC GAGATGGGTG AGCGCGCACA TCAACTGTTT AAAGATAAAT	1680

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	AAGCGATTAT TCGATGTAGT GAGTTCAATA TATGGTTTAG TAGTTTTAAG TCCGATTCTG	1800
	TTAATTACAG CATTACTAAT TAAAATGGAA TCACCTGGAC CAGCCATTTT CAAACAAAAA	1860
5	AGACCGACGA TTAATAATGA ATTGTTTAAT ATTTATAAGT TTAGATCAAT GAAAATAGAC	1920
	ACACCTAATG TTGCAACTGA TTTAATGGAT TCAACATCGT ATATAACAAA GACAGGGAAG	1980
	GTCATTTCGT AGACCTCTAT TGATGAATTG CCACAATTAT TGAATGTTTT AAAAGGAGAA	2040
10	ATGTCAATTG TAGGTCCTAG ACCAGCGCTT TATAATCAAT ACGAATTAAT CGAAAAACGT	2100
	ACAAAAGCGA ACGTGCATAC GATTAGACCA GGTGTGACAG GACTAGCTCA AGTGATGGGG	2160
	AGAGATGATA TCACTGATGA TCAAAAAGTA GCGTATGATC ATTATTACTT AACACATCAA	2220
15	TCTATGATGC TTGATATGTA TATCATATAT AAAACAATTA AAAATATCGT TACTTCAGAA	2280
	GGTGTGCATC ACTAATGAGA AAAAATATTT TAATTACAGG CGTACATGGA TATATCGGTA	2340
	ATGCTTTAAA AGATAAGCTT ATTGAACAAG GACATCAAGT AGATCAAATT AATGTTAGGA	2400
20	ATCAATTATG GAAGTCGACC TCGTTCAAAG ATTATGATGT TTTAATTCAT ACAGCAGCTT	2460
	TGGTTCACAA CAATTCACCT CAAGCAAGGC TATCTGATTA TATGCAAGTG AATATGTTGC	2520
25	TGACGAAACA ATTGGCACA AAGGCTAAAG CTGAAGACGT TAAACAATTT ATTTTTATGA	2580
	GTACTATGGC AGTTTATGGA AAAGAAGGTC ATGTTGGTAA ATCAGATCAA GTTGATACAC	2640
	AAACACCAAT GAACCTACG ACCAACTATG GTATTTCCAA AAAGTTCGCT GAACAAGCAT	2700
30	TACAAGAATT GATTAGTGAT TCGTTTAAAG TAGCAATTGT GAGACCACCA ATGATTTATG	2760
	GTGCACATTG CCCAGGAAAT TTCCAACGGT TAATGCAATT GTCAAAGCGA TTGCCAATCA	2820
	TTCCCAATAT TAACAATCAG CGCAGTGCAT TATATATTAA ACATCTGACA GCATTTATTG	2880
35	ATCAATTAAT ATCATTAGAA GTGACAGGTG TGTACCATCC TCAAGATAGT TTTTACTTTG	2940
	ATACATCGTC AGTAATGTAT GAAATACGTC GCCAATCACA TCGTAAAACG GTATTGATCA	3000
	ACATGCCTTC AATGCTAAAT AAGTATTTTA ATAAGTTGTC GGTCTTTAGA AAATTATTCTG	3060
40	GCAATTTAAT ATACAGCAAT ACGTTATATG AAAATAATAA TGCACTTGAA ATTATTCCTG	3120
	GAAAAATGTC ACTTGTTATT GCGGACATCA TGGATGAAAC GACAACCAA GATAAGGCAT	3180
45	AAGTCATCTA TTAAATAAAA TCAACATACA AATCGTTTTA TTTGGAGGTT ATAGTATGAA	3240
	GTTAACAGTA GTTGGCTTAG GTTATATTGG TTTACCAACA TCAATTATGT TTGCAAAACA	3300
	TGGCGTCGAT GTGCTTGGTG TTGATATTAA TCAGCAAACG ATTGATAAGT TACAAAGTGG	3360
50	TCAAATTAGT ATTGAAGAAC CTGGATTACA AGAGGTTTAT GAAGAGGTAC TGTCATCGGG	3420
	AAAATTGAAG GTATCTACAA CGCCAGATGC ATCTGATGTT TTTATCATTG CCGTTCCGAC	3480

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	TAGTATTTTA	TCATTTTATAG	AAAAAGGAAA	TACCATTATT	GTAGAGTCGA	CAATTGCGCC	3600
	TAAAACGATG	GATGATTTTG	TAAAACCAGT	CATTGAAAAT	TTAGGGTTTA	CAATAGGTGA	3660
5	AGATATTTAT	TTAGTGCATT	GTCCAGAACG	TGTACTGCCA	GGAAAAATTT	TAGAAGAATT	3720
	AGTTCATAAC	AATCGTATCA	TTGGCGGTGT	GACTGAAGCT	TGTATTGAAG	CGGGTAAACG	3780
	TGTCTATCGC	ACATTCGTTT	AGGGAGAAAT	GATTGAAACA	GATGCACGTA	CTGCTGAAAT	3840
10	GAGTAAGCTA	ATGGAAAACA	CATATAGAGA	CGTGAACATT	GCTTTAGCTA	ATGAATTAAC	3900
	AAAAATTTGC	AATAACTTAA	ATATTAATGT	ATTAGATGTG	ATTGAAATGG	CAAAACAAACA	3960
	TCCGCGTGTT	AACATCCATC	AGCCTGGTCC	AGGTGTAGGC	GGTCATTGTT	TAGCTGTTGA	4020
15	TCCGTACTTT	ATTATTGCTA	AAGACCCTGA	AAATGCAAAG	TTAATTCAAA	CTGGACGTGA	4080
	AATTAATAAT	TCAATGCCGG	CCTATGTTGT	TGATACAACG	AAGCAAATCA	TCAAAGTGTT	4140
20	GAGCGGGAAT	AAAGTCACAG	TATTTGGTTT	AACTTATAAA	GGTGATGTTG	ATGATATAAG	4200
	AGAATCACCA	GCATTTGATA	TTTATGAGCT	ATTAAATCAA	GAACCAGACA	TAGAAGTATG	4260
	TGCTTATGAT	CCACATGTTG	AATTAGATTT	TGTGGAACAT	GATATGTCAC	ATGCTGTCAA	4320
25	AGACGCATCG	CTAGTATTGA	TTTAAAGTGA	CCACTCAGAA	TTTAAAAATT	TATCGGACAG	4380
	TCATTTTGAT	AAAATGAAGC	ATAAAGTGAT	TTTTGATACA	AAAAATGTTG	TGAAATCATC	4440
	ATTTGAAGAT	GTATCGTATT	ATAATTATGG	CAATATATTT	AATTTTATCG	ACAAATAAAA	4500
30	TGTGTCAAAC	TAGGGCATAAC	ATGATTAAGG	AAAGATAAGC	TGTCATGTGT	TTGAACTTCA	4560
	GAGAGGATAA	TGTTATGAAA	AAAATTATGG	TTATTTTCGG	TACGAGACCC	GAAGCAATAA	4620
	AAATGGCACC	ATTAGTAAAA	GAAATTGATC	ATAATGGGAA	CTTTGAAGCG	AACATTGTGA	4680
35	TTACAGCACA	ACATAGAGAT	ATGTTAGATA	GTGTGTTAAG	TATATTTGAT	ATTCAAGCTG	4740
	ATCATGATTT	AAATATTATG	CAAGATCAAC	AAACATTAGC	AGGCCTTACG	GCGAATGCAC	4800
	TTGCTAAACT	TGATAGCATC	ATTAATGAGG	AACAACCGGA	TATGATTTTA	GTACATGGTG	4860
40	ATACTACAAC	GACTTTTGTA	GGAAGTTTGG	CAGCATTTTA	TCATCAAATT	CCGGTCCGAC	4920
	ATGTAGAAGC	TGGACTTCGA	ACACATCAGA	AATACTCACC	ATTCCTGAA	GAGTTAAATC	4980
45	GAGTCATGGT	AAGTAATATT	GCTGAATTGA	ATTTTGCGCC	AACAGTAATT	GCAGCTAAAA	5040
	ATTTACTTTT	TGAAAACAAA	GACAAAGAGC	GTATCTTTAT	TACTGGAAAT	ACAGTTATTG	5100
	ACGCATTGTC	AACAACAGTT	CAAAATGATT	TTGTTTCAAC	GATTATTAAT	AAACATAAAG	5160
50	GCAAGAAAGT	TGTTTACTA	ACAGCGCATC	GTCGTGAAAA	TATTGGGGAA	CCGATGCATC	5220
	AGATTTTTAA	AGCAGTAAGA	GATTTGGCAG	ATGAATATAA	AGATGTTGTC	TTCATTTATC	5280

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	GGATTGAATT AATTGAGCCA TTAGATGCGA TTGAGTTCCA TAATTTTACA AATCAATCGT	5400
	ACCTCGTGCT GACAGATTCT GGTGGTATTC AAGAGGAGGC TCCTACATTT GGAAAACCTG	5460
5	TGTTGGTATT AAGGAATCAT ACAGAGCGTC CCGAAGGCGT TGAGGCGGGA ACATCGAGAG	5520
	TAATTGGCAC AGATTATGAC AATATTGTTC GAAATGTGAA ACAATTGATT GAGGATGATG	5580
	AAGCGTATCA ACGTATGAGT CAAGCGAATA ATCCATATGG TGATGGACAA GCATCACGAC	5640
10	GTATTTGTGA AGCAATAGAA TATTATTTTG GATTGCGCAC AGACAAGCCG GATGAATTCG	5700
	TACCTTTACG TCACAAATAA TAAAAAACCC CTAATCATGA AGTTGGTTTA GACAACCAGC	5760
	GGTGACTAGG GGTTTTTAAT ATATTTATTT TTGATAGTGG TAGCCAATAT CATATTTGAA	5820
15	TACTTTATTT GATAATATTG GACTTTGCTG TCCATCGTCA TCACTTTTTA AACGTACATT	5880
	TTTATGAGCT TCTTTAAATA CATCGGAATT CAACCAATTA TTAAAGCTAT CTTGAGATTC	5940
20	CCAAATAGTT AAGATTTTAA CTTGCTCTGT ATCCTCGGTA TTTAATGTTT TAGTGACAAA	6000
	CATTTGTTGG AAGCCTTCAA TAGTTTCAAT ACCTTGCTCA TTGTAAAAAC GTTCAATCGT	6060
	TTCTTCCGCA CTGCCTTTTT GTAATTGTAA TCTATTTTCT GCCATAAACA TGGGCAATCA	6120
25	CTCCTCTATT TTATGATTTG ATTTGGGTAA TGTTTTTACA AATGTAAAGA GTACAGCGGT	6180
	TTGTATGATA ACCATTATGA TTAATCCTAC ACGGACTGCA AGAACATCCA CCATATAAAT	6240
	TGAAAAACCT ATTACAATGT ATAAGCTAAT TAAAATTTTA ATTTTCTGTT GTAGCGTGTA	6300
30	GCCTCGATGT AAATAAAAGT TTTCTACATA TTCTTTATAA ATTTTTTGAT TAATAAGCCA	6360
	ATTGTAAAAG CGATCTGAAC TTCGAGCAAA GCAAAAAACT GCTACGAGTA AAAAAGGGGT	6420
	CGTTGGCAGT AAAGGTAATA CGGCACCTGC AATACCAAGC GCTGTAAATA TTAAGCCAAT	6480
35	GACGATTAAA ATAAGTCGCA TTGAAAAAAC TCCATTCTAG TACTAATGCG CATGTAATAT	6540
	TGTTTTAGTA ATATAACTCA TGCTAAATAT AATGTGTATG ATAAGTGCAA TGA CT CAGTA	6600
	AAATGAAACG ATGTTGAATT ATCCTTGTC AATTAAACGCA TTTTAAGCGC GACTTTCATA	6660
40	ACAACCAAAC TATTTAATGA GAATTATTCT CAAGTATTAT AGTTATATTA TGTGTTTTAT	6720
	TTTTGAAAAG TGCAATATGT TTTCGAAAAT AAGATTATTT TTATGTGCAA AAACGACGCA	6780
45	AAAGTTTTAA AAATGAGACT TCTGTGAGCT GATTATTTTA TAAAATGTAA ACGCTTACTA	6840
	TATAATGTGA ATCATATCGT TTAAAAGCAT TATTAAATAT GATGCTAAGA GATTTATATT	6900
	ATAGCCAATA AACAAAGGAG AGATAATATG GCAGTAAACG TTCGAGATTA TATTGCAGAG	6960
50	AATTATGGTT TATTTATCAA TGGGGAATTT GTTAAAGGTA GCAGTGACGA AACAATCGAA	7020
	GTGACTAATC CAGCAACTGG AGAAACACTA TCACATATTA CAAGAGCAAA AGATAAAGAT	7080

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	TCAGAACGTG CACAAATGTT GCGTGATATT GGTGATAAAT TAATGGCACA AAAAGATAAA	7200
	ATTGCAATGA TTGAAACATT AAATAATGGT AAACCGATTG GTGAGACAAC AGCAATTGAT	7260
5	ATTCCATTG CTGCAAGACA TTTCCATTAT TTCGCAAGTG TTATTGAAAC AGAAGAAGGT	7320
	ACAGTGAATG ATATCGATAA AGACACAATG AGTATCGTAC GACATGAGCC GATTGGCGTC	7380
10	GTAGGTGCTG TTGTTGCTTG GAACTTCCCA ATGCTATTAG CTGCATGGAA GATTGCGCCA	7440
	GCCATTGCTG CAGGTAATAC AATTGTGATT CAACCTTCGT CTTCAACACC ATTAAGTTTA	7500
	TTGGAAGTTG CTAAAATTTT CCAAGAGGTA TTACCTAAAG GTGTTGTCAA TATACTAACG	7560
15	GGTAAAGGTT CAGAATCAGG TAATGCAATT TTCAATCATG ATGGTGTAGA TAAATTATCA	7620
	TTTACGGGCT CAACTGATGT AGGTTATCAA GTTGCCGAAG CTGCAGCAA ACATCTAGTA	7680
	CCCGCTACAT TAGAGCTTGG TGGTAAAAGC GCCAATATCA TATTAGATGA TGCTAATTTA	7740
20	GACCTTGCAG TTGAAGGTAT TCAGTTAGGT ATTTTATTCA ACCAAGGTGA AGTATGTAGT	7800
	GCAGGTCTC GATTATTAGT TCATGAAAAA ATTTATGATC AATTGGTGCC ACGTTTACAA	7860
	GAGGCATTTT CAAATATTAA AGTTGGAAAT CCACAAGATG AAGCTACACA AATGGGTAGT	7920
25	CAAACCTGGTA AGGATCAATT AGATAAAATT CAATCATATA TTGATGCAGC AAAAGAATCA	7980
	GATGCACAAA TTTTAGCAGG CGGTCATCGC TTAACGAAA ATGGATTAGA TAAAGGGTTC	8040
	TTCTTTGAGC CGACATTAAT TGCTGTGCCA GACAATCATC ACAAATTAGC ACAAGAAGAA	8100
30	ATATTTGGAC CAGTGTTAAC AGTGATTAAA GTGAAGGACG ATCAAGAAGC AATTGATATA	8160
	GCTAATGATT CTGAGTATGG TTTAGCAGGC GGTGTATTTT CTCAAATAT CACACGTGCA	8220
	TTAAATATTG CTAAAGCTGT ACGTACAGGA CGTATTTGGA TTAACACTTA CAACCAAGTA	8280
35	CCAGAAGGCG CACCATTGG TGGTTATAAA AAATCAGGTA TCGGTCGAGA AACTTATAAA	8340
	GGTGCTTAA GTAACATCA ACAAGTTAAA AATATTTATA TTGATACAAG CAATGCTTTA	8400
	AAAGTTTGT ACTAGAATAA ATATCGTTTC TGAAGCGTGT TTGTAGGTCA GTCTAGCGGT	8460
40	AAGTCTTAAC ATTTAACGGC GTTGTTTAGA TTTTAAGCAA AACAAAATAT ATAGGAACAC	8520
	GTATCATGAT ATTAGGATAT AATGACTAAA ATAATAGCAG TAGGATGGTT TTTAATTGCA	8580
45	AATCATCTTA CTGCTGTTTT TAATTATGCT AATTTGCGAT GCGGCTATTA TAAGGACAGA	8640
	GTTGTTTATT AATTATGGTG ATTTAGAAAT ATGAAGTTCA ATATGCAAAG TCATCGTTTG	8700
	TTTTAATATG CGGAACAATC ATTAAAGTTA TTGCGATTTT TTGAACTTAA TGAAACTAAA	8760
50	CAATAAATTT GAGATACTTT TTTGTCAATT TTATGTAACT AACACAATAA TCTCGTACAT	8820
	TATTAAAATT TTCTATATGA TAGGAATAAA GCAAAGCGCG AGTGTGCTGT AAAAGTTTTC	8880

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	GATGATGTAT	AAATCATGGT	TAATTACGGA	AGCATTAATA	TTAACCTGAG	AAGCTATAAA	9000
	GAATTATTTT	TAAAAGCGAC	AATATTAAAT	ACGACGCATT	TATTTAGGAG	TGGCAAACGT	9060
5	ATGAATGGGA	AAAAGGCGAA	TACGATAAAC	AGATACAAAT	ATTTTCATCA	TGTCAATCAT	9120
	CAAAAAATTC	AACAAAGTTC	TAAAAAGACG	CTGTGGGCAT	CACTAATCAT	CACATTGTTA	9180
	TTTACAGTGA	TTGAATTTGT	CGGAGGTTTA	GTATCTAATt	CATTGGCATT	ACTGTCAGAT	9240
10	TCATTTTCATA	TGCTTAGTGA	TGTATTAGCA	CTTGGTTTAT	CTATGTTGGC	CATTTATTTT	9300
	GCAAGTAAAA	AGCCGACTGC	ACGATACACA	TTTGGATATT	TAAGATTTGA	GATATTAGCT	9360
	GCATTTTAA	ATGGTTTAGC	ATTAAATGTA	ATTTCAATCT	GGATTTTATA	TGAAGCTATT	9420
15	GTACGTATTA	TTTATCCGCA	ACCAATTGAA	AGTGGCATT	TGTTTATGAT	TGCTAGTATT	9480
	GGTTTACTCG	TCAATATTAT	TTTGACTGTT	ATCCTTGTAA	GGTCTTTAAA	ACAAGAAGAC	9540
20	AATATCAATA	TTCAAAGTGC	ATTATGGCAT	TTCATGGGAG	ACTTATTGAA	CTCTATTGGT	9600
	GTCATCGTTG	CAGTTGTATT	GATTTACTTT	ACAGGATGGC	GCATCATCGA	CCCAATCATT	9660
	AGTATTGTAA	TTTCACTCAT	CATTTTACGT	GGTGGTTATA	AAATTACGCG	TAATGCGTGG	9720
25	TTAAATTTTAA	TGGAAAGTGT	GCCTCAACAT	TTGGATACTG	ATCAAATTAT	GGCAGATATT	9780
	AAAAACATAG	ATGGCATATT	AGATGTACAT	GAATTTTCATT	TGTGGAGTAT	TACAACAGAG	9840
	CATTATTCAT	TAAGTGCCCA	TGTTGTGTTA	GATAAAAAAT	ATGAGGGTGA	TGATTATCAA	9900
30	GCGATTGATC	AAGTATCATC	ATTGTTGAAA	GAAAAATATG	GCATTGCACA	TTCAACGTTG	9960
	CAAAATTGAAA	ACTTGCAATT	GAATCCATTA	GATGAGCCAT	ACTTCGACAA	ATTAACATAA	10020
	ATAAAACATT	GTAGCGCCTA	AAACATTAAT	CTATGTCATA	GGCGCACGTT	TCGTTTATA	10080
35	CTTATGTTGC	ATCATTTTAA	TGATTTTCGT	CAATTTCTTT	GATGCTATCT	ACATCTAACA	10140
	CGACATCTTT	AGGTTTCAAA	ATATGAATAT	GTTTTTCATC	ATTTGTATGT	AAAATGCGTT	10200
	CTATGATGTA	CCTTTGACCG	GCCATTGTTT	CTACAGCAAT	CTTTTGTGTT	CTAGCTAAAC	10260
40	TTGCTACGAC	AGATTCTTTA	TCCATAATGA	TAGCCCCCTA	TATATATGTT	TATTTACTTA	10320
	TACCCTAACA	TGATTTTTAT	ACTCTTTGAA	AATATATTTT	ACAGAATTTT	ATCTAAATAT	10380
	TTAAAAAAT	ATCTTAATAT	CCTTGTAATC	CGATAAGAAT	TATAGTAATA	TTTTTTCAAC	10440
45	CATtGTTATA	GGAGGTCTTA	TTAATGACAT	TATTTTATT	AGAAGCTAAC	AATCTTGATT	10500
	TTGCATCAAC	GAAAGAAGAA	CTAGAAGCAA	AGGCAGCATC	ACTATCTACG	AAGACAATTC	10560
50	CAACATTAAT	TGAAGTACAA	GCTACTGAAA	ATTTAACTCA	TGTTTATTTT	ATTGTGGAAG	10620
	CAAATGACGA	aGCAGAAGCT	AAACAATTTT	TAACAGAAGC	AGATATTAGT	ATTCAATTAG	10680

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	TTGATTACCT TGTAACCTGG AACATTCCGG AAGGCATTAC GATGGATCAA TATTTAGCAC	10800
	GTAAAAAGAA AAATTCTGTT CATTATGAAG AAGTGCCAGA AGTTGAATTT AAACGCACAT	10860
5	ATGTATGTGA AGATATGTCT AAATGTATTT GTTTATACAA CGCACCTGAT GAAGAAGCGG	10920
	TACGTCGCGC GCGCAAAGCA GTTGATACAC CGATTGATGG CATCGAAAAA CTTTAATAAG	10980
10	ACAACAAGTT GATGAGATAT ATGTATATAG GTTTGGCATG GATTTTCGATT GCAGTTAATT	11040
	AGAATAGCTC AATGCTATAA ATGTAAGTAG TTGATATGAA GAAACTAATG AACTAAATGC	11100
	AAGTATTGTC TAAAACAATC ATTTTATTGA AATTAGTAG AGCTGAAATT AATATAACGT	11160
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	ATATAACAAT TCACGATATA AGGGCTGTGT TTGGCATAGC CCTTTAGATA TACACTTAAT	11280
	TCCTATTAAA ATAGTAGGGA TTAAAAGGGG GCTTGTCTAG ATTAAAATTC AACAATTACA	11340
20	ACATCACTTT GGATCACATA AAGTAATTCA TAACTTTAAT TTGGACATTA GCAAGGGAGA	11400
	AATAGTCACT TTCATAGGGA AAAGTGGTTG CGGAAAGTCT ACTTTACTCA ATATTATCGG	11460
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	TGACAACATT AGGATTGGAT TACAACAGAA AATTAGTGAT GAAGAGATTA ACGCACAGCT	11640
	TAAATTAGTT GATTTAGAAG ACAGGGGAAA GCATTTTCCC GAGCAACTGT CCGGGGGTAT	11700
30	GAAACAACGT GTGGCACTAT GTCGAGCGCA TGTGCATAAG CCTAACGTTA TATTGATGGA	11760
	TGAGCCATTA GGTGCATTAG ATGCATTTAC ACGTTATAAA CTTCAGGATC AACTAGTGCA	11820
	aCTAAAACAT AAAACGCAAT CAACTATTAT TTTAGTGACG CATGACATTG ATGAAGCTAT	11880
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	AATTACAGCA TCACATCCAC GCAGTCGTAA TGATAGCCAC CTACTTAAGA TTCGTAATGA	12000
	AATTATGGAA ACATTTGCAT TGAATCATCA TCAAGTTGAA CCTGAATATT ATTTATAAGG	12060
40	AGTGAGTGAC GATGAAAAGG TTAAGCATAA TCGTCATCAT TGGAACTTTT ATAATTACAG	12120
	GATGTGATTG GCAAAGGACG TCTAAAGAAC GGTCTAAAAA TGCCCAAAT CAGCAAGTGA	12180
45	TTAAAATTGG ATATTTGCCG ATTACACATT CAGCTAATTT GATGATGACT AAAAAATTAT	12240
	TATCACAATA CAATCATCCG AAATATAAAC TAGAATTAGT TAAATTCAAT AATTGGCCAG	12300
	ATTTAATGGA CGCATTAAAC AGTGGTCGTA TTGATGGTGC ATCAACTTTA ATAGAGCTAG	12360
50	CGATGAAATC AAAACAGAAG GGCTCAAATA TAAAGGCTGT GGCATTGGGC CATCATGAAG	12420
	GCAATGTCAT TATGGGACAA AAAGGTATGC ACTTAAATGA ATTTAATAAT AATGGCGATG	12480

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	GTAAACAATT AAAGATTAAA CCGGGGCATT TTAGCTATCA TGAAATGTCG CCAGCAGAAA	12600
	TGCCAGCCGC ATTGAGTGAA CACAGAATTA CAGGGTATTC TGTAGCCGAA CCATTCGGTG	12660
5	CACTGGGTGA AAAGTTAGGC AAAGGTAAGA CTTTGAAACA TGGTGATGAC GTTATACCTG	12720
	ATGCGTATTG CTGTGTGCTA GTACTGAGAG GGAATTGCT TGATCAACAC AAGGATGTAG	12780
	CGCAAGCATT TGTACAAGAT TATAAAAAGT CTGGCTTTAA AATGAATGAT CGCAAGCAAA	12840
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	CATGGACATC CTATGGTGAT TTAACAATTA AGCCATCCGG CTATCAAGAA ATTACGACAT	12960
	TGGTAAACA ACATCATTTG TTTAATCCAC CTGCATATGA TGACTTTGTT GAACCGTCAT	13020
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20	TGGAGAAATT TTCCAACATT TAGCAATTAG TTTATGGAGA TTTGTAGCGG GCTTTGTTGT	13260
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	TGTTGTTCTA TGGTTTGGA TTGGTAGTTT GCCAGCGATT GCGATTATTT TTATCGCTGC	13440
	TTTTTCCCA ATTGTGTTCA ATACTATTAA AGGCGTTAGA GACATTGAAC CTCAATATTT	13500
30	AAAAATAGCA GCAAATTTAA ATTAACTGG GTGGTCATTG TATCGCAATA TATTATTTCC	13560
	CGGGGCATTT AAACAAATCA TGGCTGGGAT ACATATGGCG GTAGGAACAA GTTGATATT	13620
	TTTAGTTTCT GGTGAAATGA TTGGTGACA ATCGGGATTA GGTTTTAA TCGTTGATGC	13680
35	ACGAAATATG TTGAACTTAG AAGATGTTTT AGCAGCAATA TTCTTTATCG GATTATTTGG	13740
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	GTCTTGTTTG ACAACAGGAT TTTGTTTATG GTGCCAATTA GCTTTTCAA CGTATTTAGA	14040
45	AAATGCCACG CAGCCACATT TAAATAATGA CTTACAACAG CAATTGTTAT CTGGAGAAAT	14100
	ATTAGGTGCT ACCGGATTGT CTAATCCGAT GAAGTCATTT AATGATTTAG AAAAGTTGAA	14160
50	CCTTGAACAC ACTTATGTTG ATGGACAATT GGTGTGAGT GGACGTATGC CAGCTGTAAG	14220
	TAATATTCAA GAAGACCATT ATTTTGGTGC GATTTCGAAA CATGAATCAT CAGATGAATT	14280

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	TTTAGGAGTC AACGGGTCAG CAACGTATCA AATCACATTG AATCAAGTCG TAGTGCCACA	14400
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5	TGCTTACCAA ATTCCAATAG GATTAGGCTC AATTAAGT TCTTTAGAGT TAATTGATGC	14520
	ATTTTCAAAT GTGCAAAACG GAATAAATCA ATATTTAGAG TATGATGTTG AAGCTTTTAA	14580
	AAAACGTTAT CGTCAACTTA GAGAGGAATA TTATGCAATA TTAGATGACG GTAACCTAAC	14640
10	TTCACATTTA AATGAATTAA TATCATTGAA GAAGGACATC GGCTATTTAT TGTTAGATGT	14700
	AAATCAAGCT TCTGTTGTCA ATGGTGGTTC TAGAGCGTAC ACACCATATT CGCCACAAGT	14760
15	TCGCAAGTTA AAAGAAGGAT TCTTCTTCGC AGCATTGACA CCGACATTAA GACATTTAGG	14820
	TAAACTTGAA GCAGAGTTGA AGGGGTAAGT GTGATAAGCT GATTTTTTGT TTAGATGCGT	14880
	TTGTTGAAAC ATTTTTTAAA ATAATATAAA TCTTAGTTTA TAAACATTTT CTGTTAATTT	14940
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	AAAAGTGTTA ATAAGGTGTA TAATGAAAAT GTGAACAATT AATGAACCTC TTATTTTTAA	15060
	GAAGGTGAAT ACTATAGATA CGCATACTAA AGAACAACAA TTCTCGAATC TAGTAAGATC	15120
25	TTATCGTAAA GAATACGTGG GTAAAGGACC CAATAGTATT CGAGTGTCTG TTAAAGATAA	15180
	TTGGGCGATT GCACATATGA CAGGTGTTTT GAGTAAAGTT GAGAGTTTTT ACCTAAACGA	15240
	CAACGCAAT GAATCGATGC TCCATTATAC ACGCACAGAG AAGATTAAAC AGATGTATAA	15300
30	AGAAATAGAT GTAAATGAGA TGGAAAGTCT TGTAGGCGCT AAGTTTGTA AATTATTTAC	15360
	AGATATTGAT TTGAATGATG ATGAAGTCAT TTCAATATTT GTTTTCGATA AGTCAATAGA	15420
	ATAAGTGTTG CTGGTGTAAG GTACACGGTG CTGTTTGCTA ACTTCGCTTT GAATTTAACA	15480
35	ATAATTCAAG GGGGTGGTAT GTCAAACGGT GCCGTTTTTT TGTCAATTTT TTAAAACAAG	15540
	CAACATGCAA CACGTACTTT AAGGAAGTCA AAATTTATCA TTTAGGAGAG ATGGATATGA	15600
	AAATCGTAGC ATTATTTCCA GAAGCAGTAG AAGGTCAAGA AAATCAATTA CTTAATACTA	15660
40	AAAAAGCATT AGGATTAAAA ACATTTTATG AGGAAAGAGG ACATGAGTTC ATTATATTAG	15720
	CAGATAATGG TGAAGACTTA GATAACATT TACCAGATAT GGATGTGATT ATTAGTGCCG	15780
45	CATTTTATCC TGCATATATG ACTCGTGAAC GTATTGAAAA AGCACCGAAC TTGAAATTAG	15840
	CAATTACAGC AGGTGTAGGA TCTGACCATG TAGATTAGC GGCAGCAAGT GAACACAATA	15900
	TTGGTGTCGT TGAAGTTACA GGAAGTAATA CAGTTAGTGT GGCAGAACAT GCGGTTATGG	15960
50	ATTTATTAAT ACTTCTTAGA AACTATGAAG AAGGTCATCG TCAATCAGTA GAAGGTGAAT	16020
	GGAACCTGTC TCAAGTAGGT AATCATGCGC ATGAATTACA ACACAAAACA ATTGGTATTT	16080

TACAACACTA TGATCCAATC AATCAACAAG ACCATAAATT GTCTAAATTT GTAAGCTTTG 16200
 ATGAACTTGT TTCAACAAGT GATGCGATTA CAATTCATGC ACCATTAACA CCAGAAACTG 16260
 5 ATAACCTTATT TGATAAAGAT GTTTTAAGTC GTATGAAAAA ACACAGTTAT TTAGTGAATA 16320
 CTGCACGTGG TAAAAATGTA AATCGCGATG CGTTAGTTGA AGCGTTAgCA TCCGAGCATT 16380
 TACAAGGATA TGCTGGTGAT GTTTGGTATC CaCAACcTGC ACCTGCTGAT CATCCATGGA 16440
 10 GAACAATGCC TAGAAATGCT ATGACGGTTC ACTATTCAGG TATGACTTTA GAAGCACAAA 16500
 AACGTATTGA AGATGGAGTT AAAGATATTT TAGAGCGTTT CTTCAATCAT GAACCTTTCC 16560
 AAGATAAAGA TATTATTGTT GCAAGTGGTC GTATTGCTAG TAAAAGTTAT ACAGCTAAAT 16620
 15 AGAATAAGGA TGCTGGGCTA GCGATTAACG CTTTCAATTT TATATAAATG AATCATATAA 16680
 GCACTACTGC TGTTGTAAAG ATGGCAGTAG TTTTTTATG ATTACATCTA AGTATAGTCA 16740
 CGGCTATGTT AGGACAATGA TTTAACATTT ACGCACATAT GTGTTCACTT ACGCAATTAT 16800
 20 TGAnAAATnt CATTATGTG GnAATC 16826

(2) INFORMATION FOR SEQ ID NO: 47:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4012 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

TTCAATGAGA GTAGTGGGCT GATGTTTAGC GATATCGCGT AAGATTAACC ATTGGCCATA 60
 35 ATATATATTG TGTTTTCTA AAATCGGCTC GGCTAATTTT AAATAGGGGC GATATATTGT 120
 TATAAACTA TTGAAAAATT CTGTGATAG CATAGTGACA TCTCCTAAGA CAAAATAGTT 180
 AGCTTAGCTA mCCTTTTTAC AACAAATAGTA ATTATAAAC GGGAGCAATT AGAAATCAAT 240
 40 ATATAATTAT TAAGAGCAAA AATAATTATA CTTTGTTAAA ATAAGCGTAA TTACATGTAA 300
 ATAGGGGGAT ACTAATGATA TTGAAATTTG aTCACATCAT TCATTATATA GATCAGTTAG 360
 ATCGGTTTAG TTTTCCAGGA GATGTTATAA AATTACATTC AGGTGGGTAT CATCATAAAT 420
 45 ATGGAACATT CAATAAATTA GGTATATCA ATGAAAATTA TATTGAGCTA CTAGATGTAG 480
 AAAATAATGA AAAGTTGAAA AAGATGGCAA AAACGATAGA mGGCGGAGTC GCTTTTGCTA 540
 CTCAAATTGT TCAAGAGAAG TATGAGCAAG GCTTTAAAAA TATTGTTTG CGTACAAATG 600
 50 ATATAGAGGC AGTTAAAAAT AACTACAAA GTGAGCAGGT TGAAGTAGTA GGGCCGATTC 660

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	ATCAGGATGA TGATGAAATT AAGCCACCAT TTTTATTCA ATGGGAAGAA AGTGATTCCA	780
	TGCGTACTAA AAAATTGCAA AAATATTTTC AAAACAATT TTCAATTGAA ACTGTTATTG	840
5	TGAAAAGTAA AAACCGATCA CAAACAGTAT CGAATTGGTT GAAATGGTTT GATATGGACA	900
	TTGTAGAAGA GAATGACCAT TACACAGATT TGATTTTAAA AAATGATGAT ATTTATTTTA	960
	GAATTGAAGA TGGTAAAGTT TCAAAATATC ATTCGGTTAT CATAAAAGAC GCACAAGCAA	1020
10	CTTCACCATA TTCAATTTTT ATCAGAGGTG CTATTTATCG CTTTGAACCA TTAGTATAAA	1080
	TATACGTAAG TGCTATGAGC GAGAATGCC ATATGAATAA TGACAAGCAC AATGGAAAGA	1140
	ATCGTTAATA TATTATTTAA TCGTGATGAC TTAATTAAAA TGAAAAAGAT TGATAATATA	1200
15	AATGTGAAAA AGATAAGTAT AACCCGTAAA CTAAAGTAAT TCACGGTGAG AGGTTGACTC	1260
	AATGTCATAA TGATTGCAAC GATGTTTATA ATTATAAATA GACTTAAAAA AATTGTTCTC	1320
	ATATCAAACA CCTCATTGTT AGATTATTGA CATTATAACA GGGGTAATTG TATATGAACA	1380
20	TTAATGTGGT TGCTTGAGGA AAAATTTATT CATTGAAGTC AAGTTGGTTC ATTTTAGAAA	1440
	TGAATATCGT GTTAGATGAT GAAAGTATAT TGAAGTATAG GTAAGTAGTT GAAAAGTATT	1500
25	AATTGTACGA TAACATTAAA TTTAACACGA AACATAGATA TAAAATGATT CACAATTAAA	1560
	ATGGGTAAAT TTGAACCTGC TAACTATTA ATTGGAGCAT GGACATTTCA AAAATAAGAG	1620
	TTCAAATCTT ACACAAGCTC TGAATCGACA CTATAAGATA CAACTGTAT AATTAAAGGT	1680
30	ATTGTTAAAT AGAAGGAGAT ATCATAAATC ATGGAAAAGA TGCATATCAC TAATCAGGAA	1740
	CATGACGCAT TTGTTAAATC CCACCCAAAT GGAGATTTAT TACAATTAAC GAAATGGGCA	1800
	GAAACAAAGA AATTAAGTGG ATGGTACGCG CGAAGAATCG CTGTAGGTCG TGACGGTGAA	1860
35	GTTCAGGGTG TTGCGCAGTT ACTTTTTAAA AAAGTACCTA AATTACCTTA TACGCTATGT	1920
	TATATTTTCG GTGGTTTTGT TGTGATTAT AGTAATAAAG AAGCGTTAAA TGCATTGTTA	1980
	GACAGTGCAA AAGAAATTGC TAAAGCTGAG AAAGCGTATG CAATTAAAAT CGATCCTGAT	2040
40	GTTGAAGTTG ATAAAGGTAC AGATGCTTTG CAAAATTTGA AAGCGCTTGG TTTTAAACAT	2100
	AAAGGATTTA AAGAAGGTTT ATCAAAGAC TACATCCAAC CACGTATGAC TATGATTACA	2160
	CCAATTGATA AAAATGATGA TGAGTTATTA AATAGTTTTG AACGCCGAAA TCGTTCAAAA	2220
45	GTGCGCTTGG CTTTAAAGCG AGGTACGACA GTAGAACGAT CTGATAGAGA AGGTTTAAAA	2280
	ACATTTGCTG AGTTAATGAA AATCACTGGG GAACGCGATG GCTTCTTAAC GCGTGATATT	2340
	AGTTACTTTG AAAATATTTA TGATGCGTTG CATGAAGATG GAGATGCTGA ACTATTTTTA	2400
50	GTAAAGTTGG ATCCAAAAGA AAATATAGCG AAAGTAAATC AAGAATTGAA TGAACCTCAT	2460

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CAAAATATGA TTAATGATGC GCAAAATAAA ATTGCTAAAA ATGAAGATTT AAAACGAGAC 2580
 CTAGAAGCTT TAGAAAAGGA ACATCCTGAA GGTATTTATC TTTCTGGTGC ACTATTAATG 2640
 5 TTTGCTGGCT CAAAATCATA TTACTTATAT GGTGCGTCTT CTAATGAATT TAGAGATTTT 2700
 TTACCAAATC ATCATATGCA GTATACGATG ATGAAGTATG CACGTGAACA TGGTGCAACA 2760
 ACTTACGATT TCGGTGGTAC AGATAATGAT CCAGATAAAG ACTCAGAACA TTATGGATTA 2820
 10 TGGGCATTTA AAAAAGTGTG GGGGAACATAC TTAAGTGAAG AGATTGGTGA ATTTGATTAT 2880
 GTATTGAATC AGCCATTGTA CCAATTAATT GAGCAAGTTA AACCGCGTTT AACAAAAGCT 2940
 AAAATTAATA TATCTCGTAA ATTAAAACGA AAATAGATTA ACGACTGAAA TCTGAACGCT 3000
 15 CATAAGACTG TCATTTGCGT TCAGATTTTTT TTACACAATA TAGAATGGTT GAGTAAATA 3060
 TTTTTGAATA TAGTGAAAGA GGGGAAGTA CTGTGATAAA AAAGCTATTA CAATTTTCTT 3120
 TAGGGAATAA GTTTGCTATC TTTTAAATGG TTGTTTTAGT TGTCTTGGGC GGTGTATATG 3180
 CGAGTGCTAA ATTGAAATTA GAATTACTAC CAAATGTACA AAATCCAGTT ATTTTCAGTTA 3240
 CAACAACAAT GCCGGGTGCA ACGCCACAAA GTACCCAAGA TGAAATAAGT AGTAAAATTG 3300
 25 ACAATCAAGT AAGATCATTG GCATATGTGA AAAATGTTAA AACGCAATCC ATACAAAATG 3360
 CTTCAATTGT AACAGTTGAA TATGAAAATA ATACAGATAT GGATAAAGCA GAAGAACAGC 3420
 TTAAAAAGA AATCGATAAA ATTAAATTTA AAGATGAAGT TGGTCAACCA GAATTAAGAC 3480
 30 GTAATTCGAT GGATGCTTTT CCGGTTTTAG CATATTCATT TTCAAATAAA GAGAATGACT 3540
 TGAAAAAGT AACGAAAGTA CTGAATGAAC AATTAATACC AAAATTGCAA ACGGTAGATG 3600
 GTGTGCAAAA TCGCAATTA AATGGGCAGA CGAACCGTGA AATCACCCTT AAATTTAAGC 3660
 35 AAAATGAACT TGAAAAATAT GGGTTGACTG CTGATGATGT AGAAAACTAT CTAAAAACGG 3720
 CAACAAGAAC AACGCCACTT GGATTGTTCC AATTTGGTGA TAAAGATAAT CAATTGTTGT 3780
 TGATGGTCAA TATCAATCTG TTGATGCTTT TAAAAACATA AATATTCAT TAACGTGGCA 3840
 40 GGAGGACCAA GGGCATCTCA TCCCAAAGTG ACCATAAACC AAATTCAGCC ATGTCAGACG 3900
 TTATCAGGCA TCACCACAGC AAATTCAAAG CGTCAGCnCC AATATATAGT GGATGCCGCA 3960
 nGAACTAGGG GTTTAGCGnT ATCAGTGGTG TGGCGACTCT ATTCTAAACG AT 4012
 45

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

	CAATATAGGT CGCCGAGTTT CAACTaCATC AACTGGTTCA GTTACATTAG ATAATGCGCT	60
5	AGGTGTAGGT GGCTATCCTA AAGGACGAAT TATTGAAATT TATGGTCCTG AAAGTTCTGG	120
	TAAGACAACA GTAGCGCTTC ACGCTATTGC TGAAGTACAA AGTAATGGCG GGGTGGCAGC	180
10	ATTTATCGAT GCTGAACATG CTTTAGATCC AGAATATGCT CAAGCATTAG GCGTAGATAT	240
	CGATAATTTA TATTTATCGC AACCGGATCA TGGTGAACAA GGTCTTGAAA TCGCCGAAGC	300
	ATTTGTTAGA AGTGGTGCAG TTGATATTGT AGTTGTAGAC TCAGTTGCTG CTTTAACACC	360
15	TAAAGCTGAA ATTGAAGGAG AAATGGGAGA CACTCACGTT GGTTTACAAG CTCGTTTAAT	420
	GTCACAAGCG TTACGTAAAC TTTCAGGTGC TATTTCTAAA TCAAATACAA CTGCTATTTT	480
	CATCAACCAA ATTCGTGAAA AAGTTGGTGT TATGTTCCGT AATCCAGAGA CTACACCAGG	540
20	TGGACGTGCA TTAAAATTCT ATAGTTCAGT AAGACTAGAA GTACGTCGTG CAGAACAGCT	600
	TAAACAAGGA CAAGAAATTG TAGGTAATAG AACTAAAATT AAAGTCGTTA AAAATAAAGT	660
	GGCACCACCA TTTAGAGTAG CTGAAGTTGA TATTATGTAT GGACAAGGTA TTTCTAAAGA	720
25	GGGTGAACCT ATTGATTTAG GTGTTGAAAA CGACATCGTT GaTAAATCAG GAGCATGGTA	780
	TTCTTACAAT GGCGAACGAA TGGGTCAAGG TAAGGAAAAT GTTAAAATGT ACTTGAAAGA	840
	AAATCCACAA ATTAAAGAAG AAATTGATCG TAAATTGAGA GAAAAATTAG GTATATCTGA	900
30	TGGTGATGTT GAAGAAACAG AAGATGCACC AAAGTCATTA TTTGACGAAG AATAGTACAC	960
	AAATTTATAT CTATAGTTAA ACTTAGCAAA TATCCTTATA GGATTGATTG AAAGTGATAT	1020
	TCATCTCATA AAGCTAGAAT AATATCTAAC TTTATGGGAT ACACTACAAA TCGAGACTAT	1080
35	AAGGTTTTTT ATTTTATTTA TTATTACATT ATCAATAGTT TTATAATCGA GCTTCAAAAC	1140
	TTTAGAAAAAT AGTAGAAATA GCATTCAATA TAGTGCAAAA GTGCAAATTG ATAACCTGAC	1200
	ACTTATCTCC TATAAACCGT ACAATTAAAT TGTATGATTT ATATATAATT TCATAAAGTC	1260
40	ATATTGAATT TCATATAAAG AGCAAACCCT AGAAAAGGAG GTGTTTGTGT GAATTTATTA	1320
	AGCCTCCTAC TCATTTTGCT GGGGATCATT CTAGGAGTTG TTGGAGGGTA TGTGTTGCC	1380
45	CGAAATTTGT TGCTTCAAAA GCAATCACAA GCTAGACAAA CTGCCGAAGA TATTGTAAAT	1440
	CAAGCACATA AAGAAGCTGA CAATATCAAA AAAGAGAAAT TACTTGAGGC AAAAGAAGAA	1500
	AACCAAATCC TAAGAGAACA AACTGAAGCA GAACTACGAG AAAGACGTAG CGAACTTCAA	1560
50	AGACAAGAAA CCCGACTTCT TCAAAAAGAA GAAAACCTAG AGCGCAAATC TGATCTATTA	1620
	GATAAAAAAG ATGAGATTTT AGAGCAAAAA GAATCAAAAA TTGAAGAAAA ACAACAACAA	1680

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	CGCATCTCCG GTCTCACTCA AGAAGAAGCT ATTAATGAGC AACTTCAAAG AGTAGAGGAA	1800
	GAAGTGTAC AAGATATTGC AGTACTTGTT AAAGAAAAAG AAAAGAAGC TAAAGAAAAA	1860
5	GTGATAAAA CAGCAAAAGA ATTATTAGCT ACAGCAGTAC AAAGATTAGC AGCAGATCAC	1920
	ACAAGTGAAT CAACGGTATC AGTAGTTAAC TTACCTAATG ATGAGATGAA AGGTGGAATC	1980
10	ATTGGACGAG AAGGACGAAA CATCCGCACA CTTGAAACTT TAACTGGCAT TGATTTAATT	2040
	ATTGATGACA CACCAGAAGC GGTTATATTA TCTGGTTTTG ATCCAATAAG AAGAGAAATT	2100
	GCTAGAACAG CACTTGTTAA CTTAGTATCT GATGGACGTA TTCATCCAGG TAGAATTGAA	2160
15	GATATGGTCG AAAAAGCTAG AAAAGAAGTA GACGATATTA TTAGAGAAGC AGGTGAACAA	2220
	GCTACATTTG AAGTGAACGC ACATAATATG CATCCTGACT TAGTAAAAAT TGTAGGGCGT	2280
	TTAAACTATC GTACGAGTTA CGGTCAAAAT GTACTTAAAC ATTCAATTGA AGTTGCGCAT	2340
20	CTTGCTAGTA TGTTAGCTGC TGAGCTAGGC GAAGATGAGA CATTAGCGAA ACGAGCTGGA	2400
	CTTTTACATG ATGTTGGTAA AGCAATTGAT CATGAAGTAG AAGGTAGTCA TGTTGAAATC	2460
	GGTGTAGAAT TAGCGAAAAA ATATGGTGAA AATGAAACAG TTATTAATGC AATCCATTCT	2520
25	CATCATGGTG ATGTTGAACC TACATCTATT ATATCTATCC TTGTTGCTGC TGCAGATGCA	2580
	TTGTCTGCGG CTCGTCCAGG TGCAAGAAAA GAAACATTAG AGAATTATAT TCGTCGATTA	2640
	GAACGTTTAG AAACGTTATC AGAAAGTTAT GATGGTGTAG AAAAAGCATT TGCATTGAG	2700
30	GCAGGTAGAG AAATCCGAGT GATTGTATCT CCTGAAGAAA TTGATGATTT AAAATCTTAT	2760
	CGATTGGCTA GAGATATTAA AAATCAGATT GAAGATGAAT TACAATATCC TGGTCATATC	2820
	AAGGTGACAG TTGTTGAGA GACTAGAGCA GTAGAATATG CGAAATAATT TTTGTCTCCC	2880
35	TCACAAATTA GTGAGGGAGC TTTTAAAGT TGTAGTCTTA ACTAGTTAG ACAGCACTTT	2940
	ATCGGTAATA ACTATATTAA ACAGTAGTTA TTTGAAAGTA AGACGGACCT TATATTAAAT	3000
	AAGAAGTTAT TGCTTTTAAT AAAAATGTTT TAGGCTTCGT AATTACTATA TTTATATTAT	3060
40	GTAAACCTAT AAAGATGATT GGTTTTCTAT CCAATAAAAA AGAAGAGAAG ATGTAACACA	3120
	TCTTCTCTTC YGCAATATTA ATTAGGATTT ATTTCTAAGT TGAGTTATTT TAATTGTAAT	3180
45	TCTGTTTTCT TTAATCTTTT TATAACTTCT GCAGTATCAT AACAATTTGT TGCAATTGTT	3240
	GAATATCTCT CTGCTAAACG ATATGCATTA ATGTAAAGCT TTAACTTTTCT TTTAGCTATA	3300
	TCCTCTGCAT CTTCGAATTT TGATGGGTGA GACATAACCA CTAATCTGTC AAATTTTTCT	3360
50	GGATCAATAT TAATAGACAT GTATTTATTT ACAACTCCTA TTTATTTTGA TGTCTTAATA	3420
	CTAACATATT GAAGTTTTCA GACAAAGTAA TGTCTCTCTA TAATTGAAGA AAAATAATTC	3480

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	GGATGAACAA AACATGAGAA TAATGTTTAT AGGGGATATC GTAGGTAAAA TTGGACGAGA	3600
	CGCAATTGAA ACGTACATAC CTCAACTGAA GCAAAAGTAT AAACCAACAG TTACAATTGT	3660
5	AAATGCTGAA AATGCAGCAC ATGGTAAAGG TTTGACTGAA AAAATATATA AACAATTACT	3720
	AAGAAATGGT GTAGATTTC A TGACTATGGG TAATCACACA TATGGTCAAC GTGAAATTTA	3780
	TGATTTTATA GATGAAGCAA AACGACTAGT AAGACCAGCG AATTTTCCGG ATGAAGCGCC	3840
10	GGGAATTGGT ATGAGATTTA TACAAATTAA TGATATTAAA CTTGCAGTTA TTAATCTGCA	3900
	AGGAAGAGCG TTTATGCCAG ATATTGATGA TCCTTTTAAA AAGGCAGATC AATTAGTCAA	3960
	GGAAGCACAA GAACAACTC CGTTTATATT TGTTGATTTT CATGCAGAAA CAACTTCTGA	4020
15	AAAGTATGCA ATGGGATGGC ATTTAGATGG TAGAsTAGCG CTGTTGTTGG AACGCATACA	4080
	CACATTCAAA CAGCAGATGA ACGTATTTTA CCAAAGGGGA CAGGGTATAT AACGGATGTT	4140
20	GGTATGACAG GTTTTTATGA TGGCATTTTA GGAATAAATA AAACAGAGGT AATTGAGCGT	4200
	TTTATCACTA GTTTGCCACA AAGACATGTT GTTCCAAATG AAGGTAGAAG TGTATTATCT	4260
	GGTGTGTTA TTGATTTAGA CAAAGAAGGT AAAACAAAGC ACATCGAACG TATATTGATA	4320
25	AATGATGACC ATCCATTTTC AACATTTTAA AATTACGTAA GTAAACATTC GAATTGGACC	4380
	CTATCGTCCA TTAGTATGAA TTTAATATAG TACCACTGTT TACATAGTAA ATCGGTGGTT	4440
	CTTTTGTGA TCATTTAATA TGAAATATAT CCATAGGAGG CATATACTA TGAAACCACA	4500
30	ATTATCGTGG AAAGTTGGCG GTCAACAAGG CGAAGGTATT GAATCAACTG GGGAAATCTT	4560
	CGCTACGGCT ATGAATAGAA AAGGATATTA TTTATATGGA TATAGACATT TTTCAAGTCG	4620
	TATCAAAGGT GGACATACGA ATAATAAAAT TAGAGTTTCT ACGACGCCTG TTCATGCAAT	4680
35	TAGTGATGAT TTAGATATTT TGATTGCATT TGACCAAGAA ACAATTGATG TTAACCATCA	4740
	TGAAATGAGA GAAGACAGTA TTATTTTArC TGATGCCAAG GCTAAACCTG TGAAaCCAGA	4800
	AGGATGTCAT GCACAGCTTA TTGAATTACC TTTTACAGCA ACCGCTAAAG AATTAGGTAC	4860
40	AGCATTAAATG AAAAACATGG TTGCAATAGG TGCTACTAGC GCATTGATGA ATTTGAATAC	4920
	AAATACATTT GAAGAACTTA TTAATAATAT GTTTTCTAAA AAAGGTGACA AGGTAGTTGA	4980
	AGTCAATATC CAAGCATTAA ACGAAGGTTA TCAATTAATG CAATCTCGCT TACCTGAAAT	5040
45	CTACGGGGAC TTTGAATTAG AGTCAACAGA TGCACTACCA CATCTATATA TGATTGGTAA	5100
	CGATGCCATT GGATTAGGTG CAATTGCTGC AGGTTTACAA TTTATGGCGG CATATCCTAT	5160
50	TACACCTGCG TCTGAAGTTA TGGAATATAT GATTGCCAAT ATATCTAAAG TAAACGGAGC	5220
	GGTTATTCAA ACAGAAGATG AAATTGCTGC TGTAACATG GCTATTGGTG CAAATTATGG	5280

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	TGGATTATCT	GGTATGACTG	AAACGCCATT	AGTCATTATT	AATACCCAAC	GAGGTGGACC	5400
5	TTCTACTGGA	TTACCTACGA	AACAAGAACA	GTCAGATTTA	ATGCAAATGA	TTTATGGTAC	5460
	ACATGGTGAT	ATTCCAAAA	TTGTTGTAGC	ACCAACAGAT	GCAGAAGATG	CATTTTATTT	5520
	AACTATGGAA	GCATTTAATT	TAGCAGAACA	ATATCAATGC	CCTGTTATAG	TTCTAAGTGA	5580
10	TTTGCAATTA	TCTTTAGGTA	AACAACTGT	TGAAAAATTA	GATTATAATC	GTATTGAAAT	5640
	TAAACGTGGT	GAAATCATT	AATCTGATAT	TGAACGTGAA	GAAGATGATA	AAGGTTATTT	5700
	CAAGCGTTAT	GCGTtAACAT	CCGATGGTGT	TTCTCCTAGA	CCTATCCCCG	GTGTTAAAGG	5760
15	AGGTATTCAT	CATATAACTG	GTGTGGAaCa	CAATGAAGAA	GGTAAACCTA	GTGAATCTGC	5820
	GTCAAATAGA	CAACAACAAA	TGGAAAAACG	AATGCGTAAA	ATTGAGCAGT	TACTAATTGA	5880
20	ATCGCCAGTA	GAAGCTAACT	TACAACATGA	GGATGCAGAT	ATTCTTTATA	TCGGTTTTAT	5940
	TTCTACAAAA	GGTGCAATTC	AAGAAGGTAG	TAACCGTTTG	AATCAACAAG	GCATAAAAGT	6000
	TAACACTATA	CAAATTAGAC	AATTGCATCC	ATTCCCAACA	AGCGTTATTC	AAGATGCAGT	6060
25	TAATAAAGCG	AAGAAAGTCG	TTGTAGTGGA	GCACAATTAT	CAAGGACAAT	TGGCTAGTAT	6120
	TATAAAAATG	AATGTCAATA	TTCATGATAA	GATTGAAAAT	TATACAAAGT	ATGATGGGAC	6180
	ACCTTTCCTA	CCACATGAAA	TCGAAGAAAA	AGGCAAAATA	ATTGCTACTG	AAATAAAGGA	6240
30	GATGGTATAG	ATGGCGACAT	TTAAAGATTT	TAGAAATAAT	GTTAAGCCTA	ACTGGTGCCC	6300
	CGGATGTGGC	GATTTCTCAG	TACAAGCTGC	AATTCAAAAA	GCAGCCGCAA	ATATAGGGTT	6360
35	AGAACCTGAA	GAAGTAGCTA	TCATCACCCG	TATAGGATGT	TCTGGCCGTC	TTTCAGGATA	6420
	TATTAATTCT	TATGGCGTTC	ATTCTATTCA	CGGACGTGCA	TTACCTTTAG	CTCAAGGTGT	6480
	AAAAATGGCG	AATAAAGATT	TAACTGTTAT	TGCATCGGGA	GGAGATGGTG	ATGGTTATGC	6540
40	TATAGGTATG	GGGCATACAA	TCCATGCTTT	AAGAAGAAAT	ATGAACATGA	CGTATATAGT	6600
	CATGGATAAT	CAAATTTATG	GTTTGACAAA	GGGACAAACA	TCGCCGTCAT	CAGCAGTAGG	6660
	ATTTGTTACT	AAAACAACGC	CAAAAGGTAA	TATAGAAAAA	AATGTTGCGC	CTTTAGAATT	6720
45	AGTATTATCA	TCTGGTGCCA	CATTTGTAGC	CCAAGGTTTT	TCAAGCGATA	TTAAAGGATT	6780
	AACAAAATA	ATTGAAGATG	CAATTAATCA	TGATGGATTT	TCATTCGTTA	ATGTCTTTTC	6840
50	ACCATGTGTG	ACTTATAATA	AAATTAACAC	ATACGATTGG	TTTaAAGAAC	ATTTAACAAG	6900
	TGTTGATGAc	ATTGAAAATT	ATGATTCTAC	AGATAAACAA	TTAGCGACTA	AAACTGTTAT	6960
	TGAACATGAA	TCTTTAGTAA	CTGGTATTGT	TTATCaAGAT	AAAGAAACAC	CATCATATGA	7020
55	ATCtCAAATT	AAAGAGTTAG	ATGATmCACC	ACTTGCTAAA	AGAGATATCa	AAATTaCTGA	7080

TGTATTTATA ACAGATCCAT TTATGCTACT CAGTTTTTTA CTATTACAAA AAATAAAGGA 7200
 GTTTTTAAAA ATGAAAGACA CATTAAATGAG TATACAAATA ATTCCTAAAA CACCAAACAA 7260
 5 TGACAATGTT ATACCTTACG TAGACGAGGC GATTAAAATA ATTGACGAAT CTGGTTTGCA 7320
 TTTTAGAGTA GGTCCGTTAG AAACGACAGT ACAAGGAAAT ATGAATGAAT GTTTAATTTT 7380
 10 AATACAATCA TTAAATGAAC GAATGGTGGA ACTTGAATGT CCAAGTATTA TTAGCCAAGT 7440
 TAAGTTTTAT CATGTGCCAG ATGGCATCAC TATTGAACT TTAAGTAAA AATATGATGA 7500
 ATAACATTAA AAGTGAAGTA AACTGGATTT GAATTGGCTT GTTAGAGATG ACGTATAACT 7560
 15 TTAAGTGTTC TTGCACTTTA TAGTTAAATT TAATATAATT ATTAAATGAT ACGGGCAAAT 7620
 AGAAAGGATT TTGTAAAGTG AACGAAGAAC AAAGAAAAGC AAGTTCTGTA GATGTTTTAG 7680
 CTGAGAGAGA TAAGAAAGCA GAAAAAGATT ATAGTAAATA TTTTGAACAT GTTTATCAGC 7740
 20 CGCCTAATTT AAAAGCAAGC GCAAAAAAG AGGTnAAA 7778

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

AGATGAAGTT GTTACgAAAA TTGCGTACGC TGTTTCAGAA CATGTCAAAA TAGAAACAGG 60
 35 TAATCCATTC TTTCAAACAT CACATAGTGG TTGTGCGACG GGCGGATCCT GTAATTGTTC 120
 ATTATAAAAA ACATCGAGTC AGAAAAAGGT GGTATTGAA CCACTAACTA GCATCTGACT 180
 40 CGATGTTTTT ATTTATTCGG GATTGTTTGT TTGAATTGTT GTGCTAAATC TGGTCGATCT 240
 GTCACAATCG TGTGTGCACC TTTTGGTAT AAATCATTCA TCAGATTTAT ACTATTTACG 300
 CCATAATAGC CTGGAATGAT ATTCATATCA TTTAACCATT TGATAAAACG AGATGAAGTC 360
 45 AAATCAATGC CTTTAAATG AGTAGGCATT TGGACGTTT GTGCTAATGG TTGGTAGTAC 420
 CTACCACCTA ATAAATGATA TTTTAAAAAT GCTTCTGTAA CTTCTGTGTT GCTAGCACCA 480
 ATTGCGACGG ATCCTTGTGC AATTTTATTA AACGAACGA TTTGTTCTTT ATAAAACTT 540
 50 GTCACAAGAA CGCGGTCAAA TGCTTGATTT TCTGCAATTG TATCAAACAT AATTTGTGGT 600
 GCGATTGAGC CTTCATAGGA TTCAGGAGCA TCTTTAAGT CTACGTTTAT ATACATATCA 660
 55 GGATATTGCT TCAGCAACTc ATCGAAGGTT AGTATAGCTG TGTGTGCATG ACCACGATAT 720

AATGTATGGG CACTAACTTT TCCAGAGCCG TTCGTCGTTT TATCAACAGT TCGGTCATGA 840
 AAAACGATAA GCTGTTGATC TTTTGTGAGT CTCACATCTG TTTCAAAGCC ATCAACGCCT 900
 AATTGTTTAG CATAGTCAAA TGCAAGTTGC GTTTGCTCTG GTCTTAAAGC CATACCACCG 960
 CGATGCGCAA ATATATATGG TGCATTGCCT TTGAAAAAAG CAGGGATGGT TTGCTTTTTA 1020
 GTAATCACTT TATTTTTATT GATCATTAAAT AGACTACTTA AAAATCCAGC ACCGACTAGT 1080
 ACCGCATTTA AAATGTTTCT GTTTACnTTT TTCATAAAAA ATTCCTCC 1128

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

CAAGCAAACA ATCGTCGATA AAATTGCTAA AATAATAAAA GTAATTCGAA CTTTCATCAT 60
 GATCATCCTT TGTTTATAGA GTCAATATAA GTATGGAATA TGTTAGGTAT ATAGTCAAAT 120
 GCGTCAACTA ATGGGAATTT TGGCATAGAT AGAGAATTTA AGGCAATTAA AAAGGCATCA 180
 AACAGTAATA TGCTGCTTGA TGCCCAAATG ATGACTTTAG CTAAATTGAT TAGTCACTTT 240
 TAAAGATAAA GAATTGTCAT GAATTAAAC TCATGTAATG ATGTGTTACA TTTGCAATG 300
 ATGGCTTTCA GTTATTTATC GATAACATCA CTCTTGATAC CTTTAGATT TAAGAAATCT 360
 TTAATTTTAT CTTGTTGCTT TTTATTAACA TCACCGGCAT ATTTTGTTGG CACGTCGACA 420
 ACATTGATTT TATTTTGCGG TTGATAGCTA AGCTTTTCAA TATCTTCATC AACATTGGCG 480
 ATTGFACTAT TTAAAGCTTT GAAGTAATTC ATCATTAAAT CAACGGGTTT CTTATATTCT 540
 TTAGGAATAT TGTTTTAGT GACAAATTTT TTGAAATGCA AATCGTTTTT AACAGCTAAG 600
 TTAGATAAGT GGCTAAGTGT TTCTGCTTGT TTTTCAGTCA CTTTGTGTTG ACTGTCAATT 660
 TGTTTATCTA GTTTATGTTG CATAATATAT TTGTTATCAA GTATATCGCT ATTTACAGAC 720
 AAATACTTTT CTATAGCTTG CTTCATCTCT GCATCACTAA TATCACTATT TTTCTTATCT 780
 GAGTTAAAGA TATCTTTTGT TCTAATTTT TTAGCGCTTT TAGGTGCATG GATGCCAGTA 840
 CTTGTATGAT GATCTTCGTT ATCAGATTTA TCGGACGCGC AACCTGTAAG AATTAATGTC 900
 GATGCTAAAA ATGTACTTAG TAGTAATCTC TTTTTCATAA TGTAATATAA CTCCTTAGTT 960
 TATCTTTAAT TGAAAAAATA TGTATTCATG TTTAATAGAG TAACATTGAA TTAGTTTGGA 1020

	TCTATCAATA ATGCATCATT TTGGACGTTG TTAAGGATAG CTTTATCTAT AAATAACTGC	1140
5	ATAATTGGTT GTACTAATTT AGACGTAGGT ATCGTACGTA AAAGCATAAT AATTTTCGTTT	1200
	ACATACTTTT CTTTCTCAAT ATCATTTTTT ATATTGATTT GTTGCGAGA GGTACATACT	1260
	TTAAGCATT TCGCACATCT CGTTGTATAT ATTAAGTTTA TCATAACATG ATTTTATGTC	1320
10	GGGATAAAAA AATAACAGCA TCTTAACAAA TGTAAGATAC TGTCAGTGAA ATGAATGAAA	1380
	CTTTAGTTTC TGaTAATATA GTCAAAGGCA TTTAATGCTG CATTTGCACC AGCGCCCAT	1440
	GAAATGATAA TTTGTTTGTT CTTCTGATCT GTGACATCGC CAGCAGCAA TATTCCAGGA	1500
15	ACATTCGTAT TATTGTTACG ATCAATCACA ATTTACCAC GTTCGTTTAA TTCAACAGCA	1560
	TCGTTTAACC ATGATGTGTT TGAAGTAAA CCAATTTGAA CAAAGATACC ATCTAAGTTA	1620
	AGTAGATGTT CTTGCGCGGT GTTCATGTCT TCGTAACGTA TACCTGTAAC ATGGTCTTCT	1680
20	CCGACAACTT CAGTAGTTTT GGCATTTGTT TTGATATCAA CATTTGATAA AGAACGTAAA	1740
	CGATCTTGTA ACACGTTGTC TGCTTTTAAT TCGCTAGCGA ATTCGAATAA TGTAACATGA	1800
25	TTAACGATAC CAGCAAGGTC AATTGCTGCT TCAACCCAG AGTTACCGCC ACCGATAACT	1860
	GCTACGTCTT TATTTTCAA TAGAGGTCCG TCACAGTGAG GGCAGAATGC AACACCTTTA	1920
	TTAATCAATT GCTCTTCACC TGAATGTTT AGCTTACGCC AACCTGCACC AGTAGCAATA	1980
30	ATGACTGTTT TACTTTCTAA GACAGCACCG TTTTCTAAG TAACTTTAAT TGCTTCGTCA	2040
	GTCTTTTCGA TATCTGTAGC ACGTATACCT GTCATTGCAT CAATGTCATA TTGATCAATG	2100
	TGCGCTGCTA AGTTAGAAGA AAATTCAGAA CCAGTTGTTT CTTTAACAGT AATGAAGTTC	2160
35	TCAATACCAG CAGTATCATT AACTTGGCCA CCGATACGAT CAGCAACTAT ACCAGTACGT	2220
	AAACCTTTAC GTGCTGTGTA AATCGCTGCA CTACCACTAG CAGGACCACC ACCAACGATT	2280
40	AAGACATCAT AAGGTTCTTT ATTTTCAAAC TCAGATGCAT CTGCCGTACT GCCTAGTTTC	2340
	GAAAGAATAT CTTGGATTGT CATACGACCA TTGCCAAATT CTTGCCATT TAAAAAGACA	2400
	GCAGGGACTG CCATGATGTT TTCAGATTCT TCACGGAACA CTGCACCATC AATCATAGAA	2460
45	TGCGTGATGT TAGGGTTGAT CACACTCATT AAGTTAAGTG CTTGAACGAC ATCAGGACAT	2520
	TTTTGACACG TTAACTAAT GAATGTTTCA AAATGGAATG AACCTTCTAA TTTTTTAATT	2580
	TGGTCAATGA TTGACTGTTT TTCTTTAGGT GCACGACCAC TAACCTGTAA AATTGCTAAA	2640
50	ACAAGTGAGT TAACTCGTG ACCTAATGGA ATACCTGCAA ATGTTACACC TGTTTCTTCG	2700
	CCAGGACGAT TGA CTGAGAA ACTTGGTGTA CGTTTAAAG ATTTTTCAGA AAGAGATAGT	2760
55	CTAGGTGACA TATCAGTAAT TTCTGTCAAC AAATCTTTAA GTTCTTTGGA TTTATCATCT	2820

	TGTTGTTTTA AATCAGCATT AAGCATGGTT GTAATGCCTC CTTAGATTTT ACCTACTAAA	2940
5	TCTAAACCAG GTTGCAATGT TTTAGCGCCT TCTTCCCATT TAGCTGGGCA TACTTCGCCA	3000
	GGGTTTTTAC GAACATATTG AGCTGCTTTG ATTTTGTGAG CTAATGTACT AGCGTCACGG	3060
	CCAATCCGT CAGCGTTAAT TTCAGATGCT TGTACAACAC CGTCTGGGTC GATAATGAAT	3120
10	GTACCACGTT GAGCTAAACC AGTAGCTTCA TCTAATACAT CAAAATTACG AGTGATTGTT	3180
	TGTGATGGGT CACCAATCAT AGTGTAAGTG ATTTTGCTAA TTGCATCTGA ATGGTCATGC	3240
	CATGCTTTGT GTACGAAGTG AGTATCAGTT GATACTGAGA ATACATTTAC GCCTAATTTT	3300
15	TGTAATTCTT CATATTGGTT TTGTAAGTCT TCTAATTCAG TTGGACAAAC GAATGAGAAG	3360
	TCAGCAGGAT AGAAGCATA CACGCTCCAA GAACCTTTTA AATCTTCTTG TGTAACCTCT	3420
	TTAAATTGAT CTTTTTTTGG ATCGAAATCT TGCGCTGTAA ATGGTAAGAT TTCTTTGTTA	3480
20	ATTAATGACA TAAATATCTT CCTCCTAAGA ATTTAAGTAT GAATTAGAAC TATCAATTGA	3540
	TTGCGCTTAA TTATAATAAT TCTAATCTCT TAGTTAGCAT TATTACATTT TGATCCAGAA	3600
25	TAGTCAACTG GATAACTTTG TAAAGTGAAT GATTACTTTT AAAATAAAGA AAGATAATAT	3660
	AAAGTGCTTT GATAATGGAT TTGTAGTTG ATGATTTAAA AGGTTGTGTC TATATTTAAT	3720
	ATCTTGATTT TAATGTAAAA AATGTAAAAA AAGAAGATTT GTATTCTCAA CTAAGTCAAC	3780
30	CTTATTGATA ATGGTATGAG AATATTGTG CGAGATGGAT GAAGGTAATG AGTGAGAAAC	3840
	TGGATTTTTA AAGTATGAGA CAATATTTTA AAAAGTTCAA TTATTAACTT ATAAGCAAAT	3900
	AATTGCTATA AAAAAGTTTG GACGTGTACA ATTGCAATAT GAAGATTTTA AATTAATTGT	3960
35	AAAGTATCGA GGAGTGGGTA ACGTGTGAGA ACATGTATAT AATCTTGTGA AAAAGCATCA	4020
	TTCTGTTAGA AAATTTAAGA ATAAACCTTT AAGTGAAGAC GTTGTTAAGA AATTGGTAGA	4080
40	AGCTGGACAA AGCGCTTCGA CGTCAAGTTT CCTGCAAGCA TACTCAATTA TTGGTATCGA	4140
	CGATGAGAAG ATTAAAGAAA ATTTACGAGA AGTTTCTGGA CAACCTTATG TTGTAGAAAA	4200
	TGGCTATTTA TTCGTCTTTG TTATTGATTA TTATCGTCAT CATTAGTTG ATCAACATGC	4260
45	TGAAACTGAT ATGGAAGATG CATATGGTTC AACGGAAGGT TTGCTAGTAG GTGCAATCGA	4320
	TGCAGCATTG GTTGCCGAAA ATATTGCGGT AACTGCTGAA GATATGGGGT ATGGCATTGT	4380
	CTTTTTAGGA TCATTAAGAA ATGATGTTGA ACGCGTTCGA GAAATTTTAG ACTTACCTGA	4440
50	CTATGTCTTC CCGGTATTTG GTATGGCAGT AGGGGAACCC GCAGATGACG AAAATGGTGC	4500
	AGCCAAGCCA CGCTTACCAT TTGACCATGT CTTCCATCAT AATAAGTATC ATGCTGATAA	4560
55	GGAAACACAG TATGCACAAA TGGCAGATTA CGACCAGACA ATCAGCGAGT ACTATGATCA	4620

	CAAAGCAAGA TTAGATATGT TAGAACAATT GCAAAAATCA GGCTTAATAC AGCGATAGCA	4740
	AGATACCAAA ATAACCCGCC CCCCTCTAGC TTAAATGAT AAGTATAGCT AGAGGGGGCG	4800
5	GGTATTTCTT GCAATGAATT AGTGTGAAGT TAATGCAGCA TTATCATTTG AATCGAAAGT	4860
	ATCTTTATCC CAATGTTTAG TTAACCTGGC GGTACCTGTA CCAGCTAGCA TTGAATCGTT	4920
10	CACGTTTAAT GCTGTTCTAC CCATGTCAAT CAATGTTTCA ACGGAGATGA GCACGCCGGC	4980
	TAAAGCGACT GGCAAGTTTA ACGTTGACAA CACCAATATG GATGCAAATG TAGCCCCGCC	5040
	ACCGACGCCA GCAACGCCGA ATGAACTAAT AATCAGACA GCGATTAACG TTACAATAAA	5100
15	TTGTAAATCA ATTTCTACAT TAGCGACGGG TGGCACCATA ATTGCAAGCA TGGCAGGGTA	5160
	AATGCCTGCA CAACCATTTT GTCCAATCGA CAATCCAAAT GTCGCAGCGA AATTGGCAAT	5220
	ACCTTCTGGC ACGCCTAGAC GTCTTGTTTG TGTGTTGACA TTCAATGGTA AGGCACCCGC	5280
20	GCTTGAGCGT GATGTGAATG CAAAGATTAA TACTTCCAAA GTCTTTTAA CATAGCGAAT	5340
	TGGGCTAATA CCTAACAGGC TTAAAATAAT TAAGTGAATG ATATACATCG TAATTAATGC	5400
	AGCGTACGAT GCGATTAAGA ATTTTCCTAA AGTCCAAATG GCGCCAAAGT CACTTGTCGA	5460
25	TAATGTGTTG GCCATAATTG CTAATACACC GTATGGCGTT AAACGTAAGA CGAACGTCAC	5520
	AATCGCCATT ACTAGTGAAT AGATAGCGTC AATCGCACGC TTAAGCAATT CACCATGATC	5580
30	AGGTTGTTTG CGTnTACGCG TAAATAAGCA AATCCTATAA ACGAAGCAAA TATCAGACA	5640
	GCAATCGTGG aAGTTGCACG TTGTCCaGTG AAATCTAAGA ATGGATTTTT AGGCAATAAT	5700
	TCCAAAATTT GTTGTTGTA CGTATGTGCT GTTAAATCTT TCGCTTGTTT AGCAATTTCTG	5760
35	CTTCCACGTG CTTGTTTCTG GTTACCAAGG TTAATTGTTG ATGCATCTAA ACCAAACACC	5820
	AAGGCATACA CAACACCAAC AATCGCAGCA ATGGTGACAG TGCCAATTAA AAAGATAAAA	5880
	ATGAACTAC CAATTTTAGC AAATTTTCT CCGATTGAA TTTTAGTGAA TGCAGCTACA	5940
40	ATAGAAATGA AAATTAAAGG CATAACAATC ATTTGCAACA ATGCAACGTA ACCTTGTCGG	6000
	ACAATGTTGA ACCAGTCACT TGTTGATGTA ATAACATTCG AATGTGTGCC ATAAATAAGA	6060
45	TGCAATAACA CACCGAATAC TATACCAATC CCTAAAGCTG TAAACACACG TTTCGCAAAA	6120
	GATATATGTT TGGAGCCAT CATGTGCAAT ATTACGATGA AAATCACCAA TACAATAATA	6180
	TTAATCAGTG TAAGAAAAGC ATTCATGAAC GTCACCTCTT AAATTTTGA ATATAATTCC	6240
50	GACTAGTATG CT	6252

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6730 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

	ATCAAATCnC AAAATATTTA TTAATnAnAA GGGGATTATC CaTGtGAGAA ACAAAGTAAT	60
10	GCTCTTTTTT TACCTCTTGT GGGTTGAAAA aTGGATCATC AGAGATAGAC TTCTTCTTTT	120
	TCGAAGATGA CATTGTATAC TTAAATCTTC TAAAACCATA ACTTGTCGCA TCAAAAATGC	180
	CTTCTTGTA C AAGTAAAATC AAAAATATGC TAATAAAAAT AATTAATGAA ACATAAAACA	240
15	ATATATTTAA ATATGTAATG ATAGTATGGC TATTA AAAAAG CCATATAATA AACGTTAATA	300
	TTGGCGTTAT TAGTGCCATT CCAAGCCATT TTTTCAACAT TTGATCACTC CCAC TTATAG	360
	AAAACTCTTA CGCATAGTTT ACATTAAAAAT CAGACATTGA GGAATGATTT TTTAATTTCT	420
20	TCAGCTTTAT TGAAATTCTA AAATCAATCA TTCTTCATTA GTTTAAAGCA AAAAAATATT	480
	GATATATAGT AAATATTGTA TATATAATAT TAGTTAAGAT TTCaGAAAAT TTTGAAGGGA	540
25	ATGGAAATTT AGAAATCGGA ATTTGTTAGA GGAGGGGATT AGATGGGGAA ATATATTTTC	600
	AAACGATTTA TTTATATGCT TATTTCTTTA TTTATTATTA TTACAATTAC ATTTTCTTA	660
	ATGAAATTAA TGCCAGGTTT GCCATTTAAC GATGCTAAAT TAAATGCTGA ACAAAAAGAA	720
30	ATTTTAAATG AAAAATATGG ATTAAATGAT CCTGtAGCTA CGCagTATTT ACATTATTTA	780
	AAAAATGTTG TTACAGGCGA TTTTGGTAAT TCATTCCAGT ATCATAATCA ACCTGTGTGG	840
	GATTTGATTA AACCGAGACT ACTACCTTCT TTTGAAATGG GTCTTACAGC AATGTTCaTC	900
35	GGTGTGATAC TGGGACTTAT TTTAGGTGTT GCAGCAGCTA CTAAACAAAA TTCTTGGGTT	960
	GACTATACAA CTACAGTTAT TTCAGTTATT GCAGTATCTG TACCATCTTT TGTACTTGCT	1020
40	GTACfTTTAC AATATGTATT TGCAGTTAAA TTAAGATGGT TCCCAGTAGC TGGATGGGAA	1080
	GGTTTTTCGA CCGCGGTATT ACCGTCACCTT GCATTATCTG CAGCTGTTTT AGCAACTGTC	1140
	GCCAGATACA TAAGAGCAGA GATGATAGAG GTATTAAGTT CAGACTATAT TTTATTAGCG	1200
45	AGAGCTAAAG GTAATTCGAC AATGCGTGTA CTTTTTGGAC ATGCACTTAG AAATGCTTTA	1260
	ATTCCAATTA TTACAATTAT CGTTCCCATG TTAGCAAGTA TTTAACAGG CACTTTAACA	1320
	ATTGAAAATA TTTTGGAGT TCCTGGATTA GGGGATCAAT TCGTACGTTT AATTACAACA	1380
50	AATGATTTCT CAGTAATCAT GGCAATCACA CTATTATTTA GCACACTGTT TATCGTTTCT	1440
	ATTTTTATTG TAGATATTTT GTACGGTGTG ATAGATCCAC GAATTCGTGT TCcAAGgAGG	1500
55	TAAAAAATAA TGGCTGAAAA TAAAAACAAT TTGTCGATTA ACGACGATCA TTCTAATGCA	1560

	TGAATCAGGA	ACCTGAAATG	CAACGAGAAA	GCAAAAACCTT	TTGGCAAGAT	GCTTGGGCTC	1680
	AGTTAAAACG	AAATAAGTTA	GCTGTTGTCG	GTATGATAGG	TTTAATTATC	ATTGTAATAT	1740
5	TTGCTTTTAT	CGGTCCAGTT	ATAAATAAAC	ATGATTATGC	TGAACAAAAT	GTAGAACATA	1800
	GAAATCTTCC	GGCAAAAATA	CCTGTATTAG	ACAAAGTTCC	ATTTTTACCT	TTTGATGGTA	1860
10	AAGATGCAGA	TGGCAAGGAT	GCTTATAAAG	CAGCAAATGC	TAAAGAAAAT	TATTGGTTTG	1920
	GTACTGATCA	GTTGGGTCGA	GATTTATGGA	CAAGAACATG	GAAAGGTGCT	CAAATTTTAT	1980
	TGTTTATCGG	TGTTGTTGCA	GCGATGTTAG	ATATTTTTAT	TGGTGTGTA	TATGGTGCGA	2040
15	TTTCTGGATT	CTTCGGTGGA	CGTGTGATA	CGATTATGCA	ACGTATACTT	GAAGTCATAG	2100
	CATCTATTCC	GAATTTAATT	GTCGTAATTT	TATTTGTATT	AATTTTTGAA	CCATCCATTT	2160
	GGACAATTAT	ATTGGCTATG	TCTATCACAG	GCTGGTTAGG	CATGAGCAGA	GTTGTACGTG	2220
20	GAGAATTTTT	AAAATTAAAA	AATCAAGAGT	TTGTCATGGC	TTCGAAAACA	TTGGGGGCTT	2280
	CAAAATTCAA	ATTGATATTT	AAGCATATTT	TACCTAATAC	ATTAGGTGCT	ATCGTGGTTA	2340
25	CATCAATGTT	TACAGTACCT	AGTGCTATTT	TCTTCGAAGC	ATTTTTAAGT	TTCATTGGTA	2400
	TAGGTGTACC	CGCACCTCAA	ACATCGTTAG	GGTCATTAGT	AAATGATGGG	CGCGCAATGT	2460
	TATTAATTTA	TCCACATGAA	TTATTTATAC	CAGCAATGAT	TTAAGTTTA	TTAATTCTAT	2520
30	TCTTTTACTT	ATTTAGTGAT	GGATTACGTG	ATGCATTTGA	TCCGAAAATG	CGTAAATAAA	2580
	AAGGGGGCAT	AGCATATGAC	TGAAAGAATA	TTAGAAGTAA	ATGATTTGCA	TGTTTCCTTT	2640
	GATATTACAG	CAGGGGAAGT	GCAGGCAGTG	AGAGGCGTAG	ATTTTTATTT	GAACAAAGGG	2700
35	GAAACATTGG	CAATTGTTGG	TGAATCAGGT	TCAGGTAAAT	CTGTAACAAC	AAAAGCAATT	2760
	ACAAAATTAT	TCCAAGGGGA	CACAGGAAGA	ATTAAAAAGG	GAGAAATTTT	ATTTTTAGGG	2820
	GAAGATTTAG	CAAAAAAACC	TGAAAATGAG	TTGATTAAAT	TACGTGGCAA	AGATATTTCA	2880
40	ATGATCTTTC	AAGATCCAAT	GACATCTTTA	AACCCAACGA	TGCAAATTGG	TAAACAAGTC	2940
	ATGGAACCAT	TAATTAAGCA	CAAAAATTAT	AGTAAAGCAC	AAGCTAAAAA	GCGCGCATTG	3000
45	GAAATACTAA	ATCTTGTAGG	TTTACCAAAT	GCAGAAAAAA	GATTTAAAGC	ATATCCTCAT	3060
	CAATTTTCAG	GTGGACAAAG	GCAAAGAATT	GTTATTGCAA	CCGCATTAGC	TTGTGAACCT	3120
	AAAGTGCTCA	TTGCTGATGA	ACCAACGACT	GCATTAGACG	TAACGATGCA	GGCACAAATT	3180
50	TTAGATTTAA	TGAAAGAACT	ACAACAAAAA	ATCGATACAG	CAATTATTTT	TATAACGCAT	3240
	GATTTAGGGG	TTGTTGCGAA	TATTGCTGAT	AGAGTGGCAG	TTATGTATGG	TGGTCAAATG	3300
55	GTTGAAACAG	GAGATGTTAA	CGAAATATTT	TATGATCCAA	AGCATCCATA	TACATGGGGA	3360

	GGAGCGCCAC	CTGATTTATT	ACACCCACCT	AAAGGTGATG	CATTTGCGAG	ACGTAGcAAT	3480
5	ATGCATTAGA	TATTGATTTT	AAAGTAGAAC	CACCGTGGTT	TAAAGTTTCA	CCGACACATT	3540
	TTGTGAAATC	TTGGTTATTA	GACGCACGTG	CACCAAAAGT	TGAACTACCC	GAGCTGGTAA	3600
	AACAACGTAT	GAAACCGATG	CCTAATAATT	ATGAAAAACC	ACTCAAGGTA	GAAAGGGTGT	3660
10	CGTTCAATGA	AAAATGATGA	AGTGCTATTA	TCTATTAAAA	ATTTAAAGCA	ATATTTTAAc	3720
	GCAGGAAAGA	AAAACGAAGT	GgaGCGATTG	AAAATATTTc	GTTTGATATA	TACAAAGGGG	3780
	AAACATTAGG	TTTAGTAGGA	GAATCGGGGT	GTGGTAAATC	TACAACTGGT	AAATCAATTA	3840
15	TTAAACTTAA	TGATATTACA	AGTGGAGAAA	TTTTGTATGA	GGGTATTGAT	ATACAAAAGA	3900
	TTCGTAAACG	TAAAGATTTG	CTTAAATTTA	ATAAAAAGAT	ACAGATGATT	TTTCAAGACC	3960
	CATATGCGTC	TTTAAATCCT	AGGTtAAAAG	TAATGGATAT	AGTAGCTGAA	GGTATTGATA	4020
20	TCCATCATTT	AGCAACTGaT	AAGCGTGACC	GAAAAAAACG	TGTCTATGaT	TTACTTGaAA	4080
	CTGTTGGATT	AAGTAAAGAA	CATGCCAATC	GCTATCCTCA	TGAATTTTCA	GGTGGaCAAC	4140
25	GCCAACGTAT	TGGaATTGCC	CGTGcATTAG	CCGTTGaACC	AGAATTCATT	ATCGCGGACG	4200
	AACCAATATC	GGCATTGGAT	GTTTCAATCC	AAGCTCAAGT	AGTTAATTTA	TTATTAAAT	4260
	TACAACGTGA	AAGAGGGATT	ACGTTcCTAT	TTATAGCTCA	TGATCTATCA	ATGGTGAAGT	4320
30	ATATTTcAGA	TCGTATTGCA	GTCATGCATT	TTGGGAAAAT	AGTTGAAATT	GGACCGGCAG	4380
	AAGAAATTTA	TCAAAATCCA	TTACACGATT	ATACTAAGTC	TTTATTATCA	GCCATTCCAC	4440
	AACCTGATCC	TGAATCAGAA	CGCAGTCGCA	AACGATTTAG	TTATATTGAT	GATGAAGCAA	4500
35	ATAATCATTT	AAGACAATTA	CATGAAATTA	GACCGAATCA	CTTTGTCTTT	AGTACTGAAG	4560
	AAGAAGCGGC	ACAACTACGA	GAAAATAAAT	TGGTGACACA	AAATTAAGGG	GAAGGGGGAA	4620
	ATGcAATGAC	GAGAAAATTT	AGAACACTTA	TTTTAATTTT	GATTGCTACA	ATTGCATTAA	4680
40	GTGGTTGTGC	TAATGACGAT	GGTATTTATT	CAGATAAAGG	TCAAGTATTC	AGAAAAATTT	4740
	TGTCATCAGA	CTTAACATCC	CTTGATACAT	CATTAATAAC	GGATGAAATA	TCTTCTGAAG	4800
45	TGAcTGCGCA	AACATTcGAA	GGTTTATACA	CATTAGGAAA	AGGTGACAAA	CCGGTGTTAG	4860
	GTGTTGCGAA	AGCTTTTcCT	GAAAAGAGTA	AAGATGGTAA	AACTTTAAAG	GTAAATTTAA	4920
	GAAGCGATGC	TAAATGGAGC	AATGGTGACA	AAGTGACTGC	ACAAGACTTT	GTTTATGCTT	4980
50	GGAGAAAAAC	AGTTGACCCT	AAAACAGGTT	CTGAATTTGC	ATACATTATG	GGGGACATTA	5040
	AAAATGCGAG	TGATATTAGT	ACTGGTAAGA	AACCTGTAGA	GCAATTAGGT	ATCAAAGCAT	5100
55	TAAATGATGA	AACATTACAA	ATTGAATTAG	AAAAGCCGGT	TCCATATATT	AATCAATTAT	5160

ACGGTACGGC AGCTGATAGA GCGGTATACA ATGGTCCaTT TAAAGTTGAT GATTGGAAAC 5280
 AAGAAGATAA AACCTTACTA TCTAAAAATC AGTATTATTG GGATAAAAAG AATGTAAAAT 5340
 TAGATAAAGT GAATTATAAA GTTATTAAAG ACTTACAAGC CCGTGCAATCA TTGTATGATA 5400
 CTGAATCAGT AGATGACGCA TTTATTACTG CAGATCAAGT AAATAAATAT AAAGACAACA 5460
 AAGGATTAAA CTTTGTGTIA ACGACTGGGA CATTTTTTTGT AAAAATGAAT GAAAAACAAT 5520
 ATCCTGATTT TAAAAACAAA AATTTAAGAT TGsTATCGCA CAAGCAATAG ATAAAAAAGG 5580
 ATACGTTGAT TCAGTGAAAA ACAATGGCTC AATTCCTTCC GATACACTAA CAGCCAAAGG 5640
 AATTGCGAAA GCGCCTAATG GCAAAGATTA TGCGAGTACC ATGAATTCGC CTTTAAATA 5700
 TAATCCTAAA GAAGCAAGAG CACACTGGGA CAAAGCTAAA AAAGAGTTAG GTAAAAATGA 5760
 AGTGACATTT TCAATGAACA CAGAAGATAC ACCAGATGCA AAAATATCTG CTGAATATAT 5820
 CAAATCGCAA GTTGAGAAAA ATTTACCAGG AGTTACTTTG AAAATTAAGC AATTACCGTT 5880
 TAAACAAAGA GTATCACTAG AACTGAGTAA CAATTTTGAA GCATCACTTA GTGGTTGGTC 5940
 TGCAGATTAC CCTGATCCTA TGGCTTATTT AGAAACAATG ACCACAGGTA GCGCACAAAA 6000
 TAATACAGAC TGGGGTAATA AAGAATATGA TCAATTACTT AAAGTAGCAA GAACCAAATT 6060
 GGCACCTCAA CCGAACGAAC GATATGAAAA CTTGAAAAAA GCAGAAGAAA TGTTCTTAGG 6120
 AGATGCACCG GTAGACCAA TTTATCAAAA AGGTGTtGCA CATTtaACAA aTCTCAAGT 6180
 AAAAGGATTA ATttACCATA AATTTGGTCC AAATAACTCA CTTAAACATG TATATATTGA 6240
 TAAATCGATA GATAAGAAA CAGGTAAGAA GAAAAAATAA TATGCTTTGT AAATTAGGCT 6300
 GGAGACATAT CTCCAGTCTT TTTGTGTTGG ATAAAAaCTT TGGGAATAAA AATTTAAAAT 6360
 AAGTCGTTTT TTAAATTACT GAAATTGATT AAATGCATAA ATAAGTGAAT ATTCTAAAAA 6420
 TAAACTTGTA ATAATTTTTT CTATGAGTAA ACTAAAAAGA AAAAATTAGA TTGAAAGTAG 6480
 GAGGCATATG TATGGGGAAG CTAATTAAAT ATATTTCAAT ACTTCTTATT GTCGTTTTAG 6540
 TGTTGAGTGC TTGCGGAAAA AGCAGTAATA AAGATGAAGG AGTAAAAGAT GCTACTAAAA 6600
 CGGAAACCTC AAAACATAAA GGTGGTACCT TAAATGTAGC ATTAACAGCA CCGCCAAGTG 6660
 GTGTTTATTC TTCGTTATTA AATAGTACAC ATGCAGATTC TGTAGTTGAG GGATATTTTA 6720
 ACGAAAGCTT 6730

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

5	AATTTTGTGC ATTATTAAAA ACCTCGCTTT TAAAAGATTG AAAAGTAAAT GAGTGAAATT	60
	AAAGATTATG CACATTAAAA TCACGCCACA ATTTAATTGT GAAAAATATC ACAAATATAT	120
	TATAACACTA AATTTCCCAA AATTCAAAAG TGTGTTTAT TGCAGAAAAC TTATAACAYG	180
10	TGCACAAGTT ATAGTGAATT GCAAACGGAT TACTTTAGTC TTTTAAAAC ATGAAGTATA	240
	ATTTGTATAG CAATAAATAT AAAAATGGGA GGCTATGTTT AATGAGCAAT ATGAATCAAA	300
	CAATTATGGA TGCATTTTCAT TTCAGACATG CCGACTAAGCA ATTCGATCCA CAAAAGAAAG	360
15	TTTCGAAAGA AGATTTTGAA ACAATATTAG AGTCAGGTAG ATTGTCTCCA AGTTCTCTTG	420
	GGTTAGAACC TTGGAAGTTT GTCGTGATTC AAGATCAAGC GTTACGTGAT GAATTAAAAG	480
	CGCACAGTTG GGGCGCAGCA AAACAATTAG ATACAGCGAG CCATTTTGTG CTAATTTTGTG	540
20	CGCGTAAAAA TGTAACGTCA AGATCACCGT ATGTACAACA TATGTTAAGA GATATTAAAA	600
	AATATGAGGC ACAAACGATT CCAGCTGTTG AACAAAAATT CGATGCATTC CAAGCAGATT	660
25	TCCATATTTT TGATAATGAT CAAGCCTTGT ATGACTGGTC AAGTAAACAA ACGTATATTG	720
	CATTAGGCAA TATGATGACG ACAGCCGCAT TGTAGGTAT TGATTCATGT CCGATGGAAG	780
	GTTTTAGTCT GGATACAGTG ACAGACATTT TAGCAAATAA AGGGATCTTA GATACTGAGC	840
30	AATTTGGTTT ATCAGTGATG GTCGCATTTG GCTACAGACA ACAAGAGCCA CCGAAAAATA	900
	AAACACGCCA AGCTTATGAA GATGTTATTG AATGGGTTGG ACCAAAAGAA TAAATAGAAT	960
	ACCGTATGTC TAAATATATA AAATTAAAAA GTTAGCAATA AAAAAGCCTG CGATTACATA	1020
35	AATGAATCGC AGGCTTTTGC GTGAAAAAAT TGTATTAATA AAGTATGGAT GATTATTTTT	1080
	CTGGTACAAG GTCAGTATTT GAATGAACTG TGATGTCAAA CCCTTCTGGT GCCGTAAATG	1140
	TATGTGTTGA GGCCTCGGGT TGATAAATAT CAACATGTGT TAATCCATAA CTTTGTGAAT	1200
40	TGTTTTGTCT TGCTTGATTG GATTGCCAAG TATTAGCAGC AATATGATGG TGATAATGAT	1260
	TCGTTGACAT AAATAGCGCA CGTGGAAAT CAGACACATG TTGGAATCCT AATTGTTCAA	1320
45	TGTAACATTG ATATGCTGCG TCTAAATCAT GTGTTTTTAA ATGTAAGTGT CCAATCATGC	1380
	CTTTTGCTGG CATTCCTTGC CAACCTTCAT CAGTACGATG TGTTAATAAG GTTTGGCTAT	1440
	CAACTTCTAA AGTATCCATT TTAACCTTGC CATTTTGCCA TTCCCATGAA GATGAAGGTC	1500
50	TATCGCGATA GACTTCAATA CCATTACCTT CGGGGTCGTT GAAATATAAA GCTTCACTTA	1560
	CTAAATGATC ACCAGCGCCG ATGCCCATAT TTTTTTGTGC CACGAAATAT AAGAAGTTAG	1620

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aAGTCTGACG GcCGTCTTCT AATAAATGTA ACGTTAGAGT ATGGcCACCA GTCCCAACAG 1740
 ATAATACGGT TGTATTATCG TCAGAACTTT TAACGGATAG TCCTAAAATG TTTTGTGAAA 1800
 5 ATGTTGTCAT TAAGTCTAAG TCTCTTACGT TCAGTACAAT GTTTGTCACT TGTGTGCTG 1860
 TTTTATCGTG AAATGCCATT ATGCATCGCC TCTTTTTCTA TTTTCTATA AGTTAGTATA 1920
 AAAAGTATAC CAGAAAAGAA AATGAATTGA TAGCATAAAG TTTGAAATGC AAAATAACTA 1980
 10 GTCGTTTTGC AATTTTATcAT TGATGCGAAC AAAAAAGCGA TGGTACAGTT GCACCATCGC 2040
 AAAATTTATT TAACCAAGAT ATACATCTTG ATATGAATCT TCTTTTTCTA ACATATGTTT 2100
 15 GGCAAAATGAA CATGAGGCAA TAATTTTCAA ATTATTTTCT CGAGCGTGTT CAACAAC TGc 2160
 TTTAAGTAGT TTTTGGCCAA CACCTTGACC ACCAAGTTCA TCAGATACGC CTGTATGATC 2220
 AATGTTAATT TCATTATTAT CCACAAAACG GTATGTGATT TCAGCTAAAG CATTATTTTC 2280
 20 ATCATCACCA ATATAGAATT TGTTCTCGCC TTGTTTGATT TCAAGGTTAC TCATACATAT 2340
 CAACTCCTAT CATGATTGAT TATAGTATTT CCCTATTCTA TTTTAACTTA AACGAAGTCA 2400
 AAGGTGCATG ACAGTCATGT GACGACATTG CCACATCTAT GTAGTCGTTT TTATTAAGCA 2460
 25 CAGTTTGAAA TGAAGATGAA AACACGTATC TTGACATTAA ATCTATTCAG CTATATAATT 2520
 TATCTCGAAA TCGAAATAAA ATAAAAAAGT TGGTGATCAT ATGGATCGAA CGAAACAATC 2580
 TCTCAATGTT TTTGTCGGAA TGAATAGGCG GTTAGACACA TTAGAGCAAA TTACAAAAGA 2640
 30 AGACGTAAAG CGATATGGCT TAAATATTAC TGAATTTGCA GTGCTCGAGT TGCTTTATAA 2700
 TAAAGGTCCG CAACCAATTC AACGTATTAG AGACCGCGTA TTAATTGCAA GTAGCAGCAT 2760
 35 TTCATATGTT GTAAGTCAAT TAGAGGACAA AGGTTGGATT ACACGTGAAA AGGATAAAGA 2820
 TGATAAACGT GTATATATGG CTTGTTTAAAC TGAAAAAGGT CAAAGTCAAA TGGCAGATAT 2880
 TTTcECTAAG CATGCTGAGA CATTAAACAA AGCGTTTGAT GTGTTAACAA AGGATGAATT 2940
 40 AACAACTCTTA CAACAAGCGT TTAAGAAACT AAGTGCACAA TCTACAGAAG TGTAAGGCGT 3000
 GCACTAAAAA TTTACATTAA AGTATCTCGA TTTGAGATA AATGCACTAA AAATATAAAG 3060
 AGGGTATATA AAATGATAAA TAATCATGAA TTACTAGGTA TTCACCATGT TACTGCAATG 3120
 45 ACAGATGATG CAGAACGTAA TTATAAATTT TTTACAGAAG TACTAGGCAT GCGTTTAGTT 3180
 AAAAAGACAG TCAATCAAGA TGATATTTAT ACGTATCATA CTTTTTTTGC AGATGATGTA 3240
 50 GGTTcGGCAG GTACAGACAT GACGTTCTTT GATTTTCCAA ATATTACAAA AGGGCAGGCA 3300
 GGAACAAATT CCATTACAAG ACCGTCTTTT AGAGTGCCTA ACGATGACGC ATTAACATAT 3360
 TATGAACAGC GCTTTGATGA GTTTGGTGTT AAACACGAAG GTATTCAAGA ATTATTTGGT 3420

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	TTAAATGAAG	GGGTAGCACC	TGGTGTACCT	TGGAAGAATG	GACCGGTTCC	AGTAGATAAA	3540
	GCGATTTATG	GATTAGGCCC	CATTGAAATT	AAAGTAAGTT	ATTTTGACGA	CTTTAAAAAT	3600
5	ATTTTAGAGA	CTGTTTACGG	TATGACAACT	ATTGCGCATG	AAGATAATGT	CGCATTACTT	3660
	GAAGTTGGCG	AAGGAGGCAA	TGGTGGCCAG	GTAATCTTAA	TAAAAGATGA	TAAAGGGCCa	3720
10	GCaGCACGTC	AAGGTTATGG	tGAGGTACAT	CATGTGTCAT	TTCGTGTGAA	AGATCATGAT	3780
	GCAATAGAAG	CGTGGGCAAC	GAAATATAAA	GAGGTAGGTA	TTAATAACTC	AGGCATCGTT	3840
	AATCGTTTCT	ATTTTGAAGC	ATTATATGCA	CGTGTGGGGC	ATATTTTAAT	AGAAATTTCA	3900
15	ACAGATGGAC	CAGGATTTAT	GGAAGATGAA	CCTTATGAAA	CATTAGGCGA	AGGGTTATCC	3960
	TTACCACCAT	TTTTAGAAAA	TAAAAGAGAA	TATATTGAAT	CGGAAGTTAG	ACCTTTTAAT	4020
	ACGAAGCGTC	AACATGGTTA	ATTGGAATGA	GGAGGATTG	TGATGGAACA	TATTTTTAGA	4080
20	GAAGGACAAA	ATGGTGCGCC	AACACTAATA	TTATTGCATG	GTACAGGTGG	TGATGAGTTC	4140
	GATTTATTAC	CGTTAGGCGA	AgcATTGAAT	GAAAATTATC	ACTTGTTAAG	TATTAGAGGA	4200
	CAAGTTTCAG	AAAATGGGAT	GAACCGTTAT	TTCAAACGTC	TTGGTGAAGG	TGTTTATGAT	4260
25	GAAGAAGATT	TGGCATTTCG	TGGACAAGAA	TTGTTGACGT	TCATTAAAGA	AGCTGCTGaa	4320
	CGTTATGATT	TTGaTATTGA	AAAAGCAGTA	CTTGTTGGAT	TTTCAAATGG	ATCAAATATA	4380
30	GCGATTAACT	TAATGTTGCG	TTCAGAAGCA	CCATTTAAAA	AAGCATTGTT	ATATGCACCG	4440
	TTATACCCAG	TTGAAGTAAC	GTCAACAAAG	GATTTATCAG	ATGTCAGTGT	GTTGCTTTCT	4500
	ATGGGGAAAC	ATGATCCAAT	TGTGCCATTA	GCTGCAAGTG	AACAAGTCAT	TAACTTGTTT	4560
35	AATACACGTG	GGGCACAAGT	CGAAGAAGTT	TGGGTGAAGG	GCCATGAAAT	TACAGAAACT	4620
	GGATTAACGG	CTGGTCAACA	AATACTTGGG	AAATAACAGT	TCTATTAAGA	AGCGGACAGA	4680
	TGGAaAAGAT	TTTTACTTTT	CATCTGCCCG	CTTTTTTGAT	TTTGAAGTGC	TGTACTAAAT	4740
40	TTTACAATAG	TATAGATATT	TTAATCGATA	TGAGATTTGC	CGGTAATACG	CTTAATTAAA	4800
	CCTTTATAGA	GTACAGGTAT	GAGTAAGATG	AAACCGAACA	ATCCCATAAT	AGGGAATACT	4860
	TTTCCAATTA	ATGAAATGaa	ACCGATAAAT	GTAATAATAT	AAGTGATGAC	AGCCATTGTA	4920
45	ATAATAATGA	TGAAGTAACG	TCTGCTGAAT	GGAACGCTGA	AACGTGACGC	AAATGCATAC	4980
	ATTAATCCAA	CAACAGTATT	GTAGATGACA	AGTATCATAA	TGACAGACAT	AATAATACCA	5040
50	ATTGACGGAG	ACATTTGTGT	CGCTAATTTT	AATGTAGGTA	GATCTACGTG	TTTAATTTTA	5100
	TCGAATTGAG	AAATTAAACC	TAGATTAATC	ATCATGAGTA	AAAATGTAAT	GATTAAACCG	5160
	CCAATCAAGC	CCCCGTATAA	CGTTGAGTCA	CGATATTTAA	CTTTACTACC	CATCACTGAT	5220

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CCAGGTGATA ATGATTTCTG CTTATGAATC TGAGCATCAT TATTAGCGGC AGTAAATCA 5340
 AGATGACTTG TTGTGAAATA GTAGACCGCA ATCATAATGA CAATCGCAAT TAAAAATGGG 5400
 5 GTAACACCGC CAAGCACAGC AATTAAACGA TCGAATTTTA GAAACAGTGT TGCTAAAATA 5460
 AAGGCGACTA ATATGAGTGC GCTCAGCCAA TACGGTAAGT TGAAACTTTG ATGAATGGTT 5520
 10 GACGCACCAC CTGCAGTCAT AATAATAGCT AAAGACAACA TAAACATTGT TAAAATAATA 5580
 TCAAAACCTC TTGCAATAGA GGGGTATAAG AAATAGTTAA TTGAATCAGA ATGATTTCTG 5640
 GACTTTAGAT GATGACCTGT ATGCATGACA ACCATTCCAC CTAAAGTAAT CAATAGTCCT 5700
 15 GTTACAATAA TGCCTGAAAT GCTATATGCG CCATGACTTG TGAAAACTG GAAAATTTCT 5760
 TGACCAGTAG CAAAGCCGGC ACCAACGACA ACACCAACAA AGGCAAATGC CACAATAATG 5820
 GACTCTTTTA AGATACGCAT GATTTAAAAA TGTCCCTTCG TAATTTTAAG TAATATAGAA 5880
 20 AATGTAACAT ACATGTTAAT GAAAAATATA GTACTAATAT AGTATTTTGT TAAATTGGAG 5940
 TAGAAGCGAG GGTGTCGGTC ATTTTCATTAA TTTATTAGTT GATTTTGCAT TTTTTTGCTG 6000
 TAAAGTTGTT ATAATACAGT TAACAGGAAT TAGCATAGAT ACACCAATCC CCTCACTACT 6060
 25 CGCAATAGTG AGGGGATTTT TTTCGGTGTA GCTAGGTCGC CTATTTATCA TCGTGTTCG 6120
 GTAGCaATGC GTAAACACAG TACCACTAAA TAAGTGACG ATACATGCAT CAAATGTCGT 6180
 CTTTAGTcTA AGTAACGATC ATGCATTAA ATTTTCAAAA TATCTATTG AGCTTGAAGA 6240
 30 TCTTTACCAA TATTGGTATC ACGAATCTTC TTACGTTGTA ATTCTTTATC TACGACGCGC 6300
 TTTATAGAAA GTTCATCGAT ACCTTCGGAA AGTATTTTTn CTTTAGCGTT AAATTGTTGG 6360
 35 TGTGCAACGA GTTGCAATACC GAATGAATTA TACAATAGTG TATAGCCTGC AATGCCAGTn 6420
 GTTGACTGAT AAGCTTTTGA AAAGCCACCA TCAATGACAA GCATCTTTCC ATCAGCCTTG 6480
 AT - 6482

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16592 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ATTTAAGGCG ATTGCTTG TG TATTTCTCTC TTTTGTAGGC AAACCTGCAC TCGTTCCAAA 60
 AAATGTAAC TCCATATATG CCCCTCCTTT TCTTCAATTC ATTTTATCAT AAAATTGTA 120

	AATTTTCTA	ACTTTAACGT	AGACATAACT	ATATAAATTT	TGATAATTAC	GTTATACTTA	240
	TCATTAATAA	GTATCACATT	AAACATGATA	CATGAATCGA	TATTTCAATTT	AAGACACTGC	300
5	ATACAGTCGA	GCATATTGTA	TGACCTACTG	AATGGATTAT	CTTATAATAA	TAAATCATAT	360
	ATCTAATTAA	GAATTGAGGT	TTTAATCTTG	AGTACTAAAA	ACAAACACAT	CCCATGTTTA	420
10	ATCACAATCT	TTGGTGCACT	GCGTGACTTA	AGCCATCGTA	AGTnGTTTCC	ATCAATATTC	480
	CATCTCTACC	AACAAGACAA	TTTAGATGAA	CATATTGCCA	TcATCgGTAT	TGGACGTCGT	540
	GACATkwnTA	ATGATGATTT	CCGTAATCAA	GTAAAATCAT	CAATTCAAAA	GCACGTAAAA	600
15	GATACAAACA	AAATTGACGC	GTTTATGGAA	CATGTCTTCT	ATCATAGACA	TGATGTTAGT	660
	AATGAAGAAA	GCTATCAAGA	ATTACTAGAT	TTTAGTAATG	AATTAGATAG	CCAATTTGAA	720
	TTAAAAGGTA	ATCGACTATT	CTATTTAGCA	ATGGCACCAC	AATTCTTTGG	CGTTATTTCT	780
20	GATTATCTAA	AATCTTCTGG	TCTTACTGAT	ACAAAAGGAT	TTAAACGCCT	TGTTATCGAA	840
	AAACCATTCTG	GTAGTGATTT	AAAATCAGCC	GAAGCATTAA	ACAATCAAAT	TCGTAAATCA	900
	TTTAAAGAAG	AAGAAATTTA	TCGTATTGAC	CACTATTTAG	GAAAAGACAT	GGTTCAAAAT	960
25	ATCGAGGTAT	TACGTTTTGC	GAATGCGATG	TTTGAACCAT	TATGGAATAA	CAAATATATT	1020
	TCAAACATCC	AAGTTACATC	TTCTGAAATA	CTAGGTGTTG	AAGATCGTGG	TGGTTATTAT	1080
30	GAATCAAGTG	GCGCGCTAAA	AGATATGGTG	CAAAACCACA	TGTTACAAAT	GGTTGcATTA	1140
	TTAGCTATGG	AAGCACCTAT	TAGTTTAAAT	AGTGAAGATA	TCCGTGCTGA	GAAAGTAAAA	1200
	GTACTTAAAT	CACTGCGTCA	TTTCCAATCT	GAAGATGTTA	AAAAGAACTT	TGTTTCGTGGT	1260
35	CAATATGGCG	AAGGCTATAT	CGATGGTAAA	CAAGTTAAAG	CATACCGTGA	TGAAGATCGC	1320
	GTTGCAGATG	ACTCTAACAC	ACCTACCTTT	GTTTCAGGTA	AATTAACAAT	TGATAACTTT	1380
	AGATGGGCTG	GTGTACCATT	CTATATTCGT	ACTGGTAAAC	GTATGAAATC	TAAAACAATT	1440
40	CAAGTTGTCG	TTGAATTTAA	AGAAGTACCA	ATGAACCTTAT	ACTATGgAAA	CTGaTAAACT	1500
	GTTAGATTCA	AACCTATTAG	TAATCAATAT	CCAACCTAAT	GAAGGTGgTA	TCTTTtACAT	1560
45	CtAAATGcTA	AGAAAAATAC	ACAAGGTATC	gAAACAGrAC	CTGtCCmATT	GtCTTACTCm	1620
	ATGaGCGcTC	aAGaTAAAAAT	GaATACTGTA	GATGCATATG	AAAATCTATT	ATTTGATTGT	1680
	CTTAAAGGTG	ATGCCACTAA	CTTCACGCAC	TGGGAAGAAT	TAAaATCAAC	ATGGAAATTT	1740
50	GTTGATGCAA	TTCAAGATGA	ATGGAATATG	GTTGaTCCAG	AATTCCTTAA	CTATGAATCA	1800
	GGTACTAATG	GTCCATTAGA	AAGTGATTTA	CTACTTGCTC	GTGATGGTAA	CCATTGGTGG	1860
55	GGACGATATT	CAATAATTGA	ATTAAAACGC	ACATGTTAAA	CAAAAATAAA	TGAGCGAATG	1920

	TATATTATGA	AATTATATTT	TACAATGCCC	AAACTATTTT	TAATAATCAT	TGAACAAATG	2040
	GGTGATAAAT	TTATAGAAAT	AATGTAGAAT	AAAAATAAAT	GATTGAATTA	ATTGGAGTGA	2100
5	AAGTTTGGGA	CGTTATCAAG	CAAATACAAC	AGGCAATTGT	TTATATTGAA	GATCGTTTAT	2160
	TAGAGCCTTT	CAATTTGCAA	GAATTAAGTG	ATTACGTTGG	TCTTTCGCCA	TACCATCTTG	2220
	ATCAATCATT	TAAAATGATT	GTGCGCTTAT	CTCCAGAAGC	TTATGCACGC	GCGCGTAAAA	2280
10	TGACACTCGC	TGCAAATGAT	GTGATTAATG	GTGCTACACG	ACTTGTAGAT	ATCGCTAAAA	2340
	AATATCACTA	TGCAAATTCA	AATGATTTTG	CAAATGATTT	TAGTGATTTT	CACGGCGTAT	2400
	CACCTATTCA	AGCCTCTACT	AAAAAAGATG	AATTACAAAT	TCAAGAGCGA	TTATATATCA	2460
15	AATTATCAAC	TACTGAGAGA	GCACCTTATC	CATACAGATT	AGAAGAGACA	GATGATATTT	2520
	CATTGGTTGG	ATATGCACGA	TTTATAGACA	CTAAGTATTT	GTCACATCCT	TTAATGTTC	2580
20	CGGATTTTTT	AGAAGACTTG	CTCATTGATG	GTAAAAATTAA	AGAGTTACGA	CGATATAATG	2640
	ACGTTAGTCC	ATTTGAACTA	TTTGTATTAT	GTGTCTCTCT	TGAAAATGGT	TTAGAAATAT	2700
	TTGTAGGTGT	ACCAAGTGAA	CGTTATCCTG	CACACTTAGA	AAGTCGATTT	TTACCTGGCA	2760
25	AACATTGTGC	GAAATTCAAT	TTACAAGGTG	AAATTGATTA	TGCAACTAAT	GAAGCTTGGT	2820
	ACTATATTGA	ATCAAGTTTG	CAGTTAACAT	TGCCATATGA	ACGAAATGAT	TTATATGTTG	2880
	AAGTGTACCC	TCTCGATATT	TCATTTAATG	ACCCATTAC	TAAAATTCAG	CTTTGGATTC	2940
30	CTGTTAAACA	GAGTCCTTAT	GACGAAGATT	AAATAATAAA	AAACAAAGAA	GCCCCCTAAT	3000
	ATATCTATAG	GTCTACAAAT	GGCCTTAGAT	TCTATTAGGG	GGCATATTAA	TATGTTAATT	3060
	TAGTTCGATA	ACACATGCTT	CATATGGACG	TAAGTGTTTT	AAATTAACTT	TGGCATCATA	3120
35	ATTAAATAGC	TTTACTTCTC	CATGGCTTAA	ATCAAATGGT	ACAGTTAATT	CTGCTTCGTG	3180
	GTTAGTAAGA	TTACCTACAA	TAAGAACTTG	CTTTTCATTT	AATGTTCTCG	TGTACGCAAA	3240
40	AACTTGTGAA	TTTTTCAGCAT	CTACTAAATC	AAATTGACCA	TATACGTATA	CATCATTAGA	3300
	CTTTCTTAAT	TGAATTAAAT	CTTTATAAAA	TTGTAATACT	GAATGCTCAT	CTTCTAATTG	3360
	TTGTGCAACA	TTGATAGTTT	TATAAATCGG	ATTCACGGG	AACCACGGTT	CACCATTTGT	3420
45	AAATCCTCCA	TTTAACGTAT	CATCCCATTG	CATTGGTGTG	CGAGAATTAT	CTCGTTCTC	3480
	ATCTTTATAT	TTGCAAGTA	AAGCGTCTAC	ATCTCCACCT	TGAGCTTTCA	CTATTGATA	3540
	GTCATTTTTA	ACAGCAACAT	CGTTAAACGT	TTCAATACTT	TCAAATGGAT	AATTCGTCAT	3600
50	ACCAATTTCT	TGACCTTGAT	AAATGAATGG	CGTACCTTGT	TGCAAGAAAT	AAACAGCTGC	3660
	ATGACTTGTT	GCTGATTCAT	ACCAATACTT	GTCATCGTCA	CCCCACGTGC	ATACACGTGC	3720

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	CCATCTATTT AATACAGATT TATACGAATT TACATCAAAG TGAGAATCAC CACTATTCCA	3840
	CAGTCCCAA TGTTCAAAT GGAATATCAT ATTAAATTTA CCATTTTCTT CCCCACCCA	3900
5	GTCATCAGCA TCATCAGGGC TTACACCATT CGCTTCACCA ACAGTCATAA TGTCACTT	3960
	ACTTAATGAG CGATCTTTCA TCTCTTGTA CCAAGTTTGT ATACCTGGCT GATTCATATC	4020
	TACATCAAAT GCTGGGGCAT ATGTTTTACC CTCAGGTACA GGTAAGTCAC CCGCTTCAA	4080
10	CGTCTTCTTA ATATGCGTAA TTGCATCTAC TCTAAATCCA TCAATGCCTT TATCAAACCA	4140
	CCAGTTCATC ATTTCAAATA CAGCATCTCT AACTTCCGGA TTACCCCAAT TCAAATCAGG	4200
	TTGTTTTTTA CTGAATAAAT GGAAATAATA TTGCTCAGTA TTAGCATCAT ATTCCCATGT	4260
15	AGATCCATTA AATATACTTT CCCAGTTGTT AGGTTGAGAG CCATCTGGCT TTGGATCTTG	4320
	CCAAATGTAC CAATCACGTT TGGGATTGTC TTTACTAGAT TTGGATTCTA TAAACCAAGG	4380
20	ATGTTTCATCA GATGTATGAT TTACAATAA ATCTAAAATA AGCTTCATGC CTCTATCATG	4440
	AACACCTTTT AATAAACGAT CAAAGTCTTC CATCGTTCCA AATTCATCCA TAATCTCTTG	4500
	GTAGTCACTA ATATCATAAC CATTGTCATC ATTAGGTGAT TTAAACATTG GACTGAGCCA	4560
25	AATGACATCG ATACCGAAAT CTTTTAAGTA GTCCAATTTA TCAATCATTC CAGGTAAATC	4620
	CCCAATACCA TCGTGATTAC TATCATTAAA ACTTCTTGGA TATACTTGAT ATGCTACTGC	4680
	TTCTTTCCAC CATTGCTTAT TCATTTTAAA ACTCCTTTGC TATCGCTGTG TTGATTTTCT	4740
30	TATTTTAAAT TCTGTATCTA TAATGACGAG TTCAATAACA TCCTGTGCTT TGTTTTTCAA	4800
	TATATTTAAA ATTGCTGCAC CAGCCTGTTG ACCTAACATT CGAGGCTTGA TGTCAATACA	4860
35	GGTTTGTGGT GGTGACGCAA TTTGCGTTAA ATAAGAATCA TTGAACGTTG CTGTCATTAC	4920
	ATCTTTCCGA ATTTCAATAT TAAGTTCATA TAGGACACTT AAAATCGCTA AATGTAACAT	4980
	AGCATCTAAC GAAATGATTG CCTGTTTAAAT ATTTGGGTCC TTCAAACGCG TATGTAGATT	5040
40	TTGCATGTAA TTAATAATA CTTCTCTTTC ATTACTAGTC TCAATAATTT GATAATTAAT	5100
	TTTATTTTGA GAAGCTATCG TTTCAAATCC TTGAATTCTA TCTTTTGAAA CTTCAAATTT	5160
	TCCTTTTCTT GTAATAAATA TTAATTCATC TACACCTTGT TCAATAACAT GTCGTGTCAA	5220
45	ATTTTCAGAA GCTAATATAT TATCATTATC TATATGTGTA AATTGATGAT CTATATCCGA	5280
	TGTAGGCTTA CCAATCACAA TAAATGGCAT GCTTTCATCA ATTAACATTT GTTTAATCGG	5340
	ATCATTTTCT TTTGAATAGA GCAGTATAAA CGCATCAACC ATTCGTTGTT TAATCATTTT	5400
50	ATAAACTTCA TCCATTAAAT CATTATATT ATTTGAGACT GTCGTTTGTG TACCATAGCC	5460
	ATGCTGGTTA CACGTTTCAG AAATTCCTAG CAATACATTG ATGTAGAATG GATTCAGTCG	5520

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	AGTTCTAGCA GCGGTATTAG GAAAATAATT CAATTCTTCC ATAACCTTCT TCACTTTTGA	5640
	AATTGTCGCT TCGCTAATAC GTTGATTTCC TTTTATAACT CTTGAAACTG TCGAAGGAGA	5700
5	AACACCGGCT TTTAGTGCAA CATCTTTAAT CGTAACCATT TAATCACCTC CTGTTAATTT	5760
	CTGCATCGGA AAACGCTTCC AACCACTGTA TAATACCAGT TTAGTCACAC TTTCTAAAAA	5820
	AGTCAAAAGA TTTGTGCAAA CGATTGCATA AAACGATAAA AATAAACCT TCATACTGAA	5880
10	ATTCAATCCG AAAATCAATA TAAAGGTTTG TATAAATATT AAAATCGATT GTTTAGTCAC	5940
	TAACTGCAAA ATAGTTACCT TGGCCATCTT GAAAATTAAA TACACGTTGA CCATTCATTT	6000
15	CTACTATATC ATGCCCAGTT AAACCTAAAT CATTTAATTT TGAGTATAAT GCATCAAAGT	6060
	TTTTCTCTTT AAACATTAAA GATGGTGTTT CTAGGTTTAC TTCCGGGCTA TGCTTTTCAA	6120
	TAAATTCTTT TGCCATAATC GTCAATGACG TTTCAGCATC TTTGGTAGGT GATACTTCAA	6180
20	CTGCAACATA GTCCTCAGCT AACGGTGTTT CACTTACAAC AACAAATTCT AAAGTTTCTG	6240
	TCCAAAATGC TTTGCTTTT TCGACATCAT CAACATATAA CATAACTTGA TTAACTTTT	6300
	CCATAAAATA GTACCTCTAT TTCTCTATAG TACATGCTAT CATAACACAG TAAATATTTT	6360
25	ATTACTTCAC AAAATGCTTA AAAATATGGC GGGATGCTTT TAAGGTCAAG GATAATACTT	6420
	GTGTAATTTT TTATAGGTTG TAGCTACTCT ATCACACTCT CTTTTATATT TATCAAAAGA	6480
	TATAAAAAAG GATAGTATCT TTCAACTATC CTTTAATCAA TATTATTCTT CAATCCATTG	6540
30	TGTATGGAAT ACGCCCTCTT TATCTTTTCT TTCGTACGTA TGAGCACCGA AGTAGTCACG	6600
	TTGTGCTTGA ATTAAGTTTG CAGGTAAATC AGCAGCACGG TAACTATCAT AGTAATTAAT	6660
35	ACTTGATGAG AAACCAGGTG TTGGTACACC ATTTTGAACA CCAGTTGCGA CAACATCACG	6720
	TAACGCATCT TGATATTCAG TAACGATGTT TTTAAAGTAA GGATCTAGCA ATAAGTTTTG	6780
	TAATCCTGGA TTATTATCGT AAGCATCTTT GATCTTTTGT AAGAATTGTG CACGGATAAT	6840
40	GCAACCTTCT CTCCAAATCA TAGCTAAATC ACCAAGTTTT AAATTCCATT CATTATCTTC	6900
	ACTTGCTTTA CGCATTTGcG CGAAACCTTG TGCATAAGAA CAAATTTTAC TCATATATAA	6960
	TGCTTTACGA ATTTTTTCTA AAAAGTCTTT CTTGTACCA TCAAATGATG CTTTGGACC	7020
45	ATTTAATTCT TTAGAAGCAT TTACGCGCTC TTCTTTGaTT GAAGAGATAA AACGTGCAAA	7080
	TACAGATTCA GTAATGATTG TTAATGGAAT ACCTAATTCT AATGCGTTAA TTGAAGTCCA	7140
	TTTCCTGTA CCTTTTTGcC CTGCAGTATC AAGAATTTTT TCAACTAATG CTTCTTTATT	7200
50	TTCATCTAAT TTCATGAAAA TATCACCAGT GATTTCAATT AAATAACTTT CTAATTCACC	7260
	AGCATTCAG TCTTTGAACG TTTGAGCAAT GTCTTCATGA GACATGCCTA ATAATCTTT	7320

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	CATTTTCACA TAGTGTCCAG CACCATTAGG TCCAATATAA GTAACACATG AAGCACCGTC	7440
	TTTTGCCTTT GCAGCAATTG CATCAAGAAT ATCTGCAACT TTGTATAAG CTTCTTCTTG	7500
5	TCCACCCGGC ATTAATGACG GACCAGTTAA CGCTCCAATT TCACCACCAG AAACGCCCAT	7560
	ACCAATAAAG TTGATTGCAC TTTGTGyWAA TGCTTTATTA CGTCTGATAG TATCTTGATA	7620
	GTTTGTATTA CCACCATCAA TTAAAATATC TCCATCATCT AATAAAGGTA ACAAACATATC	7680
10	AATCGTTGCG TCCGTAGCTT TACCTGCTTG AACCATTAAAT AAAATTTTAC GTGGTTTTTC	7740
	TAAAGAATTA ACAAATTCTT CCAATGAATA CGTTGGATGA ATATTTTCC CTTTTGATTG	7800
	TTCAACCATT AAATCAGTTT TTTCATTGA GCGGTTAAAT ACAGATACAC TATATCCGCG	7860
15	TGATTCAATA TTCCAAGCTA GGTTTTTACC CATAACGGCT AAACCAATAA CTCCAATTTG	7920
	TTGTGTCATA TTACTTACCT CACTTGTGTA TTTTTCATTA GTATTGTATC ACAAATAGA	7980
20	CATACACTAC ACTAAATCAT TTCGAATGTC GCGCAACTAT TTTGATTATT TCTAACACTT	8040
	GACTTGCAAG CAAGTTCAAT GATTTAATCG GCATTCTCTC ATTTGTGTGA TGGATTTTTT	8100
	CATAACCCAC TCCTAAAATG ACTGAAGGAA TACCAAATGT ATTAATAATA CTGCCGCTCG	8160
25	AACCGCCACC AGAAATAATT GTATTTGCAG ATAATCCTAA ATTACGAGCA CTTTCTTGTC	8220
	CAATTTTAAC AACCGCTTCA TTATCATTA TTTTAAATCC TGGATAACTT TGCTCCACTG	8280
	TAACACTGTC TTTCCACCT AATTCTGATG CAGTAGTTTC AAACACATCA GTCATATGTT	8340
30	TGACTTGTGT TTTTATTCTT TCTGGATCGT GAGAACGTGC CTCTGCTTCT AAAATGACTT	8400
	CATCTGCAAC AATATTCGTA GCTGAACCGC CATGAAACTT ACCAATATTG GCAGTAGTTA	8460
	TTTCATCAAC TTGTCCTAAT TTCATTGAC TAATTGCTTT CGCGCAATA TTAATAGCAC	8520
35	TAACACCCTC TTTTGGCGTA CTTGCATGAG CCGTTTGGCC AAAAAATTTA GCTGAAATTA	8580
	ACATTTGCGT CGGTGCACCT ACAACCGTAG TACCGACATC AGCACTTGCA TCAATAGCAT	8640
40	AACCAAAGTC CGCGTCCAAC AACTCTGAAT TTAATTCCTT AGCACCAATT AAACCTGATT	8700
	CTTCTCCAAC AGTAATCACA AATTGAATTT GTCCATGTGG GATTTGTTGT TCCTTTATCA	8760
	CTTGCAAAAC TTCAAGCATC GCTGATAATC CTGCTTTATC ATCTGCACCT AGAATAGTCG	8820
45	TACCATCAGA GTATATGTAG CCGTCATCTT TTACAATTGG CTTTACATTA ATTGCGGGTA	8880
	CAACAGTATC CATATGGCTC GTCAAATATA ATTTAGGTAC TTCGCCTTCT TCGATAGTAC	8940
	TATTCATTGT ACACACTAGA TTATTGGCAC CTAATTTAGG ATGTTTAGCC GCTTCATCTT	9000
50	CTTTAACATC TAACCCTAAT GCTATGAATT TTTCTTTTAA AATAGGTTGG ATTGTTGATT	9060
	CATTCCCTGT CTCAGAATCG ATTTGTACAA GTTCAAAAAA CGTATTAAGT AATCTTTGCT	9120

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	GATGAAATAA AATGTTACAG TAATTGACGT TACACAGATT TATCAGGTTT GTAAATTGTG	9240
	TCATATTATT TTCAATTTAT TATATATAAT TATTGTAAC TAACTAAGC TTTGTCAAAA	9300
5	ATATATTGAT TGATTTTTC AAGATATCGT ATAATGAGGA AAATGACATA AGCAAACCTA	9360
	CTCATGTTTT TTATTATATT CCTTTATGAT GATTGCTAGT TATATCGTCT CAAGTTAAAA	9420
10	GTTTTATATC TTATGTCGTA ATTATTAATA CAAAGGTTAT TCATTTGGAG GCACACAAAA	9480
	TGCAAAATAA AGTTTTAAGA ATTATCATT TCGTTATGCT TGTATCAGTT GTATTAGCAT	9540
	TGTTATTAAC GAGTATCATT CCAATTTTAT AAATATATC TCAACTACCT ATACAAAATC	9600
15	ATACAATTAA AAATCCATCC ATTATAAAG CATGTATTAA TAAGTTATCG TATTGCAACG	9660
	ATTACTTTCA AACATGGGTC ATACGGATGG ATTATTTTTT AAGCTACTTC ACTATGCATT	9720
	TTCAATGAAC CAAATTGCGA TTTGATTTGT AAATATTCTT CTAATTCATT TAATATTGA	9780
20	ATAATACTTG CTCTCGAGTT AAGCGCTTTG TGTGTTGTTG GCAATGGCAG TTCATCCAAT	9840
	TTCAAACGCG TCTCATACAA ATTGTGTAAA CGCATTGCTG TATAGTCATT ACTATTCACA	9900
	TTTAGACCAA TTTCTTTCAG CAGTGACGCA ACATCATTTA AAAGCGGATC TTTATGACAG	9960
25	ATACTTTCGA TGAGCGGTTT CATTCTCATT AACAAATCCA CTTGCTCTTC TCGCATATCA	10020
	AAATAATGAT AGTATGAATT TTCGTTTCTA ACAAATGAT TTTTAACATC TCGGAACGCG	10080
	ATAGACTTCG CCTTTTAAAT ATTTAAAAGT AACACTTCAA ATTCAATCGC AATGGTATCT	10140
30	TCATATTTTT CACAAATATA ACTATATTTA CTAATAATAT CAGCAATTTG TTGCTCAATT	10200
	TTACATTTGT ATTCTGCTAG TTGTTTGTCT AAACCTGGCA TCATTAAATT CATGTAAAT	10260
	GCAATGCTTA GTCCAATTAA CAGTAATAAT GTTTCATTAA CAATTAAATG TGCATCAATT	10320
35	GATTTTGCAT TAAAAACATG AAGTAATATA ACGCAACTCG TAATGACACC TTCTGTACT	10380
	TTTAAATACGA CAGTTAATGG TATAAATAAC AATACGATAA TACCGAGTAC AATTGGACTC	10440
40	TGACCTAATA AACTAAATAT TGCTGAACCT AAAACAATA CTAAAAACA TGATACTAAT	10500
	CTTGAAATAA TCGCTGTAG CGAATGTACT TTTGTATGTT TAATACATAA TACGACTAAT	10560
	ATGGCGCTTG AAGCATAATT ATCTAAACCT AACAGCTTAC TAATAATTAC ACCTAAAGTC	10620
45	ATACCCACTG CTGTTTTTAT TGTTCTAAAT CCAATCTTGT AAGGATTTAA CTTTAACATG	10680
	GGTTAGCGCC TCTTATCTTT CTTCAATAA TTTATTGAAT AATGTTTGTA ATTGATTAAT	10740
	TACGTTTATC ACATCATGAC CTTGATTTG ATGTCTTTCA ATCATTTCTG TAATCTTTCC	10800
50	ATCTTTTACT AATGCAAATG ACGGACTTGA AGGCGCATAA CCTTCGAAGT ATTCACGCGC	10860
	TCTTGTGTC GCTTCTTTAT CTTGTCCAGC AAATACTGTC ACTAGACGAT CAGGTAATAC	10920

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AGAATTGATC ATAAC TAGTG TTGTACCATC TTGTTTAAGA ACTTTGTCAA CATCTTCTGC 11040
 AGTAGTTAAT TGCTCATATC CCGCAGATTC AATTTCATTC CTTGCTTGTT CTACAACACC 11100
 5 GTTCATGTAT AAATCGAAAT TCATGnCCAT AAGTTCAATC ACCTATCCCT TTATATTTAA 11160
 ACTAtCCTCA TTCTACTAAT TAATAACATA TTGTTCAATA AACTAATCTG AATCACACCT 11220
 10 ATATTTAGAC ACAATTTTAA CAATATACCA AACATTATTG TGCTTAAAAT CATGGTAACT 11280
 AATTTGTTCA CATGTTTTCA TTAATATGTT TCAAGTATGA TGTCTTATTT TGACTTTACT 11340
 GCAAAAATGC ATTCAACCAT GTTGATTATT GTTCTTTATC TTTTGTGAAT ATATTGCACA 11400
 15 TATTTTAGTG CCAAAAAATA ATACATCCAT CGACAAGAAC AAGATAAAAC AAGTTGTCGA 11460
 TAGATGCATC TATGTTATCA CTAATATATA TTTGTATTTT CTAAAGTATA CTGTTGATA 11520
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 20 ATTGAAATAC ATAAATTAAC CATGTTACGA ATTGCAATCA TATCATTAAAT TACTACTGGC 11640
 TTTTAAACGA TTGATTCTAC TTGTAAATC GCTGCTTGTC GATGATTTAT AATACCCATT 11700
 GATGATACTG AACCAAATGT ACCAGTATTA TTTACCGTAA ATGTACCGCC CTGCATATCT 11760
 25 TCAGCTGTCA ATTGCTTATT ACGCGCTTTC GTTGCTAAAG TATTAATTTT TCTAGCTATA 11820
 CCTTTGATTG ACTTTTCGTC TGCATGCTTA ATCACAGGTA CGTATAATTT ATTTTCATCA 11880
 GCAACAGCAA TTGAAATATT AATGTCTTTA TGTAAGACAA TTTCATTTCC TTGCCAGCTA 11940
 30 CTATTTAATA AAGGATATGC TTTTAAAGCA TCTGCTACAG CTTTACAAA GAAAGCAAAG 12000
 AACGTTAGAT TATATCCTTC TTTATTTTTA AAGCTGTTTT TATAATGATT TCTCGTATTC 12060
 35 ACAAGATTG TAGCATCTAC TTCAATCATC ATCCATGCAT GTGGAATCTC TGTTACACTA 12120
 TTAACCATAT TTTGCGCAAT TGCTTTACGC ACACCATTTA CTGGTATTGT GCTGTTTTCA 12180
 CTATGTCTT CAGATGATTG GTTACTTGAT GTATCTACTG ATGTTGATTT TGTTTGAACT 12240
 40 TGTTTGTGAG ATTGAGCTGT GGTACCACCA TTTTCAATAA CTGACATTAT ATCCTTCTTA 12300
 GTTACACGAC CTTCAAATCC ACTACCTACA ACTTGTGATA AATCAATGTC ATGCTCTGAA 12360
 GCGAGTTTAA ATACAACAGG TGAAAAGCGA CCATTATTAC GTGGTTGATT TTGTTTAGCA 12420
 45 GTAGATGTCT GTTCCACTGT TGCACTAGCT TTTTAGTAG ATTTCTGAGT ATGCTCATCC 12480
 ACTTTTGCTT GTATCTCTTC AGTTGTTTCA TTTGTCTTTT CATCAGCAGT TTCAATTTTA 12540
 CAGATAATTG TATCAATAGC TACTGTCTGC CCCGCTTCAA CTAAAATTTT TGTAATTGTT 12600
 50 CCTGATATCG TGGAAGGGAC TTCAGCTGTC ACTTTATCTG TAATAACTTC ACATAATGGT 12660
 TCATATTCAT CAATATGATC ACCAACAGAA ACTAACCATT GTTCAATGGT GCCTTCATGA 12720

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	AATTCACGCA	TTTTATTTAA	GATTTTTTCT	GGATTCATCA	TAATTTTCATT	TTCTAATACA	12840
	GGAGAAAATG	GCATAGATGG	TACATCTGGA	GCAGCTAAAC	GCATGATTGG	TGCATCTAAA	12900
5	TCGAACAAGC	AATGCTCTGC	AATAATCGCT	GACACTTCTG	ACATAATACT	ACCTTCTAAA	12960
	TTATCTTCAG	TTACAAGTAA	AACTTTACCT	GTATGTTTAG	CACGATCAAT	AATTGTTTCT	13020
	TTATCTAATG	GATAAACAGT	TCGTAAATCA	ACGACTTCAA	CATTGATACC	GTCTGCAGCT	13080
10	AAAATATCCG	CTGCTTGTA	ACAATAATTG	ACCATTAATC	CATAACAAAA	TACTGTTAAA	13140
	TCTTCACCTT	CACGTTTCAC	ATCTGCTTTT	CCTAAAGGTA	CAGTGTAAATA	TTCTTCTGGC	13200
15	ACTTCTTCCT	TTAAGAAACG	ATAAGCTTTT	TTATGCTCAA	AGTACAATAC	TGGATCATT	13260
	GATTCGATAG	ATGATAATAA	AAGCCCTTTA	GCATCATACG	GTGTGGAAGG	AATAACAATT	13320
	GTTAAACCTG	GCGATGAAGC	AAATATACTT	TCAATACTTT	GTGAATGATA	TAGTCCTCCG	13380
20	TGAACACCGC	CACCAAATGG	TGCACGAATC	GTTAATGGGC	ATTGCCAATC	ATTATTTGAA	13440
	CGATAACGCA	TTTCGCAGC	TTCCTAATA	ATTTGATTG	TCGCAGGTAA	AATAAAATCT	13500
	GCAAATTGAA	TTCTGCAAT	TGGTCTTTTA	CCTACCATAG	CTGCACCAAT	GGCAGTTCCA	13560
25	ACAATATTTG	ACTCAGCTAA	TGGCGTATCG	ATAACTCTGT	CTTCACCATA	TTTTTGTGTC	13620
	AGTCCTTGAG	TAGTACCAA	TACGCCACCT	TTTCTACCAA	CATCTTCACC	AAGAATAAAC	13680
	ACATCTTTAT	TTGTTGTAA	TGCTAAGTCT	TGTGCCTGCG	TATCGCCTCT	AAATAAGATA	13740
30	ATTTAGCCAT	TAGTTAAGAC	TCCCTTCTTC	GTACACAAAT	GCATAGGCTT	CTTCGACACT	13800
	TGGATATGGC	GCGTCTTCAG	CAGCCTTTGT	CGCTTTATTG	ATGATGTCTT	TnATgTCCGC	13860
	TTCTATTTCT	GCCAACCAAG	CATCATCGAT	AATGCCAGCT	GAAAGCAACT	CTTTTTTGAA	13920
35	CTTTTCATTG	CAGTCTGCTT	TTTTAAGCGT	TTCACGCTCT	TCTTTCGTAC	GATATTGGTC	13980
	GTCAATCATCT	GATGAATGAG	CTGTCATACG	ACTTGTTACT	GCTTCAATCA	AAGTTGAACC	14040
40	TTGACCAGAA	ATAGCTCGAT	CTCTTGCTTC	TTTCATCGCT	TTATACATTG	CTAATGGATC	14100
	ATTACCATCT	ACTTGTTTAC	CATGTATACC	GTAACCAAGT	GCTCTATCCG	ATAATTTTTTC	14160
	AGCTGCGTAT	TGTAATGAAT	CAGGTACTGA	AATTGCATAT	TTATTATTTA	TAATGACACA	14220
45	TACAAAAGGA	AGTTTGTGTA	CACCCGCGAA	GTTTAAACCT	TCATGGAAGT	CACCTTGTTT	14280
	TGAGCTACCT	TCACCAACAG	TTGCTGTTGC	AATTTTCTTC	TTACCATCCA	TTTTTAAAGC	14340
	TAAAGCAGCA	CCAACAGCAT	GGGTATTTG	AGTTGCTACC	GGTGAACCTT	GAGACAAAAT	14400
50	ATTCTTAGCT	CTACTACTAA	AGTGTGATGG	CATTTGTTTT	CCACCAGAGT	TAACATCGTC	14460
	TTTCTTTCCA	AACGCTGATA	AAAACGTATC	ATACGCTGAG	ATACCCATAT	AAGTAACGAA	14520

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	AATCTGAGTT	GCTTCTTGTC	CTTGACCACT	TACAACAAAT	GGAATTTTAC	CTGCACGGTT	14640
	CAATAACCAC	AGTCTTTCAT	CTATTTTTCT	ACCTAAATCC	ATCCATTTAT	ATATTACTTT	14700
5	TAGGTCTTCT	TCGCTAAGGC	CTAATGATTT	ATAATCAATC	ATGTTAAATC	CTCCTATTTA	14760
	TACGTGAATA	GCTCTACTTT	CTGCTTTCAA	TCCTAATTCC	ATCAACACTT	CAGAGATGGA	14820
10	AGGATGTGCG	TGTGTGTGTA	GTCCTAATTC	TAATGCCGAG	CCATTTCATGA	ACTGTAACAG	14880
	TGATGCCTCA	TTAATCAATT	CTGTTACATG	TGGACCAATC	ATATTAATAC	CCACAATTTT	14940
	TTCACTTGAT	TGATCAATCA	CCATTTTCGCT	ATACCCTTCG	TTTGTGTCAT	GGCTATCAAT	15000
15	CACCTGCTTTA	CCAATTGCTT	TAAATGGTAC	TTTAAAACTT	TTAACTTTCA	TTCCCTCTGC	15060
	CTTTGCTTGT	TCAATGTTTTA	AACCGATAGA	AGCAATTTCA	GGTTGTGAAT	AAATACACTT	15120
	AGGCATCATG	TTATAGTTTTA	CTGGGATTGG	GTTCCCCTCA	AACATATGAT	CAACAGCCAC	15180
20	AACACCTTCT	TTTGATCCAA	CATGTGCCAA	TTGTAATTTT	CCTATACAAT	CACCAGCTGC	15240
	ATAAATATGT	TTATCTTCAG	TTTGTGAAA	TTCGTTTCGT	AAAATATGTC	CTGATGTTGa	15300
	AAGTTTATT	TTAGTGTGT	TTAAACCAAT	ATCTGATGTG	TTAGGTTTTT	TACCAATCGA	15360
25	TAGCAACACT	TTATCTACTT	TAATTATGTC	TGAGGAAATT	TCAAACGTAA	CACCATCTTC	15420
	GTTAACATTT	ATATCATTTT	CAGAAAGTTT	TATTCCTTCA	TAGAATTTAA	CACCACGTGC	15480
30	TGACAATGAT	TTTTTTAATA	GTTGTGAAGC	TTGTTTACTT	TCAGTTGGTA	AAATTCTTTC	15540
	ACCTGCTTCT	ATAACTGTTA	CGTCAACACC	TAAATCTATC	ATCAATGATG	CAAATTCCAT	15600
	TCCGATAACA	CCACCACCAA	TAATACCAAT	ACTTGATGGT	AACGTCTTTA	ATGATAATAT	15660
35	ATCATCGCTA	GATAAAATTT	TATCATGATC	AAATGATAAG	AATGGCAACT	CTGCAGGCGA	15720
	AGAACCAGTT	GCAATTAATA	CAAATTGGTT	GGGTAATAAG	TCTGATTCAC	CATCTTCATA	15780
	TTCGACAGAA	ATTGTGCCAC	TTTGAGGTGA	AAATATAGAT	GTACCTAGAA	TACGTCCCGT	15840
40	GCCATTATAA	ATGTCAATGT	GATTGTGTTG	CATTAAATGC	TTTACACCTT	GATACATTTG	15900
	ATTAATAATG	TCTTCTTTTC	GTGCCAACAT	ATTTTCAAAA	TTAACATTAG	CATCTTTGAC	15960
	ATCAACGCCA	AACATTGCTG	CCTGTTTTAC	TGTTTGAAAT	ACTTCAGCAG	ATTTAAGCAG	16020
45	CGATTTAGTA	GGAATACAAC	CTTTATGGAG	ACAAGTACCT	CCTAATAGTT	GTCGTTCTAC	16080
	TATTGCCACT	TTTTTACCTA	ATTGAGACGC	ACGTATCGCA	GCAACATATC	CTGCAGTACC	16140
	TCCACCGAGA	ACGACTAAAT	CATATTGTTT	CTCTGACATG	TTCTTACTCC	TAATAATGA	16200
50	TATATATCCA	TTGAAAATTT	ATTAATACAT	AGTTTTCATG	TCCATTAAAT	ACCTATTTTA	16260
	CATGATTGTC	TATTTAGTTT	GAATGCACAT	AAATAAATCC	ATAAATGAGT	ATTCAACACA	16320

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TAAATCAGTA ACACTTGCAC CTGAAATCAT TCGTGCAATT TCATCTACTT TATCATCGCT 16440
 AATTAACTCT TGAACCTGTG TTGTTGTACG ATCATCTTTT GATGATTTCG AAATTAATAA 16500
 5 ATGATGGTCG CTCATCGATG CAACTTGTGG TAAGTGAGAG ATACAAATAA CTTGTATATA 16560
 TTCTGCTaTA TCTCGCATTT TCTCTGCCAT TT 16592

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13794 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

20 CCAATACAAC GTAAAAAGAT TGCTTGTGTT ATTAATGAGT TAGATAAAAT AATTAAAGGA 60
 TTTAATAAGG AAAGAGACTA CATAAAATAT CAATGGGCTC CAAAATATAG CAAAGAnTTT 120
 TTTATACTTT TTATGAACAT TATGTACTCA AAAGATTTTT TAAATATCG ATTTAATTTA 180
 25 ACATTTCTTG ATTTATCTAT CTTATATGTA ATATCATCTC GAAAAAATGA GATACTAAAT 240
 TTAAAAGATT TGTTTGAAAG TATTAGATTT ATGTATCCTC AAATTGTTAG GTCAGTTAAT 300
 AGATTAAATA ATAAAGGTAT GCTAATCAAA GAACGATCCC TTGCAGATGA AAGGATTGTG 360
 30 TTAATCAAAA TAAATAAAAT ACAATATAAC ACTATTAAAA GCATATTCAC AGATACTTCC 420
 AAGATTCTCA AACCAAGAAA ATTTTTCTTT TAAATTTAAA CAGATTTACC TCTTGATAAA 480
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 35 CTTTGTGTTT TATATTATTT CAATACCCTA CTATATATCA CAACACATAA ATTAAGCATG 600
 ACACTCATT C AATTTAGTTC ACCATTTTCGT GTTCCAATTT TACTGAGTAT CATGCTTTTA 660
 40 ATGTTATAAA CCTAATGCTT TAATAAATCG TGTTAATTCT TCTCGCATAC TGTCATCTTT 720
 CAATGCATAT TCTATGGTAG TTTTAAACGAA GCCTAATTTT TCTCCAACGT CATAACGTTT 780
 GCCTTCGAAG TCATATGCAT ACACTTGGTT ATCATTATTC ATACGTTCAA TCGCATCTGT 840
 45 TAACTGAATT TCGTTACCTG CGCCTTCTTT TTGCGTTTTT AAATAATCGA AAATTT CAGG 900
 CGTTAATACA TAACGTCCCA TAATAGCTAG GTTTGATGGT GCCGTACCTT GTGCTGGCTT 960
 TTCAACAAAC TTTTTCACCT CATACTGACG TCCGTTTTTA GTTAATGGGT CAATAATTCC 1020
 50 ATAACGATGA GTATCTGCTT CCGGAACCTC TTGGACACCT ATAACGAGT GCCCTGTTTC 1080
 TTCATAAAGC TCAATCAACT GTTTCACCTG TGGCACTTCA GATTCAACAA TATCGTCACC 1140

	TAAACCTTTT TGTTCTTTCT GCCTTACATA AAAAATATTC GCAAGTTCCG TTGAATACTG	1260
	AACTTTCTCT AGTAATTCAG ATTTACCTTT TTCTTTTAAC ACCATTTCTA ATTCTTTTGG	1320
5	ACTATCAAAA TGATCTTCAA TCGCGCGTTT GTGGCGACCT GTCACATATAA TAATATCTTC	1380
	AATTCCAGCT CTTGCAGCTT CTTCAACGAT ATATTGTATT GTGGGTTTAT CTAAGATAGG	1440
	AAGCATTTC TTTGGCATCG CTTTAGTTGC TGGTAAAAAT CTAGTCCCTA AACCAGCAGC	1500
10	GGGAATGATT GCCTTTTTTA TTTTTTTCAA AGTTAATGTG CTCCTTTTCC TAAGTATTAA	1560
	ATCTATGTAT CAACGTCATT TTAACACTAA TTAGAACGCC TTCATAGTGT CATTGAGTAT	1620
	GTAATTATTT CTTGGGAAAT TTGTTTTAAT TTTAAAAAAC AGGCTTACTT CATATAATTT	1680
15	ATGAAATAAA CCTGTCAATT TTGGATTGAT TATGCTTTGT GATTCTTTTT ATTTCTGCGT	1740
	AATAACGCTA AACCTAAAAT GCTAAATAAT CCGCCGAACA ACATGCCGTT GTTTGTTGAT	1800
20	TCTTCTCCAC CTGTTTCAGG TAGTTCAGAT TTCTTAGATT GTGCTTTTTT AGTTGGTACC	1860
	ACTGCTTTAA CCTTTTCATT GATTTCAATA ACAGGTGTTA CTACTTTACC TTGTTCCACT	1920
	GGTTTAGAAG GTTTTTTAGG TTCTTCTTTA GCAGGTGGTA TTGGTTTACC AGGTTCACTT	1980
25	GGTACCTCTG GCGTTGGCGG TGTTGGTGT TCCGGCTCGC TTGGTACTTC TGGTGTCGGT	2040
	GGTGTGGTG TTTCCGGCTC GCTTGGTACT TCTGGTGTG GTGGCGTTGG TGGCACGATT	2100
	GGAGGTGTTG TATCTTCTTC AATCGTTTGT TGACCTTCAT TATGACCACT TACTGTGGA	2160
30	AGTGTATCTT CTTCAAAGTC AACACTATTG TGTCCACCGA ATTGATAATT TGGTTTATCT	2220
	TTATTTGTAT CTTCTTCAAT AATTTCACTG TGCTTATTGA ATCCGTGAAT ATGTGGCACA	2280
	CTGTGGAAGT CGATATCAAT GATATTACCA CTTGTTCAT ACTTAGGTTT GTCTTTCTCT	2340
35	GTATCTTCTT CGAATGATTG GTTACCATT TTTGACCAT GAATTTGAGG TACACTATCG	2400
	AAATCGATAT CTACGATATT GCCACCTTGT TCATATTTTG GTTTATCTTC TTCTGTGTCT	2460
40	TCCTCAAATG ACTGATTACC GCTATTTTGG CCACCTTCGT AACCTAATTC ACTCTTAATA	2520
	TCCACGTGGC TATTTTCTTC GATTTCTTCA ATCAGCCAT AATTACCGTG ACCATTTTCA	2580
	GTTCTTAAAC CAGAAAGAGA AATATGATGA TTGTTTTTCT TAATTTCTTC GATTGGTCCT	2640
45	TGCGCTTGAC CATGTTCTTC AGGTAGTTCA TCTACTAGTT CAATCAGATT ACTTTCAGTC	2700
	GTATATTCTT TCGTATCTTC AATTGTTGTA TGATCGCTAA CAGCACCAGT TACAATACCT	2760
	TTTGTAGAAT CTTCTGCAAA TTCAACTAGG TTAGACTCAG TAGTAACCTG ACCACCACCT	2820
50	GGGTTTGTAT CTTCTTCATA TTCAACAACA TCAGCATGAT GTTTTGAATT TTCATGTGTC	2880
	GATTCTTCAA AGTCTACATG AATAGAATCT TCTTCAGTTT CAATGGTACC TTCTGCATGA	2940

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TCTTCGATTG TACCAGTCAA TTCATGCTTC TCCACTGGCG GCTCTGATTT AAATTCAAGT 3060
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 5 GCGTTATTAG AGTAAAATGC AACGCCATTT TTCCaAGTTA AATTACTTGT ATAATAATAG 3180
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 10 CCTTCATATT TTATTACATA ATTTTACTTT TGGTCTAAAT TATTAAAGTT TAAAGAATAA 3300
 CCACCATTAG TATCAAAATC TAAACTCATA TTATCAGTCA CATCTTCAAA TTTGCTGACA 3360
 TCATCAAGCT TTGCATAnTh AgctTTCAGC TAAATCGTCT GAACCAATGT GTTTATATAC 3420
 15 CTTAACTGTT GGATTATTAA CCCCTGGTTT ATTTCTTTA GTTACTTGAC CAGTTACTGT 3480
 CACAGAGCTT AACGACTGGT TGTTAGGTTT CATGTACGCA AAATGACTAA ATTTCCCATC 3540
 TACTTTATTT AAAGTATCAA TTCGACCATT AGCTGTACT CCCCAATTAT CTCTAACTCC 3600
 20 ACCTAAATAT TGAATATTAA ATATTTTGCT AACCGTAGTC TCACCCAATT TAACCTCAAC 3660
 ATTTTGTTA CCTTTTGCG TCACTGTTGT AGGATCAATA AATAGATTTA AAGATAATTC 3720
 AGCAGTTAAA TCTTTCTTTT CTGTACATA TTCTTTAAAC GTATATCTAA CTTTTCTTTC 3780
 25 TCCAATTATT TCTCCTGTCT CCATAACTTG ACCATCTGTA CTTTTTATCT CCGGAACTTT 3840
 ACGCAGTGTT GAGATACCAT GAGTTTCAAC ATTATCGCTT AATGTGAAAT CAAAATAATC 3900
 TCCCGCCTTA ATTCCTTCTC CAAATTTCCA TTTATATTTT AAGGTTACTC TTTCTGCGTT 3960
 30 ATGAGGATTT ACAACATTCG TATCTTGTTT ATGTCCTACA ATTTCACTAC CTTCTTCTAC 4020
 TTCCACTTTA TTTGTTACAT CTGTACCTGT CGCTTTAGTT TCTTCCACTA CTTCTTTCTC 4080
 35 TGCAACTGCT GTAACGTCA TGAatCTTTT ATTCTTGGTT TAATTTCTGA GACGTTACTT 4140
 GGTGAGCTA TGTCAACTTG AGTTCCTGTA GTTTCCTTAT CAGCAACTTT TTCCGATGGC 4200
 AAATCAACTC GCGAAgTTTC TACTTTTGGT GCTTGCAcAG TTTTCGGTGC TTCTTCTGTT 4260
 40 GTTACTTGTT TTGATTGTGA TGGTTGCTCA GTTGATGTCG CGCTGTATGA TTGTGTTTCA 4320
 TCTATTGTAT TAACGTTATT TGTAAGTTGT TGTGTTTCGC TTGCTTTACT TTCAGTAGCT 4380
 GAACTCCAC TTTCCTCTAC TGTAAGTATTG TTTTGTTCG ATGCTGCAGC TTCTTTTCT 4440
 45 TGTCCCATTC CAACAACGAT CATTGTTTCT AAGAATACTG AGGCCGCTCC CAATTGTGT 4500
 TTTCTTATGC CGTATCTAAG ATTGCTTTTC ACTATAATAT TCTCCCTTAA ATGCAAAATT 4560
 CATTTATTTT TAAAACTCAA TAAATGCAAT TCTATATTGT TCGGTTTTTA AAAGCAATGA 4620
 50 AAAAAAGCGA GTTAATAAAA AGTTAAGATT GTTGTTAACT TTATGTATAA TGAGTTTTTT 4680
 ATTATTTGAA ACTCACATAT ATATTGCATA CAAAGCTCTT GAACACCTTG ATATAACAGG 4740

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	TACTAAACCA	TACATAATAA	TCGCCTGTAC	AATGCATCAT	TAACAAGTCA	CTGAAACGCC	4860
	TTTCATTGTA	TTAATAACGT	CACTATAATT	TTTATATCGT	TCGGTTTTTG	TTTGATTTTA	4920
5	ATGATTATTT	ATACAAAAAC	AGCCGTATTT	CAAGCCGACA	TTTTAAATTT	AACTAAATTT	4980
	GCATCTAGTT	AATAATTGCA	TTTATCAAAT	TTGTCTTATT	GATCCAATCT	AATTTGTACT	5040
10	CACAACTAG	TTTAAAATTC	TAACCTTTATC	TCTCAGTTTCG	TTATCAATCA	TCAGACATAA	5100
	ACCAATGAAG	CAATCAGAAA	ACACTCTAAT	TTTCTATTAG	AAATTGATT	TAATATAAAA	5160
	AAACAGGCTT	ACTTCATATA	ATTTATGAAA	TAAACCCGTC	AATTTTGTGTT	TAATTATGCT	5220
15	TTGTGATTCT	TTTTATTTCT	GCGTAATAAT	GCTAAACCTA	GAATGCTGAA	TAATCCGCCG	5280
	AACAACATAC	CTTTGTTTGT	TGATTCTTCT	CCACCTGTTT	CAGGTAGTTC	AGATTTCTTA	5340
	GATTGTGGTT	TTTTAGTTGG	TGCCACTGCT	TTAACCTTTT	CATTGATTTT	AATAACAGGT	5400
20	GTTACTACTT	TACCTTGTTT	CACTGGTTTA	GAAGGCTTTT	TAGGTTCTTC	TTTGGCAGGT	5460
	GGTACTGGTT	TACCAGGTTT	AGCTGGTACC	TCTGGTGTG	GCGGTGTTGG	AGTTTCTGGC	5520
	TCACTCGGCA	CTTCTGGTGT	CGGTGGTGT	GGTGTTCGG	GCTCACTTGG	TACTTCTGGT	5580
25	GTTGGTGGCG	TTGGTGTTC	CGGCTCACTT	GGTACTTCTG	GTGTCGGTGG	CGTTGGTGGC	5640
	ACGATTGGAG	GTGTTGTATC	TTCTTCAATC	GTTTGTGAC	CTTCATTTTG	GCCGCTTACT	5700
	TTTGGAAGTG	TATCTTCTTC	AAAGTCAACA	CTATTGTGTC	CACCGAATTG	ATAACTTGGT	5760
30	TTATCTTTAT	TTGTATCTTC	TTCAATAATT	TCAGTGTGCT	TATTGAATCC	GTGAATATGT	5820
	GGCACACTGT	CGAAGTCGAT	ATCAATGATG	TTACCGCCAT	GTTCACTT	AGGTTTGTCT	5880
35	TTTTCTGTAT	CTTCCTCGAA	TGACTGATTA	CCTTTATTTT	GACCATGAAT	TTGAGGTACA	5940
	CTATCAAAAT	CGATATCTAC	GATATTGCCA	CCTTGTTTAT	ATTTAGGTTT	GTCTTCTTCT	6000
	GTGTCTTCCT	CGAATGACTG	GTTACCGCTA	TTTTGGCCAC	CTTCATAACC	TAATTCATCT	6060
40	TTAATATCAA	CGTGGCTATT	TTCTTCGATT	TCTTCAATCA	CGTCATAATT	CCCGTGACCA	6120
	TTTTCAGTTC	CTAAACCAGA	ATGAGAAATA	TGATGATTGT	TTTAGTAAT	TTCCTCGACT	6180
	GGTCCTTGTG	CTTGACCATG	CTCTTCAGGT	AATTCATCCA	CTAATTCAAT	CAGATTACTT	6240
45	TCAGTTGTAT	ATTCTTTTCG	ATCTTCAACT	GTTGTATGAT	CGCTCACCTGC	GCCAGTTACA	6300
	ATACCTTTTG	TAGACTCTTC	GTCAAATTCA	ACTAAGTTAG	ACTCAGTAGT	AACCTGACCA	6360
	CCACCTGGGT	TTGTATCTTC	TTCATATTCA	ACAACATCAG	CGTGATGTTT	TGAATTTTCA	6420
50	TGTGTAGATT	CTTCAAAGTC	AATTGGATTT	GATTCCTCAG	AGGACTCAGT	GTATCTCTCA	6480
	ACGTGACCTG	CTTCGCTATC	CACAGCAGTA	TGGTAATCGA	TATCAATAGC	TGATGAATCC	6540

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	TGGTAATCAA TGTCAAGAGT TGATGAATCA TATTCCTCTT CAACAGTAGT TACTAAATTC	6660
	TTATCATATT GACCTGTAAG AGTTTCTTTA ATTGTATCTT CTTTATATTC AAATTTATTA	6720
5	TTTTGAATAA TCGGACCATT TTTCTCATTT CCGTTCGCTT TATTACTGTA TAAAACTAAA	6780
	CCATTATCCC AAGTTAAGGT ATATCCTCTA TCATAATAAT ACTTATAAAG TTGCTCTGGA	6840
10	TGTCCTACCA TTTGTGTTCT AAAATCAACT TCATCAGTAC CATTTAAATA CTCTCCATCA	6900
	TAGTGAACAA CATAAGTTTT ATCTAGATTT TCTATATTCA ATGAATAGCT TCCATTATTT	6960
	TGTAAATTCA AATTCCCACT CATATTACTT GTGACTTCTT TAAATTTAGA AGTATCTGTC	7020
15	GTATTTGTCAT ATACACTCTT CGCTATGTCT TCATTATTAC CCAAGTATTC AAATATCCTA	7080
	ACTTTTGGTT GATTTCCATT CTGATTACTA CCTTTCATTA AAGTTCAGT AACAGTCACA	7140
	CTTGTCGTTT TACCATTATT AGGTTTAATA AATGCAACAT GCGAAAATCT ATTATTCGCT	7200
20	TTATTAAATG TCTCAATCGA TCCATTTAAA TTGGCATAAT AATCCCAAT ACCATCTTTA	7260
	TATTTAACAT CTAATTCCTT TGAAGTTTGT TCTTCATTTA GTGTTGAAGT TATAGTTTGA	7320
	TTTCCATTAG TTTGTACAGT TTTAGGATCA ATAAATAAAT TAATTTCTAG TTCAGCCGTT	7380
25	ACATCAACCT TATCTTCAAT ATCATTTGTA AATGTATATC TAATCTTCC ACCTTCTAAA	7440
	ACTTCACCTG TCGCCATTAC GACTGAACCA TTTTAAATTT CTGGTACTTT TCTAGCAGTT	7500
	GATACGCCAT GCGTATTTAC ATTATTTGAT AAAGTAAAGT CAAAGTAGTC ACCTTGATGT	7560
30	AAACCATTCT CAAATTTCAA CTTATATTTT AGTACCGCTC GTTGTCTGTC ATGAGGTTCT	7620
	ACTTTATTTG TATTGTTATG CCCCTCAATA GAACCAATTT CTA CTGTAAC TTTACTTGTT	7680
	ACATCTGTAC CCGTTTCCAC TTTCGCGTTA CTAGCTTCCT TAGCTTCCGC TACATCTGCT	7740
35	GATCTTGTCA CACGTGGCTT ACTTTCTGAT GCCGTTCTTG GCTGTGCCAC TTCAACTTGT	7800
	GTTTCTGCGA CTTGATTTTG TGTAGCCTTT TTAGGTGTTA AATCTACTTG TCTTTGATCT	7860
40	CCGCTATTGT CTGAGATTG TGTGTTTTCC TTAAGTTGAG GTTTCGCTTC TTCCTTAACT	7920
	ACCTCTTCTT TAACTGTTTC TATATTTGCT GGTGTGTCAG TTTGTGTC TGTACTGCT	7980
	TTTGGTGCTT CTTCAAGTTGT TACTTGTGTT GCGTTTGACG GTTGTCTGT TACTGTTGCG	8040
45	TTATATGATT GAGTTTCTTC TATATGATT ACGTTAGTTG CAGTTGTTTG TGTTTCACCT	8100
	GTTTTATTAT CAGTAGCTGA ATTCCCATTT TCTTCTACTG TAGTTGTCTT TTGTTCTGAT	8160
	GCTGCAGCTT CTTTGTCTTG TCCCATCCCA ACAACGATCA TTGTTCTTAA GAATACTGAT	8220
50	GCTGCTCCCA ATTTATGTTT TCTAATGCCG TACCTAAGAT TGTTTTTCAC TATAATATCT	8280
	CCCTTTAAAT GCAAAATTCA TTAATTTTTT AAACCTAATA AATGCAAGTC TATATTGTTT	8340

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	ATGTTAATTG	ATAATTTTAT	TATTTGAAAT	ATACCTATAA	ATTGTATTCA	AGTCATCAGA	8460
	AACCCTTGTC	ACACAAGGCT	TGTATTTTTT	ATACTTATTT	TTTAAATTAA	ATTCATCAIT	8520
5	ATCTAATTTA	AAACAATATA	CTAAACGTTT	CATAATTATC	GCCTGTACAA	TACGCACAAA	8580
	AACATGTCTT	GAAACGCCTT	TCATTACTCT	AAAATACCCA	ATATACTTTT	TATATCGTTC	8640
	GGATTCTGAG	TATTTTCAGAC	GATTTTCTGC	ATAAAAATAA	ACGTGTTTCA	AGGCAATATA	8700
10	TTGCAATTAC	CTAAAAACAC	GTTTACTTAA	TATTTAGTTA	AACAAATAAG	CTAATGAATA	8760
	AAATGAAGAT	GATACCTGAA	ACGGAAATAA	TCGTTTCTAA	TAATGACCAT	GTTAAGAATG	8820
	TTTCTTTTAC	AGTTAAACCA	AAATATTCTT	TAAACATCCA	AAATCCTGCG	TCATTTACAT	8880
15	GAGACAAAAT	CACACTACCT	GCACCTATCG	CAAGTACAAC	TAATGCAACA	TTTACATCTG	8940
	ATGATTGTAA	TAATGGTAAG	ACAATACCTG	TAGTTGAAAT	CGCAGCTACT	GTAGCCGAAC	9000
20	CTAATGCGAT	ACGTAGCACA	GCTGCAACAA	TCCATGCTAG	TAAAAATCGGA	GACATCTCTG	9060
	TACCTTCAAA	CATTTTAGCA	ATTGTATTTT	CGACACCGCC	GTCAATTAAT	ACTTGTTTTAA	9120
	ATGTACCGCC	ACCGCCAATA	ATCAATAACA	TCATTCCGAT	TGGATAAATC	GCATTCTGCA	9180
25	CTGATTCCAT	AATATGATTG	ATCTTACGCT	TTCTCATTAA	TCCCATCGTA	ACGATTGCAA	9240
	ATAATACTGC	TATTAGCATG	GCTGTCCCTG	CTGTTCCTAT	CATATAAATG	ATAGATTCAA	9300
	ATAGATTTGT	AGGTTTGTCA	TGCCCAGTTA	CAAGTTGCGT	TATCGTAGAC	ACTAACATTA	9360
30	ATATGACTGG	TAATGTTGCT	GTTAATAAAC	TCATACCAAA	TCCTGGCATC	TCTTGATCCG	9420
	TAAATTCTTT	TTGTGCACCT	AACGCTGAAA	TATCGCCTTC	TCGTGTATAC	GCAGACGGAA	9480
	TCATTTTTTG	TGCACTTTGT	TAAATATAGG	CCCTGCAATG	AGTGTAAGTG	GaATGGCAAT	9540
35	AATCATACCA	TACAGTAATA	CATCTCCAAC	ATTTGCCTTT	AATTCTTTTG	CGATGACTAC	9600
	CGGTCCTGGA	TGTGGTGGTA	AAAAGCCATG	TGTCACTGAT	AAAGCTGTTA	CCATAGGTAG	9660
40	TCCTAGTTTT	AACACTGAAA	CATTTGCGCG	TTTTGCTACT	GTAAATACTA	ATGGAATCAG	9720
	TAAGACTAAA	CCTACTTCAA	AGAACAATGC	AATACCGACG	ATAAATGCTG	CAACAAGCAT	9780
	TGCCCATTGT	ACATGTTTTT	GACCAAATTT	TTGAATCAAC	GTGTCTGCGA	TTCGAGTTGC	9840
45	ACCACCACCA	TCAGCAAGCA	ATTTCCCAAG	TATGGCACCT	AAACCGAATA	TCAGTGCAAT	9900
	GTGGCCGAGC	GTAAGTCCCA	TTCTTTTCTC	AATCGTCTCC	ATAATTTTAG	TCAATGGTAT	9960
	ACCTAGCATT	AACGCTGTAA	TCATCGATGT	GATAATTAAT	GAAATAAATG	TATTTAATTT	10020
50	AAACCCAATA	ATTAATACTA	ATAAAAATAA	GATACCTAAA	ACAACACTGA	TTAACGGCCA	10080
	TATTTGTTA	AACATGACAT	TCCCCTCTTT	CTCTTTTCAA	TAGAATGTAA	CACCGTCGTC	10140

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GAGTGACGTA TTTATTGTGT TTTATTTTCA GCGATATGTT GCGGTTGAAA ATCTGCAATT 10260
 TGTTTCATAAT TCTCTGTAA AGAACGACTT AAATTGATAA AAATGGATAC GATCTCTTGG 10320
 TAAACAGTGA CATTCTCTTC AATCGGCGTA TGATTGTTTG TGGCACCGAC CATCGATGAA 10380
 ACGATTGAAA AATCTTCAAT GTCACCTACA GCTTTAAGTC CGAGCACGCA GGCACCTAAG 10440
 CATGAACTTT CATAACTTTC AGGAACCACT AACTCTGTGT CAAATATATC TGACATCATT 10500
 TGACGCCATA CTTCACTTTT CGCAAAACCA CCTGTTGCTT TTATCATCTT AGGTGTTTCA 10560
 TTCATTACTT CAATAAGCGC AAGATAGACG GTATACAAAT TGTAAGAAGC ACCTTCTAAT 10620
 GCAGCGCGAA TCATATGTTC TTTTATGA GATAAAGTTA AACCGAAGAA TGAACCTCTT 10680
 GCATTGCGT TCCAAAGCGG CGCACGTTCT CCTGCTAAAT AGGGATGGAA TATTAAACCA 10740
 TCTGCACCTG GTTTAACACG CTTTGCAATT TGAGTTAAGA CATCATAAGG ATCAACACCG 10800
 AGACGTTTCG CAGTTTCGAC TTCACTCGCT AGCAACTCGT CGCGCAACCA TCTCAATACG 10860
 ACACCACCAT TATTTACAGG ACCTCCGATG ACGTAGTGGT CCTCTGTTAA GACATAACAA 10920
 AATATTCTAC CTTTGTATC AGTACGCGGT TTATCTATCA CAGTACGAAT CGCCCCAGAT 10980
 GTACCGATTG TGACAGCAAC TTCTCCTTTA CCAACACTAT TGACACCTAA ATTAGAAAGG 11040
 ACCCCATCAC TCGCACCAAT AACAAACGGT GTATCTTTAT TAAGCCCCAT TAATGTTGCA 11100
 TAACGTTCTT TCATACCTTT CACTCACATAC GTTGTGGAA CTAATTCGG CAACATTTC 11160
 TTGGAATAC CCAGCAGTTC TAATGCCTCA ACATCCCAAT CTAATGTTTC TAAATTAAC 11220
 ATCCCTGTTG CGGAAGCCAT TGAATAATCA ATGATATATG TATCAAATAA ATGATAGAAA 11280
 ATGTATGTTT TAATATCTGC AAACCTTAGCA GTACGTTGAA ATACATCTTG CCATTCTG 11340
 TTCATCCAAA AAATCTTCGC TAATGGCGAC ATAGGATGAA TCGGTGTGCC TGTTCGCTGG 11400
 TAAATCGCAT TGCCATCATG CACTTCATTT ATTACTGTTG CATATTTTGC AGCGCGTTA 11460
 TCTGCCAAG TAATATTATT TGTTAATCTT TGATGTTGCT GATCCATCGC AATCAAGCTA 11520
 TGCATTGCG CACTAAATGA CACAACTTA ATGTCGTCTT TATTAACCTT GGATTCTCTC 11580
 ATAACATATT TAATAGTCAT TAGTACTGCA TCAAATAATT CATCTGGGTT TTCTTCTGAG 11640
 ACATCAACGT TTGGTGTGTG TAAATCATAG CCTATTTGAT GTTTCATGAT AAAAGTTCCA 11700
 TTTTCATCAT ATAAGACTGA CTTGGTACTC GTCGTTCCAA TGTCGACACC AATCATATAT 11760
 TTCATGATAA ATCCTTCTTT CTTTCATTTT AATCAACCA AAATCCTTCA ATATCTTTAC 11820
 CAACATCGTC GAAATTTAAA TGAAACGCTT CTTTCAAAAT TTGACTGTGG TATTGTTCCA 11880
 CTGCATCAAT AAACACTTGA TGATTATGAT GTATGCGTTC AAAATCTTGC GGGTTCTGTT 11940

	AAAATGAGTT TAAATATTGA TGATTAGATG CTTTGATTAA TGTTTCATGA AATTCAAAGT	12060
	CATGCTTCGT AAATGATTCT GCATCCTCAA ATTTTACTGC CACTTTCATC ATTTCAAGTT	12120
5	GTTTCTTCAT TTCTTTTACG ATAGGTAGTC GCTCTTGATT TTTAACTCTT GAAAATGCAA	12180
	ATGACTCTAA CATCAGTCGC AAATCATACA TTTCTTTCTT TTCTTGTTCC CCAAACGGCA	12240
10	ACACATGTGC ACCCATTCTT TCTAATTGGA TGAGTTGATT TTGTTGCAAT AATTTAAATG	12300
	CATCTCGAAT TGGCGAACGA CTCACATTAA ATTGCTTTGC CATTTGATTT TCAGTGAGTA	12360
	ACGTACCTTC AGCTATGTGA CCATTACAA TGCCTAAGCG TAATTCTGCC GCGATACCTT	12420
15	CTCCAGTTGT CATACTTCC AACCATTTCT CTGGATATCC ATACATCATC AAAGTCACTC	12480
	CTTCATTACA CGACATACTT GTATACAAGT ATGTTAATAT AGTTATTATG AGTTTGCAAG	12540
	CGCTTTCTTT ACGAGCACTA AAATAGTGAC CACCCCTTTT CGATTTAAAT TTAAAGGAAA	12600
20	TGGTCACTAT CACACGAATG ATTTAATTGT TATGTTGTAT GTGGGATATT TCTAATTGTT	12660
	CTGTACTCAT ATGCGCTTTA GGTACTTCAA TGCAATAATG CGTTTCATGA CAGTTTGAC	12720
	ATTGAATCG ACGTGTGTGTC GCTGTATGTT TCGCTTTGAT AACTGCCCAC AAAGATGGTG	12780
25	AGAATATATG CTGGCAGTTA GGACATAAAT AGGCAACCTT TTGTTGGTAA TAAAAAGTAA	12840
	CACCAATGCC ATAACCAATC ATAAATGGTA AAGCAATTAA AAACGGCCAT TTATTTTTC	12900
	TCAAAATTGC ACTTATAATG CTAGAATATT GAATTATTCC TATAATACCA GCACTAATCC	12960
30	AAATGTTACG ACGAATACTT TTCATTTTCTG CTGATTTACT CATGACATGC TCTATGTCTT	13020
	TTAAGTGTGT GATTGGAGAC GTCGACGCTT CATTTACGTA ATATTGAACA TTTTTAATTT	13080
35	TGTTTAATAC CGCTTGTTGC TGTTTAACTT GTTGGTTAAT TTCTTGTTGT TTCATAGTTA	13140
	GTAAAGTATT GAGCGTCTTC AAAGTACCTT CACCTTTTAG CAACATATCT ATATCGCTTA	13200
	ACGCACAACC TAAATCTTTA AGCAATAAGA TTAACCTCTAA TGTTTGTCGC TGTTGTTCTG	13260
40	TATACACACG ACGCTTTCCT TCTGTAAATC CTTGTGGTTT CAAAATACCT TTGCGATCAT	13320
	AATATTGAAT CGTTCGTGTT GTCACATTGC ATAATTTTGC GAGTTCTCCA GTCGAATAGT	13380
	TAGACATAGA TTCCACCTCC TATAATTACC ATAGTTGATG ACCCGACGTC ACGAGCAAGT	13440
45	ACAATTTCCA CATTTTAAAG AAATTTATTA TACTAGGCGT CTTATTTTTA TGATTTTCGTA	13500
	CCATGTTGAT TTACAAACTC ACTCAAACCTA AGTAACACAC CTACTAAACA TCTACTCTGT	13560
	TATTTAGAA TGAATTTGTT GTAATTTATC TTCAACTTCA GTAATCTCTG TCGCACATTC	13620
50	TTTCAGTAAA TCTCGATACT TTTCCGTCTC TGCATTGTTT TTATAACGTA TTTTATGTTT	13680
	TAAACTTGcC CACATATCCA TACCTATCGT TCTAATTGGA ATTTCAACAG GCAATACCTC	13740

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(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GGATAAGTTC	AGGTAAATTC	ATTTCTTTTT	CAATTTTGAT	TTTCATTGTT	TCCGCCCTTT	60
TAAAATAAAG	TTAGTTGCTT	CTGTTCTCTCA	TATTCCAAAT	CACTTTGCTT	TATATATGTT	120
TCAAGCTCTT	CGCTGTATC	AAATGTCTTT	TTACACCTT	GCCAACCTGG	CACGATATGA	180
CCGTGAAAGT	AATAAGTGCC	ATTTACTACA	TGGATATGTG	CCACTCGTTC	GTTATCCTGA	240
TACAGATATC	TCTTAGATCC	AAAGAATTGA	TTTAGGTATT	CTTTACGCGC	GCTATCTGTC	300
ATGGTCATCA	CTCCTTTTAA	CAATTAGGCA	GACCAAACGA	CATGCATTCTG	TCGTATAGCT	360
CTTCATTACT	TATGCTTGCC	TTATAGTTTT	CAATCACATT	GCTAACTTCT	TTATGACTCA	420
TTGCTTTAAC	TTGTTGCTCT	GTATATTTTT	CGCAGTCTTC	TAATTCCAGT	TGCTCCTGTA	480
ATGACATCAC	ATATTCAACT	TGTCTTTGGG	TTGCCATCGT	TAACCCCTCCC	ACAAGTCAAA	540
AGCTCTTTGG	ACGTAAAACT	TCGCCTTTGC	TAAATCCTCA	TGACCATTCT	TTAACGGTGC	600
TCTAGACATG	TATTTGATTG	CATTACCTAT	TGCGAATGCT	AGTTGAGGTG	GATACTGTGC	660
CGTAACCTGT	TCGATAAAAT	CTATAATTTT	AATGTCGCCG	TATGTGTAGT	GCGCTGGTTG	720
CTTAACATTG	TCTTGCGCTT	CGTTCATATC	TACTTTTCTG	TTACTGATTA	CGCTCATTAT	780
GCTTCACTCC	ATTTCTTGAA	CATTTGGTTA	TAAGTGACAT	CGAACCAGTA	CGGATCACGT	840
GAATGTTTTT	GTGGCGTTCC	ATCATAAAGC	CATGGTCTTA	ATCTTCTCTT	TCTTTCCTGT	900
TCAATATCCG	CTCTCACATT	TCGTGGTAT	CGGTTCAAAA	TCGCTTTTTT	TCTGATTTTT	960
TCTCTCCCTT	TTTCTTCATC	TTTnATtTGA	CTCTnCATAT	ATTCAACTTC	TTCTGTAGAT	1020
nTTGAGTCCT	TTCTTCCACA	CAATAATTCA	nCGCCGCGC			1059

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

	GAAGTAAAG AAGAATTAAA TTAAACATTA ACAATGGATG AAATTGAATA TGTCGGGACA	60
	ATTGTAGGTC CTGCATATCC ACAACAGGAT ATGTTAACTG AGTTAAATGG ATTTCCGCGCA	120
5	TTAACCAAAA TCGATTGGGA AAACGTAACT ATCAATAATG AAATTACGGA TATACGCTGG	180
	ATTGATAAAG ATAATGATGC GTTGATTGCG CCTGCTGTCA AAGTTTGGAT TGAAACTTAT	240
10	GGTGGTAAAC ATGACAAATA ATGACACCAT CATGTTACGA CATTATGTCC CACAAGATTA	300
	TTCGATGTTA GAAGCTTTTC AATTAAGTGA AAGTGATTG AAGTTTGTTA AAACGCCAGA	360
	GGAAAATATT ACAGCTGCAA TGTCTGATAA TGAAAGGTAT CCCATCGTTG TAATGGATGG	420
15	CAGGCAATGT GTGGCCTTTT TTACATTACA TCGTGGAAAA GGGGTCGCAC CATTTAGCGA	480
	TAACCAAGAT GCAGTATTTT TCAGGTCATT TAGTGTGAT CAACGTTATC GTAATAGAGG	540
	AATAGGTAAA GTGGTAATGG AAAAATTGGC GTCATTTATC ACTTCAACAT TTCAGGATAT	600
20	TAATGAGATT GTGTTAACGG TTAATACTGA CAATCCACAT GCCATGGCAC TTTATCGCCA	660
	ACAAGGATAT CAATATATGG GAGATAGTAT GTTCGTCGGA AGACCTGTTC ATATTATGGC	720
	GTAACTATA AAATAAATTA AATTTAAAAG CATCTTTACT CATCGTCGAC CACAACAATT	780
25	AATGATGAAT AAAGGTGCTT TTTGTTATAG ATCATCGGAC AATTTACTAT AGTAAAAAGC	840
	GACCTAGTGA ACAATTGACA TATATCCACA GGTCGCTTAA CTTAAGTTAT ATTGCTAGTT	900
	GCGATTAATT GATAGACTCA TCATTTTTGC GCTGTCGAGA TGGTCTTTTT ATTA AAAATG	960
30	CCGTAATCCA AGCCGTAATC GGAATACTGA TTGCAACGGC AATACCGCCT AAAATAATAG	1020
	AAATAAATTC TTGGGCAAAT ATTTTCGAGT TTATAATATG ACCAAATGAA TATTTAAGTT	1080
35	TGAAAAACCA AATAAATAAA GCAAGTTGGC CACCAAAAAA GGCAAGGTAA ATCGTGTTG	1140
	CAGATGTGCG TAAATTTCT CTACCAACAC GCATGCCAGA TTGGAATAAT TCGTATTGCG	1200
	TAACGTTgGA TTCACTTGAT GCAATTCATA AATGGGTGAA CTAATGGTAA TTGTTAAATC	1260
40	TATCAGAGCT GCAATAACAG CAAGAATAAT AGTGAACACC ATAAATTGAA CCATATCAAT	1320
	GCCAATATTC ATTGAATACA CATATGTTTC ATCTTGTTGT TCGGTTGaAA AGCCTTGTAG	1380
	ATGACCGAAG TAGACCGATA AATAAATGAG TGTAATCAAC AATATTGTTG TAACGATagT	1440
45	GCTGgATAAA TGCaGCTTGT GTTTTAACAT TGTAACIATT GAGTACGAAT AAATTACAAG	1500
	CGCCAATAAT AATGCAGAAA AAGAATGTGA CGACATAAAT CGGTACGCCA AAAATAATCA	1560
	ATACAATACT AATAATTAAA ATAGCGAAAT TAAAAATAG GGTAAATAA GAGATGAATC	1620
50	CCTTTTTACC TCCGAAAATT ATCATCAGAA AGAGGAGCAA TAACGCCAAT ATAAATACAG	1680
	CATTCATTGT TTCGCCCTCC TTAATGTTTC AAATATTTCC ATAAACAATA TTGTGATAGG	1740

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	CATCGAAATA	GTATAAGTCA	CTGTATTGGC	ATTTTTTAAA	AAGATTAAAA	ACATAGGTAG	1860
	TGCACCGGAT	AAATATGAGA	ATAATAAGAT	GTTAGTCATT	GTTCCCATAA	TATCTTGGCC	1920
5	GATGTTTCGC	CCAGCAAGCG	CCCATCTCCT	CATTGAAATG	TGTGGCGTAC	GCTGTAAAAT	1980
	TTCATGCATA	CCACTAGCAA	TTGTAATTGC	AACATCCATA	ATAGCGCCAA	GTGAACCTAT	2040
	TAACACTGAG	GCTAGGAAGA	TATCTTTCGG	TGGTAATGAT	AAAAAGTTCA	TCGTTTCATA	2100
10	TTTAATGCCT	TTACCATCTG	TCATATATAT	GATTAATTCT	GTTAAACCTA	TACTCAAAAA	2160
	AGTTCCGATA	ATTGTACTGG	CTATGGTAAT	GAGTGACGC	ATATGCCAGC	CTGTAACGAG	2220
	CAATAAAGTG	AGTATTGTTG	AACAGATCAT	GGCAATGGTC	ATGAGTAAGA	ATAAATTAAT	2280
15	ATTGCTATGT	TGAATATGAA	TGTAAATTGC	GATTAATATG	GCAATAGAAT	TCAAGATTAA	2340
	CGATAAAATC	GATTGCAGTC	CGACTTTGCG	ACCAACCAAT	AATACAGTTA	ATAAGAACAA	2400
20	ACCAGTGATG	ATAACCGTTA	AGGTATCAGC	CTTCTTTTCT	ATAATATAAG	CATCACTCGG	2460
	CTTGTTAGAA	ATATGTAATA	ATACTTTTTC	GTGTGTGCGA	AATGCCTCAG	AATCTGCTTG	2520
	CGATTGACG	TACTGATGAT	TAATCGTCGT	CGTTTCTCCA	GCAAATTGAC	CATTTAATAT	2580
25	TTTGACTTTT	AATTGATTTT	TATATTAAAT	ATCAGGATTA	TTTTGTGCAT	CTTTTGTAGG	2640
	TGTCGAAGAA	ACATGTTTGA	CATCTATAAT	TTGACCAATT	GGTTTGTGT	AAAAGTTCTC	2700
	ATTATTGAAT	GTAATAAAAA	TAGCACCAAT	GAATGCGATG	CAGAACAAAC	CTAAAATTAT	2760
30	ATTAAATGGC	TTTGTAATAA	AATTTCTATA	TTTCAAAAAC	AAAACCCCAA	TTCTATGAAT	2820
	GAATTAATAT	GGTGATTATA	CGCCCTTAAT	TTTTTATTTT	CAAAGATATT	ACTGCTAAGT	2880
	GTAAAACGAA	AATCATCATT	GATAGCATCG	AATTACTTAA	TGGAATGTAG	ACGTTTTAGT	2940
35	CATTAATTGC	TGAATAAGTG	TTAATAATAT	GCCAATATCA	CTCTTTGTAT	AAGGCTCCTT	3000
	TGTAATAGCA	CATATCGTTC	TTTTTAATTC	AGTATGATCT	AATTTTATAT	CTATCCATGA	3060
40	TTTAGATTCT	GGTAAATGTA	TATTTTGTGA	TGAAATGATG	TAACCTTCTT	TTTGACGAAG	3120
	GAGATACTGC	GCAAGTGGTT	GGCTACTGAT	TGTGTATACA	TCTGATTTAG	TAATCTTGCG	3180
	CAATTGTTTT	TTTACAGTTT	CGGCAATGG	TGCCAAGCAA	TAAATATGAC	TATGCTCAAA	3240
45	CTGAATTAAAT	GGTGGGTGTG	TCGCCATCGT	AATTGGATCG	TCTGAAGGCG	CATATAAATG	3300
	ATAGTGCTCT	TCGAATAAAG	GTAGCATATG	TAATTGTTTG	TGTTTACGTA	TTTCTGGTGT	3360
	AAGTTCCGTG	AAACCAATGT	CTATATTCCC	ATTTAATACG	CTATTTATAA	TTGTGTCATG	3420
50	TTCTAATAAG	CTCGGTATGA	CATGTGTATC	ATTTTGTAAA	TGAAACGTTT	GGATAAGTGG	3480
	TAGTAACATG	TGGGATACGT	CACTCTCATC	ATAGCCAATG	TAGATACTTT	TATTTTTAGT	3540

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 5 AATGTTTAGT TCAAGTGCTG TTTGCGAGAT ATGTTCTCTT TTAGCGACCT CGATAAAATA 3780
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	GTTACGAATC CACCAATTGA TCGGTATCGT GAAAAAATCG TAACGAGTGA ACTTTCTTAT	5580
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	GAAGCAGTGA ATGCTGTAAA GCAAGGCGCT CAAATTCTAG TGTTAGATGA TAGTGGATTA	5820
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	GAAGTGCATC ATGTTGCTTG TTTACTCGCA TATGGCGCGA ATGCAATTGT GCCATACCTA	6000
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	AATGTTAAGA CATATACGGA TGTATTGTCA GAAGGTGTCA TTAAAGTAAT GGCTAAGATG	6120
	GGAATTTTGA CAGTGCAAAG TTATCAAGGG GCACAAATAT TTGAAGCGAT TGGCTTGTCT	6180
25	CATGATGTGA TTGATCGTTA TTTTACTGGG ACACAGTCTA AGTTATCTGG TATTTTCGATT	6240
	GATCAAATTG ATGCTGAAAA TAAAGCACGT CAACAAAGTG ATGATAATTA TCTTGCATCA	6300
	GGTAGTACAT TCCAATGGAG ACAACAAGGT CAACATCATG CTTTTAATCC GGAATCTATT	6360
30	TTCTTATTGC AGCACGCATG TAAAGAAAAT GACTATGCGC AATTTAAAGC ATACTCTGAA	6420
	GCGGTGAACA AAAATAGAAC AGATCACATT AGACATTTAC TTGAATTTAA AGCATGTACA	6480
	CCGATTGACA TCGACCAAGT TGAACCGGTA AGTGACATTG TCAAACGCTT TAATACAGGG	6540
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	GTAAGTAGTG ATTATTTACA ACATGCCAAA GAAATTCAAA TTAAAGTTGC GCAAGGTGCA	6780
	AAGCCTGGTG AAGGTGGTCA ATTACCTGGT ACTAAGGTAT ATCCGTGGAT TGCGAAGACA	6840
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	AATTTTATGC ATTTTATGTC ACAAGAATTA AGAGAAATTT TAGCATCTTT AGGTTTGAAA	7440
	CGTGTAGAAG ACTTAGTTGG AAGAACTGAT TTATTACAAC GATCATCAAC ATTAAAAGCG	7500
10	AATAGCAAAG CGGCTAGTAT TGATGTTGAA AAAGTGTAT GTCCTTTCGA TGGGCCAAAC	7560
	ACAAAAGAAA TTCAACAAAA TCATAATCTT GAGCATGGAT TTGATTTAAC AAATTTATAT	7620
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15	AATGAACAAC GTGATGTAGG GGTATTACA GGTAGTGAGA TTTCGAAACA ATATGGAGAA	7740
	GCAGGACTTC CTGAAAATAC AATTAATGTT TATACGAATG GTCATGCTGG TCAAAGTCTT	7800
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	GGTAAAGGAT TATCTGGTGG TACGGTCATT GTCAAAGCAC CTTTGAAGA ACGACAAAAT	7920
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	AAACCAGCCG TTGTGTATTA AGGAAAGGGG GAGATACGAT GGGTGAATTT AAAGGATTTA	8520
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	AAGCATATCA ACAACGATTT ACTAAAGAAG ATGCCTCTAT CCAAGGTGCA CGATGTATGG	8640
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50	CACCATGCGA AAGTGCTTGT GTGATGAAGA TTAATAGAGA ATCGATTGCG ATTAAAGGTA	8880
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5	GTATTAAGTT AATGGAAGAA GCGGGCATT A CTTTCATTAA TGGTGTGAA GTCGGTGTG	9180
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	CAAAAGATAA GAATGTCATT ATCATTGGTG CTGGTGATAC AGGGGCAGAC TGTGTAGCGA	9420
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50	TTCCAGAAGT	TCAACATGCT	TTAAACATCA	ATTCTAGTGA	ATCACTCATT	CATATTGTTA	14340

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15	CTACATATTT CCAGCGAATA TTTTTCCTGT CTGAGCTAAA TAGAAACGCA AGTGCTAAAA	29340
	AGAAGATAAT TCCGATAATC CCAATTAGAA TATGCATATA TTTCTCATTC CTTTAGTTTT	29400
20	TTCTACaATc TATCATACAA TAAAATGGAA GGGCTAACAT CATAAATTTT TGAAAATATA	29460
	AAAACAAATT AATTGAAAAA GGTCAAAATA GGTCAATATA TATAGTCAAA GAAGGTCAAA	29520
	AAGGGGTGAT ATACATGCAC AATATGTCTG ACATCATAGA ACAATAaTCA AACGTTTATT	29580
25	TGAAGAGTCG AATGAAGATG TCGTTGAAAT TCAGAGAGCG AATATCGCAC AGCGTTTTGA	29640
	TTGCGTACCA TCACAATTAA ATTATGTAAT CAAAACACGA TTCACTAATG AACATGGTTA	29700
	TGAAATCGAA AGTAAACGTG GTGGTGGTGG TTACATCCGA ATCACTAAAA TTGAAAATAA	29760
30	AGATGCAACA GGTATATATTA ATCATTTGCT TCAGCTGATT GGACCTTCTA TTTCTCAACA	29820
	ACAAGCTTAT TATATTATTG ATGGGCTTTT AGATAAAATG TTAATAAATG AACGTGAAGC	29880
	TAAAATGATT CAAGCAGTTA TTGATAGAGA AACGCTATCA ATGGATATGG TTTCTAGAGA	29940
35	TATTATTAGA GCAAATATTT TAAAACGTTT GTTACCAGTT ATAAATTATT ACTAAATGAA	30000
	ATGAGGTGTT GAAGTGCTTT GTGAAAATTG TCAACTTAAT GAAGCGGAAT TAAAGTTAA	30060
40	AGTTACAAGT AAAAATAAAA CAGAAGAAAA AATGGTGTGT CAAACTTGTG CTGAGGGGCA	30120
	CCATCCGTGG AATCAAGCTA ATGAACAACC TGAaTATCAA GAACATCAAG ATAATTTCTGA	30180
	AGAAGCATTT GTTGTTAAGC AAATTTTACA ACATTTAGCT ACGAAACATG GAATTAATTT	30240
45	TCAAGA	30246

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

	TATTCCCCCA TCGGTTTATT AAATCGTCCA TTCAATACT GTTTTCCCCC AAGATGTCGA	60
5	TAAATCCATT TCAAACGCTT GGACGATATC TGCATCGTA CATACATTAA TTTCAATGTC	120
	TTTTAATAAT GCTAACTTTT CAACTATGTC TGGGTACTTA CGATATAAAT CAACAACCTG	180
10	CTCAAAATCT TTAGAGCCGC TTCGACTACT ACCAATCAAC GTTAATCCTT TTTCAAGTAC	240
	TAATCGTGTA TTCACCTCCA CGGGTAATTC ACTTACGCCT AACAAAGCAA TACTGCCTTC	300
	TGGTGAAATA TGTTCAACTA TTTGTTGAAG TGCAACTTGA CTTCTTTTAC CTCCAACACA	360
15	TTCAAATGCA TGATCAATTT TAAGATCATC TGGTATTTGA TTTACTGTAA AGATGTCATC	420
	TACAAATGAA AAATGACTTA ATTTATAGTC TGTCTTACCA AATACATAAG TTTTAGCTTC	480
	TGGGTACAAC TTACGTAGCA AAATAGCAGT AATATAACCT AAGTTACCAT CACCCCAAAT	540
20	ACCAAAGCTG GTTTTCAAAG GTATAGATTT ACGTTCAAAT CGTTGTATAG CATGATAACT	600
	TACTGACACT AACTCTGTGT ATGAAATCGT ACTCAAATCA ATGTCATTAG GCAGCGGAAC	660
	GATACGATCA TGTGCCATCA CAACGTAGTC TTGCATAAAA CCATCATAAC CACTAGATCT	720
25	AAAATAACTA GAGGCTAAGT AATTCTCCGC AATAATATGA TGTGCTCTG TAGGTGTATT	780
	CGGTACCATT ACTACTTTTCG TACCTTTTTT AAATACCCCT TTAATATCAA ATACAACCTC	840
	ACCAACAGCT TCATGAACTA ATGACATTGG TAATTTTTTG CGTAGTACAT TTTTATCTCT	900
30	TCGACCTGTG TAATACCTTT GATCAGCTGC ACAAATAGAC AAGTATAAAG GTCTTACGAT	960
	GACATGATTA CCATAAATAT CAACATTATT ATATGTGACG TCGAACTGTC TCGGTGCAAC	1020
35	GAGTTGATAT ACTTGATTAA TCATCGGCAA TATCACCTTG AATAATGGCA TTTGCTACTT	1080
	TTAAATCATA CGGTGTTGTC ACTTTAATGT TGTATAGTTC TCCaCGTACC AATTTAACTG	1140
	CATGTCCAGA TTCGACAATG ATTTTACATG CATCTGATAA GATTTCTTTT TGTTCACTAC	1200
40	TTAAGGCGCG ATAACATCTT TGTAATAATT TAATATTAAA TGATTGTGGT GTTTGGCCTT	1260
	GATACATTTC ATTCCTTACA GGGATACTGT GTATGTTCTG TTTATCTTTA GACATTACAA	1320
	TCGTATCAAT TGCTTCAATG ACTGTATCTA CTGCACCATA TTTGCTGCT ACTTCAATGT	1380
45	TCTCTTTAAT AATACGTTGA GTTAAAAATG GTCTTACGGC ATCATGAGTT ACAATCACAT	1440
	CATCATTATT AATTCCATT ACATTGCGAA TATGGTCGAT AATGTTTATA ATTGTTTCAT	1500
	TTGATCCGT ACCACCTGCA ACTACTTTGA CACGTTGATC TGTAATGTTA TATTTTTTTA	1560
50	AAATATCCTG TGTATGGGAA ATCCACTGTG CTGGCGTTGC GATAATAATC TCATTAAATT	1620
	CACTCACTAA AATGAACTTC TCAATTGTAT GGATTAAAAT CGGTTTATTA TCAATATCTA	1680

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	CTGCATAAAT CATGTTGTCC TCCATTCTGT CATTACATCA TTTCCATTTA TACATTACTG	1800
	ACCTATGCCC GCACATAAGC CTAACCTATT GCTCACTTGC CTCTTTTATT AATCCAAAGA	1860
5	TAGTTGTCAC AATAGTGTGA TAATTTTTTA TAAAAATGTA TTTTGTAAAC TGACCATTCT	1920
	AAGTTGTTTT GCCATGCAGT TAATCATTA A CTCTGACGAT ATTAAATTGT TAAAGGTATT	1980
10	AATGTTTACT CTTTTTCAAA TTCATTATTA CTGCCATCAT TTTACCATAT ATTATAATAA	2040
	ATTTATCTTA TTAAGTGGCT GTACTTGATT TTCACTTTAA AAATTATCAA ATATTGCCAT	2100
	CTCATTTTAA GTATACAAA TGCAAAACAA CCGATTACAA AGCATATTTT ACACAAGTAA	2160
15	ACCGGCTATT TATCAACGTA TATTGGAAGA TGAATTATTT CGATAGTATC TATAGACCAG	2220
	ACGGCATTG CACTTTCATA GCTATAACTA TACCAGCGTT TTCGTCCTCA AAGGTGCATA	2280
	CTAATAAATC GTAAACATGA CTTTATCAAA TCGTTCCTTC TTGTTAACTA ATTTATCAAA	2340
20	TGTCTCCGGG CCTTTTCTA ACGGTAAAAA ATGAGAAATA ATAGGCTTTA CATTAAATATC	2400
	TTTCGTCTTC ATATAATGTA AGGTTGCCGT CCACTCTTTG CCCGGAAAAT TACTGGACAA	2460
	ACAGTTCCAA GAGCCACATA CTGTCAACTC GTTACGCAGA ATTTTTTCAA AATGAACGCG	2520
25	ATCAATCTCA ATATCATCAT ATGGTATTCC GAGTAATACC ACCTCGCCAC CTTTTTTAGG	2580
	TAGCGTCAAT ATTTGACCAA TCGTAACTTT AGCACCTGAT GATTCTATAG CTAAATCGAT	2640
	TTGATTGGCG TAATGATTTT CGATGAATTT CTCAAGATTT TCTTCTTTTG AATTGATTGT	2700
30	TTGATGTGCG CCAATGATG TTGCAATATC TAGTTTATGC GCATCTATAT CTATAGCGAT	2760
	GATATGTGCA GCACCAAATA TTCGTGCCCA TTGAATAGCT AACAAACCTA TACTGCCACA	2820
35	CCCCATTACT GCAACAGTCA TACCAGGTTG TATATTGAT TTATAAAACC CATGCGCAAC	2880
	AACGGCTGAT GGCTCAACCA TTGCTGCTTC AATGTAATCA ACATTGTCTG GAACCTTTAA	2940
	AACATTTTGC GCTGGCAATT TGACATATTC CGCGAACGAT CCAGGTTTAT ATGAGCCAAT	3000
40	GACGAATAAC TTTTCACATC GTGCATATTC ACCTTTTAAA CAATACTCGC ATTGATAACA	3060
	AGGTATTGCT GGGCAACCTG TCACTTTGTC GCCCACATTA ACATGCGTAA CATCACTTCC	3120
	AATGGCATCT ACTACACCTG AAAATTCATG ACCAAATGGC ATACCTTTAA TGTATGGCCC	3180
45	CATTTTTTTT TATCGTGACG TGTCTGAACC ACATATGCCA GTCGCTCGTA CTTTAATAAT	3240
	AACGTCATTC GCACTTTCAA TGACTGGCTT TTCATTATCC TCATACCGTA AATCTTCCAC	3300
	GCCATATAAT TTCAATGCTT TCACTTGTA ATCACCTCAA ATTTGATTTA ATTCACAACT	3360
50	TTTTTCTTTT TAAAAATACC TGTCGCAAAA TAACCTGCAA TGACAATGGA ATTACTTACG	3420
	AGTAAATGTT CCATATAAAA ATCAGTGATT TGTCTTAATG GCCCAAGCAT AAAAGTTAGC	3480

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	TGCTTTAATA CCTTCGCCGG ATTTTAAATG TTGATACGCC TCGTCCCATT TCGAAATATC	3600
	ATATATTTTT GTCACCAAAG CTTCAGCATT TACTAAACCA TCCGCCATAA GTTGCAATGA	3660
5	AGGTTCCCAA TCTGCTGGCT TTTGACTTCT ACTACCAACA ACTGTTATTT CTTTTGAAT	3720
	CACTTTTTTC ATATCAAATG GAATTTTCAGC ATCCTTAAAA ATACCTATTT GACTGTAGAA	3780
	ACCTTTTTTG CGTAAATAT CCAAACCTTG TCGTGCTGCT GGAACGTCAC CTGAACATTC	3840
10	AACAACAACA TCTGCACCGT AACCGTCTGT AATTCATTG ATATACGTTT TTAAGTCTGT	3900
	TTGTTGTAAA TTGACTACAT AATCCATGTG CAATGCTTCT GCTTTATCTA ATCTGACTTT	3960
	GTCATTGTCC AATCCAGTTA CCACAACAGT TCGCCTTTA CTTTTTAAACA CTTGTGCTAC	4020
15	AAGTAATCCG ATTGGCCCAG GTCCCATTAC AACTGCTACA TCGCCTGAAT TGACTTGAAT	4080
	CTTAGAAACG CCATGATGTG CACATGCTAA TGGTTCGTG ATAGCTGCAG ACTGATACGA	4140
20	TATTCGCTCG GAATATGATG CAAACTTTCT TCACGTGCAA TGACATAATT AGTAAATGCG	4200
	CCATCAACTT GTGTTCCAAT ACCTTTTCGA TGGTTGCATA AATTATAGTC TTTTGATTTA	4260
	CAGTATTCAC ACTCATTACA AACATAGAAT GTCGTTTCAG ATGtGACACG GTCACCAACT	4320
25	TTAAAATCTT TAACGTCTGC TCCAACCTCA ACGATTTTAC CAGAAAATTC ATGACCTAAT	4380
	GTCACTGGAA AATTAACTTT ATAATGACCT TCATAAGTAT GAATATCTGT GCCACAAATT	4440
	CCTGCATAAT GTACTTTAAT CTTTACTTTA TCATCTAGCG GTGTTGCAAC TTCTTTATCA	4500
30	AGAAGTCTA AGTTGCCATG TCCTTCTCTT GTTTTTACTA AAGCTTTTAC CACAAACACC	4560
	TCGATTTTA ATTGAATAGA CTAAATAGTT TAAAGATAAG ATAGTTAACG ATATTACCAC	4620
	CTTGATCAAT ACTTGAAATT TCAGATGAAC CTTTGGCAT TTGTACATTG GTACCTTTTCG	4680
35	CCATATCTGT GAAAATGGGT GCTACGCTG TTGCAATATA TAGTGAAATT GCAATCATAA	4740
	TCGTACCCAC AATGACAGAA TGAATAATGT TTCCTCTTGC TGCACCAACA ATAAACGCGA	4800
40	CAACAAATGG TATCGTTGCT AAGTCACCAA AAGGTAGTAC TTGGTTTCCT GGTAAATAA	4860
	CGGCTAATAA AACAGTGATA GGTACTAAAA TTAATGCTGT CGAAATAACT GCTGGATGAC	4920
	CTAATGCTAC AGCCGCATCC AATCCAATAT AAATTTACG TTCGCCAAAA CGTTTATTTA	4980
45	GCCATGTTCT TGCAGACTCT GAACTGGCA TTAAACCTTC CATTAAGATT TTTACCATTG	5040
	TAGGCATTAA TACCATTACT GCAGCCATTG ACATTCCTAA ATTAATGATG TCTCCAGGTT	5100
	TGTAACCTGC TAACACACCA ATACCTAAAC CTAAAATTAA GCCGACAAAT ATAGACTCTC	5160
50	CAAATGCGCC AAAACGTTTT TGAATTGTTT CAGGATCAGC ATCTAACTTA TTCAGACCGG	5220
	GTACTTTTTG TAACAATTTA ACTAAGTAAA TACCTGGTGC ATAAGAAATT GTACTTCCTG	5280

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	CTACTTTCAA ACAGATAATT TGGAAAATAA CTGCTGCTAA TAACGCTTGC CAAATACTGC	5400
	CTGATACGGC ATAAACCATT GCTGCTGTAA ACGTATAATG CCAAAAATTC CAAATATCTA	5460
5	CATTCATCGT CTTTGTCACT TTAGTTACTA GCAATACAAC GTTAACTATG ATTCCGAGTG	5520
	GAATAATAAA TGCTGCGACA GATGATGCCC AAGCGATAGA TGATGTTGCT GGCCAACCTA	5580
10	CATCAATCAC ATTCAGACTG ACGCCTAAAT TTTTAACCAT CGCTTGTGCT GCTGGCCCTA	5640
	AATTTTAAAC TAATAAATCG ATGACTAAGA AAATCCCTAC AAAAGCCACA CCTATTGTTA	5700
	AACCAGACCT AAATGCCGCT CCAATTTTCT GCCTAAAGAA TAGGCCAAGC AAGAATATGA	5760
15	CAACCGGTAA AATAACAGTt GCACCTAAAT CTAAAAATCC CCTTACAAA TCAGTGAAGT	5820
	AACTCATATT TAAACCCTCC CTGTTATATA TGCAATTGTCA CGATACTTTC CGATTGTGAT	5880
	TACATTTGAC GTTACAGTCA TTTCAACGAC AACCCTTGCT AAATTGCGACT GCAGTCCTTT	5940
20	TGAATTACAG tCACTGCGTT TCTATGTCAT CAACAATCAT TTGTCGTGAT AGTCATTTAT	6000
	ATGCAATTTG CATATATTAA TATGTTATCG ACCCAGCTTA CATATCAATT CCGTTATTTT	6060
	TGTAACCTCG TTAAGATTTG TTGTTTGTGTT TCTTCAATAC CAATACCAGT TAAGAAATTA	6120
25	CGTGCGTTGA TAACTGGGAA TTTATATTCT TTTTTGTCA TTGCAGTTGT AACTAATAAA	6180
	TCTGCAGTGT CTTCATAAGG TCCAACCTCT GTAATTTTGA TTTGTTTAAT ATCTACTTTA	6240
	ATATTGTGTT CTTTGGCCAT TTCTTCAATT GCATTATTTA CTACTGTTGA CGTTGCAATA	6300
30	CCTGCACCAC ACGCTACTAA TACTTGTTC ATTTTCAATT CCTCCAATTA ATTTTTAGTT	6360
	ATATTCCAAA TAATCATTGA TTAGTGTGTC TAAATGTGTT TCATCTTTCG TTCGTAGAAT	6420
35	CTGCTCCAAT TTTTCTTCAC TTTGAAAAAT TTGCATCAAC TGTTGTAACA GCTTAAGTTG	6480
	ATCATCTACT TTATCCATTG CTAACATAAA AACGATTTTC ACTTCTGTCT GTTGATCAAG	6540
	TGTTCCCAT TCAATAAACG GCACTTCTTT TTCTAGAACA GCCACACCTA TCGTTCTATG	6600
40	GTTAATATGT TCGACATCTG TATGCGGTAT AGCGACCGAA CATAGATGCG TTGGTAAACC	6660
	AGTAGCAAAT TCTTTTTCTC TGTCGATGAC TGCATCTTTA AACGTTGACT TCACGAACCC	6720
	ATTTTGAAAT AACACATCTG ACATTGTGTA CAATACGGAT TCTTTATCAG TTGCCGACAA	6780
45	ATTGAGCATT ATATTTTCTT TATGCACTAA TTGCTGTCCC ATCCATTTTC CCTCGCTTCT	6840
	TTATTTGAAT AATTTTTTAA AATCTCATTT ACATCAGAAT TTTTGCGACT TTGTATGATG	6900
	CGCTTAATTG CGTCATTGTC TTGCGCCACA TCTCTCAATT GTAGTAACGC TCTTAAGTGT	6960
50	GTCACTTTAT CAACAGCAGC AATAGGTACA ATAATATGGA TTGCTGTGCC ATCTGACATG	7020
	TATATTGGTT CTTGTAATAT CAACATACTC ATCGCTGTTT TATGTACATG CTTTTCAGAG	7080

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	TGCATCTCAT GAATATATTT AATATCAATA AAATGATTAG CAACTAACAC ATCACTTGCT	7200
5	TTAGCAATAG CTTTCATCAAT ATTTTCAACA TGATGCATTG TTTTCACGTG CCTTGCCGGT	7260
	ATCAAGTCAG CTAAATCTAA TGyCTWATTT tGTGtGACaA TCGATCCATT AATGGTTGAA	7320
	ATTGAATTAT AATTGGCAAT AAAATCTTCT AAACCATCAC GTAGTtTGTA ATGTCATTAA	7380
10	CTGTCGTTGT GCGTTCAATT AATGCCATTA ACTTGTTTAT TTCCTTATCA ATGTCAGCCG	7440
	ATTCCTTATT AATGTACTTC ATCACTTCTT TACGTAACCT TCGTTGCTCA TTTTCAGATA	7500
	AAGCTACTTT TGTGATAAAT AATTTTTTAT GTGTTAGGAC AAACATTGGT GAAAAGACGA	7560
15	TGTCATAATC TAATGTGTAA TTTTCAAATG TTCTAAGTGA AATCGCATCT AAGAAAATAA	7620
	TTTCTGGAAA TAAGTTTCGC AACTCGTATA ACATCATTTG TGATACTGAC GTGCCTTG TG	7680
	TACACACGAT AATAGCTTTT ATCTTGCCAT CGAAGTTTTT ATCTTGACGT CTCAAACCTAC	7740
20	CTCCGAACAA CATGGTTAAA TATGCTATTT CATTATCAGG CAACGATTTT CCGAAATATT	7800
	CAGTTAACGA TTGACATGAT TGTTTTACCA TATGAAATAA GGATTGATAA TTTCTTGTA	7860
	AAGGATTTAT TAATTCATCA CGATCCGTTA AGTTATATTT AATCCTATAA AAAGCAGGCG	7920
25	TTAAATGTAA CAAGAGTTGC TGTGATAATT TCTCCTTATC TTCAATGTTA ATAAAAGTGA	7980
	TTTGTTCAAA ATGGTGAATC ATTTGAGCGA TGGCCATCGT TAAATTCGAT ATGCTATCTG	8040
	ATTCCTTGCAA ATCAGTCCAT TGCACACTTG TTGAAAGTAA GTGTAATGTC AAATATAACT	8100
30	TTTCCGCTTC TGGCAAATCC GGCTCATGTT GCGTCATAAT CTCCGTTGCT TGATATTCTT	8160
	TCGTATCCCT CAAATACTGA TAATTAATAT TTAATGGATT CATCACATGA CCACTTTGAA	8220
35	TTCGTCTACG AATCACACAA AGGACATAAG GCAATGAACCT AAGTGATTTG TCTATAAAGC	8280
	GACTCTTCAA AAATTGTTCT ACCTGTTTGA TCTTGCTTTT TTGATATGCG ATATCTTCGA	8340
	ATGtTAAGTT GAGCGCCTTT AAAACTTCAC TTTTAGTAAT ATCATGATTG AACCTTTGAT	8400
40	CAATCAACTT AATGAAGAAA CGGCGAAGTT CAAATTCATC ACCAACAATT TCATAACCAT	8460
	GTTTTCGAGA ATACTTAAGT GACAAACCAT GATTTTCCAA TTGCTCTTTC ACATGATTTA	8520
	TATCGTGAAT GACAGTATTT TTAGTGACTT GTAAATCAAT TGAAAAATGG TTTAGAGACA	8580
45	TTGCGTTTTT CTTACTAAAA AGCATGAGCA TTAAATAATA ACGACGTGTT TCTATGCTAA	8640
	AAATGACATT GTTGCCGTTT AACATTTGCT GCTCCGATAC ATCTCGCTTG AATAACGTCA	8700
	TGATTTCAGA ACTTACAATA AAATTTCTTT GGCTTGTTCT TTCAAGTTTT GGATAACCTT	8760
50	CTTGTTCAAG CCACAAATTG ATTTTTTGAA TGCGATATCC TAGTTGTCTA CGAGACAAAC	8820
	CAAATATCGA TTCAAGTTCT TTACCATGAA TAGTAGGATT CAATACAATT TCTCTGAGTA	8880

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TCAATCGTCA CACCGATGTA CACACTTTGA ACACATATTT TCAAAATGAG CATGTACATC 9000
 ATTGTGATGT TTTAACAACA TTTCAATTAT ATCTATATTT TTTGTGATTT TAATCTTTTA 9060
 5 AAATAAAGCA ATTGAAATTT TTGCATATAT TTTTGTGTTT TGTGTTTTTT TGAAGCATTT 9120
 TTAACATACA TATCTCAATC ATTATCAAAT TGTCATGACC ATTGTAACCC AATACAAAAA 9180
 10 CCCTAAGGAC GCTTATATCA GGCGCCTTAG GGTAACTGT ATCTATTTAA TTAAGTATTA 9240
 TTATTCGTAT GTACGTAAC TATGGTCTAT CAAGTTCCAC ACTTCTTCAA CATCAACTGC 9300
 TGTAGCAAAA TAAGCATTGG CAGGCTTACC TGTAACATGA TTTAAATCGA CAGCCATAGT 9360
 15 GCCATAAGTT AGTGGACTTT GATGTTCAAT GTCGATATTA ACGGGTACCA TTGTAAACAA 9420
 TTCTGGTTGT AACAAATACA AAATTGTACA AGCATCATGT ATTGGACCAC CATCCATATT 9480
 AAAGTGAGTC TTGTATGTCT TCTTAAAGAA TTGCAATAAT TCTACGACGA ACTGTGCAAC 9540
 20 AGGATTATTG ATACTTTCAA AGCGTTCAAT CACGTGATCG TCGGCTAAAA CTTGATGTGT 9600
 TACATCTAAA CCAAACACAT TTATAGTAAT CCCACTTTCA AAAACACGCT TCGCTGCTTC 9660
 AGCATCTACC CAAATATTGA ATTCTGCTGT AGGCGTCCAA TTTCCAAATG TACCACCACC 9720
 25 CATCAAAGTA ATAGATTCAA TATGCTCAGC GATTCTTGGC TCACGAATCA ATGCCGTTGC 9780
 TACATTCGTA AGAGGACCTG TCGCTACAAT TGTTACAGGT GTATCACTCG TCATCACTTT 9840
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 35 TAATATCTCT AGTGGACTGT CAATTGCCCC CGCTAAAATT AATGCTATTG CATCATCGTG 10140
 TCCTEGATCA CAATCCATAA TAATCTTTCT TTTCAATTTAT ATATCCACCT TTCTTAAGTT 10200
 40 GTTATCGATA GCTTATGTAT ATTTATTTAT GTGGTGAATC ATGTTTATTT TGAAAAATAG 10260
 TTTTAACTTT CTCATATTTT TGGATACAAA CACTATTTAT CTATTTTATG GCTTATAAAT 10320
 TTATCCGATA TGCCTTATCA ACCTACCTCG CTAAAAATAG GATGTCTACA TATCTATACC 10380
 45 GACTTTTGTC AACTCATTTT CACAACAATA TAAACAGCAA TTTATATGAT TGTACATGA 10440
 TTCAAACAAT TTTTATGAAA AATAATTTCA TACACAGAAT ATATATTGAT ATTAAATTTT 10500
 TCAAAAGCTA TATTGAGAAT AATTAGGAGG GATGTTGATG AAATCTTTAT TTGAAAAAGC 10560
 50 ACAGCAGTTC GGCAAGTCCT TTATGTTACC TATCGCAATC TTACCAGCTG CAGGTCTATT 10620
 GTTGGGTATC GGTGGTGCAT TAAGTAATCC AAACACCGTT AAAGCATACC CTATTTTAGA 10680

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	AAATTTACCG GTCATCTTTG CAATTGGTGT CGCAATCGGA TTATCTAGAA GCGATAAAGG	10800
	TACTGCAGGT tTAGctGCGC TGCTCGGTTT CTTAATTATG AACGCAACTA TGAATGGCTT	10860
5	ATTAACATATC ACGGGCACAT TGGCAAAAGA TCAGCTTGCA CAAAATGGAC AAGGCATGGT	10920
	GCTCGGTATA CAAACGGTTG AAACCGGTGT TTTTGGCGGG ATTATCACAG GTATTATGAC	10980
	CGCAATACTT CACAACAAAT ATCACAAAGT GGTATTACCA CCGTATTTAG GTTCTTTTG	11040
10	TGGCTCTAGA TTTGTCCCTA TTGTCACAGC ATTTGCCGCA ATCTTTTTAG GTGTATTGAT	11100
	GTTTTTCATT TGGCCAAGCA TACAAGCCGG CATTTATCAT GTTGGTGGAT TTGTAACGAA	11160
	AACAGGTGCC ATCGGTACTT TTGTTTATGG CTTTCATCTA AGATTGTTAG GTCCACTCGG	11220
15	TTTACACCAT ATTTTTTACT TACCGTTTTG GCAGACGGCA CTTGGTGGTA CTTTAGAAGT	11280
	CAAAGGGCAC TTAGTTCAAG GTACGCAGAA CATCTTCTTT GCTCAACTTG GTGATCCAGA	11340
20	TGTGACGAAG TATTATTCAG GTGTGTCACG CTTTATGTCA GGCCGTTTTA TTACGATGAT	11400
	GTTCCGGCTTA TGTGGTGCCG CACTTGCAAT TTATCACACA GCTAAACCTG AACATAAAAA	11460
	AGTTGTCGGC GGTTTAATGT TATCCGCTGC ACTCACTTCA TTTTTAACAG GTATTACCGA	11520
25	ACCTTTAGAG TTTAGTTTCT TGTTTGTGCG ACCTATTCTT TATGTAATCC ATGCCTTCTT	11580
	TGATGGATTA GCATTTATGA TGGCAGACAT TTTCAACATT ACAATTGGTC AAACCTTCAG	11640
	TGGAGGCTTT ATCGATTTCT TACTCTTTGG TGTGCTACAA GGTAATAGTA AAACAAACTA	11700
30	CCTATACGTC ATACCTATTG GAATTGTGTG GTTCTGTTT TATTACATCG TTTTCAGATT	11760
	CTTAATTACG AAATTTAATT TCAAAACACC TGGTCGAGAA GATAAAGCTG CAGCACAACA	11820
	AGTTGAGGCT ACTGAAAGAG CACAACTAT TGTTGCTGGT TTGGGAGGCA AAGATAACAT	11880
35	TGAAATCGTT GACTGTTGTG CAACGAGACT ACGCGTCACA CTTTCATCAA ATGACAAAGT	11940
	CGATAAAGTA TTAATCGAAA GTACTGGTGC CAAAGGTGTA ATCCAGCAAG GCACTGGTGT	12000
40	GCAAGTAATT TATGGGCCTC ACGTTACAGT TATCAAAAAT GAAATTGAAG AATTGCTCGG	12060
	GGATTAAGAC TAACCGAAAT ATCAACAGAA CTAATGGCAA CGATGTACGA AGTAAGAAGT	12120
	GACATCGTTG CTTTTATTTT TAATGTTACA TTTGAAGCAT TAAGTTCATC ATGCACTGTA	12180
45	GTGAGCCCGC AAATCGCCTC TGCTAGACAA TCATCTTAAT GCTATGATTA AAGCTTAAGT	12240
	GCCAGATTTG AATTTAATTT CAACAACGAC TTTCACTACA TTAAAAATAG GGCCACTCGA	12300
	CACATATAGT TGTATCAAAT AGCCCTTTAT ACAATTTTTT GGGTAAGGTT TTACAATTTT	12360
50	TGGGATGGTA TAGATTTTAT AAAAAGTTAT TTAAGTTCTT CTGCTTCAGC CATAATATCT	12420
	TTTAATGTTT TAGCTGAATG TGCGAACTTG CTTTGTCTT CGTCGTTTAA TGGGATTTCT	12480

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	TCCTCATATT CGCCTTCTAA TAATGCTGAT ACAGTCAATA CGGCATCTTC ATTTCTGAAA	12600
	ATCGCTTCAG TAATTCTAGC TAATCCCATT GCAACACCAT AATAAGTGGC ACCTTTAGCT	12660
5	TGAATAATGT CATATGCTGC ATCACGTGTT TGAACAAAAA TTTGTTCAAT TTGCGCTTTG	12720
	CCCTCAGGAC GTTGTTCAG TAATGTCTTC AAAGGTTGAC CCGCAATATT AGCGTGTGAC	12780
10	CATACTGGTA ATTCACTGTC ACCATGTTCA CCAATAATTT GAGCATCGAC GCTACGTGGC	12840
	GCAACATCGn AcgyTcGCTT AACAAATAATC TAAAGCGTGC AGAGTCTAAA ATTGTACCAG	12900
	AACCTATAAC ACGTTCCTTA GGTAACCAG AGAATTTCCA TGTTGCATAC GCTAAAATAT	12960
15	CAACAGGATT TGTAGCTACC AAGAAAATAC CATCAAATTT TGATGCCATT ACTTCACCAA	13020
	CAATTGATTT GAATATTTTC AAGTTTTTAG ATACTAAATC TAAACGTGTT TCTCCAGGTT	13080
	TTTGTGCAGC ACCAGCACAG ATGACAATA GATCCGCATC ATGACAATCA CTGTATTGCG	13140
20	CAGCTTTCAC ACGAACTGTT GTTGGAGAAT ATGGTGTGGC ATGTTTTAAA TCCATAACAT	13200
	CTCCTCGAAC TTTTTCAGTG TCTAAATCAA TGATGACTAA TTCATCAACA ATGCTTTGGT	13260
	TCACTAATGA AAATGCGTAG CTTGAACCTA CTGCACCATT ACCTATTAAT ACAACTTTGT	13320
25	TCCCTTTAAA TTTGTTCAAT ACAAAAACTC CCTTATGATT AATTCATAA CATACTGTA	13380
	GCTTCAAATA TGTTAGTTTA ATGCTGCTTA TTGACGATAC AAAAGCAAAT AAACATCTCT	13440
	TTTATTTTCA ACGCATAACT TAAAAGGTCA TGTGTCATCC GCTTTTAAGT TTGTGATTTA	13500
30	TTTCACATAT AAAATGTAAC ATGCATTAAG TACTGGGTCA ATATTAAAT GTGATTTATT	13560
	TCACATTTTA TTTAATTTT TACACCTTTT TAATTTGTAT mCGATTACAT CTTAGATGTC	13620
35	TTTAGTCTTC GTACTTCGCC AGTGATTATT TACACTTTC CATTTTTATT ATCATGTTTA	13680
	CTTTTTTCTA GGAAAAACAAC AATGTTTTTT GAATTAGTCA AATAAATGCG CTCAATCGTC	13740
	GGTGTGCAA CAGACAATTG TACACAATGC TTATTGATAA GTATTTAAAA AATTAAAAAT	13800
40	GTCATACAAT TATCAAATTT GCCATTTTAT TTATATTTTC TCAAACCAAT TAATTGAATA	13860
	TCGAAATTTT TAGTAGAATA ATCAAAATAT ACAGATTAAA GGAGGAGTAT CATGCTTACA	13920
	GAACAAGAGA AAGACATTAT CAAACAAACG GTGCCTTTAC TTAAAGAGAA AGGGACAGAA	13980
45	ATTACGTCAA TCTTTTATCC AAAAATGTTT AAAGCGCATC CTGAACTTTT AAACATGTTT	14040
	AATCAAACGA ACCAAAAACG AGGCATGCAA TCTTCAGCAT TAGCACAAGC TGTAATGGCC	14100
	GCAGCGGTTA ATATCGATAA CTTAAGTGTT ATTAAACCAG TCATTATGCC AGTCGCATAT	14160
50	AAACACTGCG CACTACAAGT TTATGCTGAA CATTATCCAA TTGTGGGGAA AAATTTATTA	14220
	AAAGCCATTC AAGACGTGAC AGGATTAGAA GAAAATGACC CTGTCATTCA AGCTTGGGCA	14280

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(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8779 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

	GGTATTTTnG GAnGGGTACC TAAAGCAATT CCGGCAAAGG GTnAATCCAG GTACCGAAAT	60
15	GGACTTCCCG TTATCGATAA TACCGACATA TATTGTGACA AGTAGATTTT ATGGACATTT	120
	AGGCTTACTT TTAATTGTGA TAATTGCATG TATGTTTACT GGTATTTATc CaTCaATACA	180
	TATCATTCAA TTATTGATAT ATGTACCGTT TTGTTTTTTC TTAAGTGCCT CGGTGACGTT	240
20	ATTAACATCA AACTCGGTG TGTTAGTTAG AGATACACAA ATGTTAATGC AAGCAATATT	300
	AAGAATATTA TTTTACTTTT CACCAATTTT GTGGCTACCA AAGAACCATG GTATCAGTGG	360
	TTTAATTCAT GAAATGATGA AATATAATCC AGTTTACTTT ATTGCTGAAT CATACCGTGC	420
25	AGCAATTTTA TATCACGAAT GGTATTTTAT GGATCATTGG AAATTAATGT TATACAATTT	480
	CGGTATTGTT GCCATTTTCT TTGCAATTGG TGCGTACTTA CACATGAAAT ATAGAGATCA	540
	ATTTGCAGAC TTCTTGTAAT ATATTTATAT GACGAAACCC CGCTAACCAT TAATAAATGG	600
30	AAGTGGGGTT CATTTTTGTT TATAATTTAA GTAAATAACA TATTAAGTTG GTGTATTATG	660
	AACGTTTTAA TAAAGAAATT TTATCATTTG GTAGTTCGAA TACTTTCTAA AATGATTACG	720
	CCTCAAGTGA TTGATAAACC GCATATCGTA TTTATGATGA CTTTCCAGA AGATATTAAG	780
35	CCTATCATCA AAGCATTAAA TAATTCGTCG TATCAGAAAA CTGTTTTAAC AACACCAAAA	840
	CAAGCGCCTT ATTTATCTGA ACTTAGCGAC GATGTTGATG TGATAGAAAT GACTAATCGA	900
40	ACATTGGTAA AACAAATTAA GGCTTTGAAA AGCGCGCAGA TGATTATTAT CGATAATTAT	960
	TACCTATTGC TAGGTGGATA TAATAAGACT TCTAATCAAC ACATTGTTCA AACGTGGCAT	1020
	GCAAGTGGTG CATTAAAAAA CTTTGGCTTA ACAGATCATC AAGTCGATGT GTCTGACAAG	1080
45	GCAATGGTTC AGCAGTACCG TAAAGTTTAT CAAGCGACGG ATTTTACTTT AGTGGGTGTG	1140
	GAACAAATGT CACAATGTTT TAAACAGTCT TTAGGTGCAA CAGAAGAGCA AATGCTGTAT	1200
	TTTGGGCTTC CGAGAATTAA TAAATATTAC ACAGCTGATA GAGCAACGGT TAAGGCAGAG	1260
50	TTAAAGGATA AATATGGAAT TACAAATAAG TTGGTATTAT ATGTACCAAC ATATAGAGAA	1320
	GATAAAGCAG ATAATAGGGC TATTGATAAA GCTTATTTTG AAAAATGTTT ACCAGGATAT	1380

	ATCGACACGT CTACATTAAT GCTAATGTCA GATATAATTA TTAGCGACTA TAGTTCGCTG	1500
	CCAATAGAAG CTAGCTTGTT AGATATTCCA ACTATATTTT ATGTGTATGA TGAAGGAACA	1560
5	TATGATCAGG TGAGAGGCCT GAATCAATTT TACAAAGCAA TACCGGATAG CTACAAAGTG	1620
	TATACTGAAG AAGATTTAAT AATGACGATA CAAGAAAAAG AACATCTATT AAGTCCGTTA	1680
	TTTAAAGATT GGCATAAGTA TAATACTGAT AAAAGTTTAC ATCAGCTCAC AGAATATATA	1740
10	GATAAGATGG TGACAAAATG AGGTTTACGA TAATCATACC TACATGTAAT AATGAGGCAA	1800
	CAATTCGACA ATTGTTAATA TCTATTGAGA GTAAAGAACA CTATAGAATC CTTTGTATTG	1860
	ATGGTGGTTC TACTGATCAA ACAATTCCTA TGATTGAACG GTTACAAAGA GAACTCAAGC	1920
15	ATATTTTCATT AATACAATTA CAAAATGCTT CGATAGCTAC GTGTATTAAT AAAGGTTTGA	1980
	TGGATATCAA AATGACAGAT CCACATGATA GTGACGCATT TATGGTCATA AAACCAACAT	2040
20	CAATCGTATT GCCAGGTAAA TTAGATAGGT TAACTGCTGC TTTCAAAAAT AATGATAATA	2100
	TTGATATGGT AATAGGGCAG CGAGCTTACA ATTACCATGG TGAATGGAAA TTGAAAAGTG	2160
	CTGATGAGTT TATTAAAGAC AATCGAATCG TTACATTAAC GGAACAACCA GATTGTATTAT	2220
25	CAATGATGTC TTTTGACGGA AAGTTATTCA GTGCTAAATT TGCTGAATTA CAGTGTGaCG	2280
	AAACTTTAGC TAACaCATAC AATCACGCAA TACTTGTCAA GCGCATGCAA AAAGCTACGG	2340
	ATATACATTT AGTTTCACAG ATGATTGTCG GAGATAACGA TATAGATACA CATGCTACAA	2400
30	GTAACGATGA AGATTTTAAT AGATATATCA CAGAAATTAT GAAAATAAGA CAACGAGTCA	2460
	TGGAAATGTT ACTATTACCT GAACAAAGGC TATTATATAG TGATATGGTT GATCGTATTT	2520
	TATTCAATAA TTCATTAAAA TATTATATGA ACGAACACCC AGCAGTAACG CACACGACAA	2580
35	TTCAACTCGT AAAAGACTAT ATTATGTCTA TGCAGCATTG TGATTATGTA TCGCAAAACA	2640
	TGTTTGACAT TATAAATACA GTTGAATTTA TTGGTGAGAA TTGGGATAGA GAAATATACG	2700
40	AATTGTGGCG ACAAAACATTA ATTCAAGTGG GCATTAATAG GCCGACTTAT AAAAAATTCT	2760
	TGATACAAC TAAAGGGAGA AAGTTTGCAC ATCGAACAAA ATCAATGTTA AAACGATAAC	2820
	GTGTACATTG ATGACCATAA ACTGCAATCC TATGATGTGA CAATATGAGG AGGATAACTT	2880
45	AATGAAACGT GTAATAACAT ATGGCACATA TGACTTACTT CACTATGGTC ATATCGAATT	2940
	GCTTCGTCGT GCAAGAGAGA TGGGCGATTA TTTAATAGTA GCATTATCAA CAGATGAATT	3000
	TAATCAAATT AAACATAAAA AATCTTATTA TGATTATGAA CAACGAAAAA TGATGCTTGa	3060
50	ATCAATACGC TATGTCGATT TAGTCATTCC AGAAAAGGGC TGGGGACAAA AAGAAGACGA	3120
	TGTCGAAAAA TTTGATGTAG ATGTTTTTGT TATGGGACAT GACTGGGAAG GTGAATTCGA	3180

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	TAAAATCAAA CAAGAATTAT ATGGTAAAGA TGCTAAATAA ATTATATAGA ACTATCGATA	3300
	CTAAACGATA AATTAACTTA GGTTATTATA AAATAAATAT AAAACGGACA AGTTTCGCAG	3360
5	CTTTATAATG TGCAACTTGT CCGTTTTTAG TATGTTTTAT TTTCTTTTC TAAATAAACG	3420
	ATTGATTATC ATATGAACAA TAAGTGCTAA TCCAGCGACA AGGCATGTAC CACCAATGAT	3480
	AGTGAATAAT GGATGTTCTT CCCACATACT TTTAGCAACA GTATTTGCCT TTTGAATAAT	3540
10	TGGCTGATGA ACTTCTACAG TTGGAGGTCC ATAATCTTTA TTAATAAATT CTCTTGGATA	3600
	GTCCGCGTGT ACTTTACCAT CTTGACTAC AAGTTTATAA TCTTTTTTAC TAAAATCACT	3660
	TGGTAAACA TCGTAAAGAT CATTTC AACATAATTTT TACCATTTA TCCTTTGCTC	3720
15	ACCTTTAGAC AATATTTTTA CATATTTATA CTGATCAAAT GAGCGTTCCA TTAATGCATT	3780
	CCCCATCATA TTACGTTGCT TCTCGCCACC AAGGTTTTTA TAGTCTCCTG CACCCATGAT	3840
20	AACTTGATTA ATTCTAAATT TACCTCGTTT GGTAGTAATC GTATGGTTGT AATTTGCTGT	3900
	ATCACTTGAT CCAGTTTTTA AACCATCTGT ACCCGGCAAA CTCATTTTGT CACCTTCCAA	3960
	TGAAAAGTTG AATGTGTAAT ACGTAACTGC ATGCGTTGTT GGTGCTAACT GCTTTGTAAA	4020
25	GTCTAATATT TTAGGTGTCT CTTTAATCAC GTGTAAATCT AAAATGGCAT AGTCTCTAGC	4080
	AGTCGTTACA GTACGTTCTT GGTCTTTATA CTTTGTGGT GCAAATGTAC GTAATCTTGA	4140
	ATTTTCAGCA CCCGTTGGAT TGACGAAATG TGATTTTTTC ATTCCGATAG CTTTAGCTTT	4200
30	GTTATTCATT AAATCAACGA AATCGCTGGT GTTTTTTGAA ACCTTCTTAG CTAAAATTAA	4260
	TGCCGCGGCA TTAGTAGAAT TAGATACTGT AATTGTGAAT AGGTCTGCCA TTGTCCATAC	4320
	TTGTCCAGGA TATAGTTTCG TATTACTCAA CTCAGGTAGT GTAGACATAA TATATTCTTT	4380
35	GTTTCGTCATT GTGACTGTGT CATCAAGTGA AAGCTGCCCC TTATTTACAG CTTCCAATGT	4440
	TAAGTACATT GTCATTAATT TAGTCATAGA CGCTGGAATC CACTTAGTAT CGATATTGTA	4500
	TTGATACAGT AATTGTCCAG TTTGACTTAC ATTAACAGCA CTCGTGCGTT CGTATGCAGC	4560
40	CGACAAACCT GCATAACCAT ATTGATTTGC TGCTTGTAACA GGGGTTACGT CACTGTTAGT	4620
	AGCTTGTCGA TATGGTGTCA TAATACTTAA TGTTAAACAT AAAATGATGA TAATAGATAT	4680
45	TAAATTTTTC ATAAAGCGTT AATCTTCCCT TTCCAATTC TTAAATATTC CCTAAAAGCA	4740
	ATGGTTATTC CTAATTACGG AAATCATTGC TAATTCATT CACCTTAATT AAATTGTTGA	4800
	AAATAAAGTT TTCTGCAGTT AATTTGAAAA ATAATGCAAA TATATTACGT GTGTAGCTAA	4860
50	AGGTGTTATA ATGTTTGTAC GAAGAGCAAA CTTACTCAA AGCGATTAAT TTTCATGTTT	4920
	TAATATAAAG ACTTTGAGAA GTTATTACAA AAAATGCAAT AGAAATATTC TATCATATAA	4980

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	AAGTATATGA TAGAAATGCA TGTATCTATC TAAATGAATT AACTATAAAT TTCAAACAGA	5100
	AGAGGTAAAA CTATGAAACG AGAAAATCCA TTGTTTTTCT TATTTAAAAA ACTATCATGG	5160
5	CCAGTGGGTC TTATCGTTGC AGCTATCACT ATTTTCATCAC TAGGGAGCTT AAGTGGACTA	5220
	TTAGTGCCAC TGTTTACTGG ACGAATTGTA GATAAATTTT CCgTGAGCCA TATCAATTGG	5280
	AATCtAATCG CATTATTTGG TGGTATCTTT GTCATCAATG CTTTATTAAAG CGGATTAGGT	5340
10	TTATATTTAT TAAGTAAAAT TGGTGAAAAG ATTATTTATG CGATACGCTC AGTTTTATGG	5400
	GAGCATATCA TACAATTAAA AATGCCATTG TTTGACAAAA ATGAAAGTGG TCAATTAATG	5460
15	AGTCGATTAA CTGACGATAC GAAAGTGATA AATGAATTTA TTTACAAAA GCTACCTmAC	5520
	TTATTACCAT CAATCGTTAC ATTAGTTGGG TCACTAATCA TGTTATTTAT TTTAGATTGG	5580
	AAAATGACAT TATTAACATT TATAACGATA CCGATATTG TTTTaATTAT GATTCCTCTA	5640
20	GGTCGTATTA TGCAAAAGAT ATCGACAAGT ACACAATCTG AAATTGCAAA CTTCACTGGT	5700
	TTGTTAGGGC GTGTCCTAAC TGAAATGCGT CTTGTTAAAA TATCAAATAC AGAGCGTCTT	5760
	GAATTAGATA ATGCACATAA AAATTTGAAT GAAATATATA AATTAGGTTT AAAACAGGCT	5820
25	AAAATTGCGG CAGTTGTACA ACCAATTTCA GGTATAGTTA TGTTGCTAAC AATTGCAATT	5880
	ATTTTAGGTT TTGGTGCATT AGAAATTGCG ACTGGTGCAA TCACTGCAGG TACATTAAIT	5940
	GCAATGATAT TTTATGTTAT TCAGTTATCT ATGCCTTTAA TCAATCTTTC CACGTTAGTT	6000
30	ACAGATTATA AAAAGGCAGT CCGTGCAAGT AGTAGAATAT ACGAAATCAT GCAAGAACCT	6060
	ATTGAACCGA CAGAAGCTCT TGAAGATTCT GAAAATGTAT TAATTGATGA CGGTGTATTG	6120
	TCATTTGAAC ATGTAGACTT TAAATATGAT GTGAAGAAAA TATTAGATGA TGTGTCGTTT	6180
35	CAAATCCAC AAGGTCAAGT GAGTGCTTTT GTAGGCCCTT CTGGGTCTGG TAAAAGTACG	6240
	ATATTTAATC TGATAGAACG TATGTATGAA ATTGAGTCAG GTGATATTAA ATATGGCCTT	6300
40	GAAAGTGTCT ATGATATCCC GTTATCTAAG TGGCGACGCA AAATTGGATA TGTTATGCAA	6360
	TCAAATTCGA TGATGAGTGG TACAATTAGA GACAATATTT TATACGGAAT TAATCGTCAT	6420
	GTTTCAGATG AAGAACTTAT TAATTATGCT AAATTAGCGA ACTGTCATGA TTTTATCATG	6480
45	CAATTTGATG AAGGATATGA CACGCTTGTA GGTGAACGAG GATTGAAACT GTCTGGCGGA	6540
	CAACGTCAAC GTATTGATAT TGCTAGAAGT TTTGTTAAAA ATCCTGATAT TTTGTTACTT	6600
	GATGAAGCAA CAGCTAATCT CGATAGTGAA AGTGAATTGA AAATTCAGA AGCTTTAGAA	6660
50	ACATTGATGG AAGGTAGAAC AACGATTGTC ATTGCGCATC GTTTGTCTAC AATTAAAAAA	6720
	GCCGGTCAAA TTATATTCTT AGACAAAGGA CAGGTAACAG GTAAAGGTAC GCATTCAGAA	6780

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	TTTTATATAT ATAAGTAAGC TTGGAGCAAA TACACATATA CCATCGAGGA AATTAAAGTG	6900
	TGGCACATTG ATGGATATAG ATGTTAATAA ATTGCTTCAA GCTTTTGTCT ATTTTAAATC	6960
5	ATTTGAGAAG TTACGACATA ATAATTCTTA AATTAATGAA ATCGATATTT TAAGAAAAAA	7020
	ATGCTCATGG TATAATACAA GTTATAAGCA AACATACATA TATTAAATAC TGTAGCCACG	7080
	AGTCATAATT CTTTCATATTT TACATAGCAA TTTAACTGAT TTTAGAGTCC ACGGTACAGA	7140
10	AGTTTGATAT TTCAATGTTT CTAATTTTTT AAAAAATTAA ATCATAGGTG GGTGCCAAAT	7200
	GTTTTTATTA ATCAACATTA TTGGTCTAAT TGTATTTCTT GGTATTGCGG TATTATTTTC	7260
	AAGAGATCGC AAAAATATCC AATGGCAATC AATTGGGATC TTAGTTGTTT TAAACCTGTT	7320
15	TTTAGCATGG TTCTTTATTT ATTTTGATTG GGGTCAAAAA GCAGTAAGAG GAGCAGCCAA	7380
	TGGTATCGCT TGGGTAGTTC AGTCAGCGCA TGCTGGTACA GGTTTTGCAT TTGCAAGTTT	7440
20	GACAAATGTT AAAATGATGG ATATGGCTGT TGCAGCCTTA TTCCAATAT TATTAATAGT	7500
	GCCATTATTT GATATCTTAA TGTACTTTAA TATTTTACCG AAAATTATTG GAGGTATTGG	7560
	TTGGTTACTA GCTAAAGTAA CAAGACAACC TAAATTCGAG TCATTCTTTG GGATAGAAAT	7620
25	GATGTTCTTA GGAAATACTG AAGCATTAGC CGTATCAAGT GAGCAACTAA AACGTATGAA	7680
	TGAAATGCGT GTATTAACAA TCGCAATGAT GTCAATGAGC TCTGTATCGG GAGCTATTGT	7740
	AGGTGCGTAT GTACAAATGG TACCAGGAGA ACTGGTACTA ACGGCAATTC CACTAAATAT	7800
30	CGTTAACGCG ATTATTGTGT CATGCTTGTT GAATCCAGTA AGTGTTGAAG AGAAAGAAGA	7860
	TATTATTTAC AGTCTTAAAA ACAATGAAGT TGAACGTCAA CCATTCTTCT CATTCTTTGG	7920
	AGATTCTGTA TTAGCAGCAG GTAAATTAGT ATTAATCATC ATCGCATTG TTATTAGTTT	7980
35	TGTAGCGTTA GCTGATCTAT TTGATCGTTT TATCAATTG ATTACAGGAT TGATAGCAGG	8040
	ATGGATAGGC ATAAAAGGTA GTTTCGGTTT AAACCAAATT TTAGGTGTGT TTATGTATCC	8100
	ATTTCGCTA TTAATCGGTT TACCTTATGA TGAAGCGTGG TTGGTAGCAC AACAAATGGC	8160
40	TAAGAAAATT GTTACAAATG AATTTGTTGT TATGGGTGAA ATTTCTAAAG ATATTGCATC	8220
	TTATACACCA CACCATCGTG CGGTTATTAC AACATTCTTA ATTTCAATTG CAAACTTCTC	8280
45	AACGATTGGT ATGATTATCG GTACATTGAA AGGCATTGTT GATAAAAAGA CATCAGACTT	8340
	TGTATCTAAA TATGTACCTA TGATGCTATT ATCAGGTATC CTAGTTTCAT TATTAACAGC	8400
	AGCTTTCGTT GGTTTATTG CATGGTAATA TGTCGAAGAG TGACTATGAT AATACATTTT	8460
50	AACTAATAAA TATGTCCAGG CATGTCGTCT ATTGATATAG GTGAGATGCT TGGACTTTTT	8520
	TATTATTGAT ATAAAGGTAT ATAAATATTT TTAAAGTTAC CGAAATTGAA GCATTATAAA	8580

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GACAGTAAGG ACTAGGTACA GTCATAGTAC TTCGAGCAAA ATTTGTTTTG TTATTATAAA 8700
 CAACACAAAG GAGATAACTT CTCTANTGAA GAAGTTAAAA ACATTATAGC AGACAATGAA 8760
 5 ATGAAAGTAA ATTAAAAAT 8779

(2) INFORMATION FOR SEQ ID NO: 59:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31096 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GTTGCAGTAG TCAAAGAATT AAACAAGGTG AAGGcGTGTA GCTTGCACAC CCGAAAATGT 60
 20 GCGTAAGTTA aCGGATGCAG GACATAAAGT AATTGTTGAA AAAAATGCTG GCATTGGTTC 120
 AGGATTTTCT AACGATATGT ATGAAAAAGA AGGCGCTAAG ATCGTAACTC ACGAACAAGC 180
 ATGGGAAGCT GATCTTGTTA TCAAAGTAAA AGAACCTCAT GAAAGCGAAT ATCAATATTT 240
 25 CAAAAAGAAT CAAATTATCT GGGGATTTTT ACATCTAGCA TCTTCAAAAG AAATAGTAGA 300
 AAAAATGCAA GAAGTTGGTG TAACTGCGAT TAGTGGTGAA ACCATTATAA AAAATGGAAA 360
 AGCAGAATTA TTAGCGCCAA TGAGTGCTAT AGCAGGTCAA CGCTCAGCAA TTATGGGAGC 420
 30 TTACTACTCT GAAGCACAAC ATGGTGGTCA AGGTACTTTA GTGACTGGTG TACATGAAAA 480
 TGTGGATATA CCTGGTAGTA CATATGTGAT TTTCGGTGGT GGAGTAGCAG CAACAAATGC 540
 AGCAAATGTT GCCTTGGGAC TAAATGCTAA AGTAATCATT ATCGAGTTAA ACGATGACCG 600
 35 CATTAAATAT CTTGAAGATA TGTATGCAGA AAAAGATGTC ACAGTAGTCA AATCAACACC 660
 AGAAAATTTA GCAGAACAAA TTAAGAAAGC AGATGTATTT ATTTCTACAA TTTTAATTTT 720
 40 AGGTGCGAAA CCGCCAAAAT TGGTTACTCG TGAGATGGTT AAATCAATGA AAAAAGGTTC 780
 AGTATTAATC GATATAGCTA TTGACCAAGG TGGAACCTATT GAAACAATTA GACCAACTAC 840
 AATTTCTGAT CCAGTGTATG AAGAAGAAGG TGTGATTCAT TATGGTGTAC CAAATCAACC 900
 45 AGGAGCAGTC CCAAGAAGCT CAACAATGGC ATTAGCACAA GGAAATATTG ATTATATATT 960
 AGAAATTTGT GACAAAGGCT TAGAACAAGC AATTAAAGAT AATGAAGCCT TAAGTACTGG 1020
 TGTAAACATT TACCAAGGAC AAGTGACAAA TCAAGGATTA GCTTCATCAC ATGACCTAGA 1080
 50 TTATAAAGAA ATATTAAATG TTATCGAATA GATAGTAATT TAAATGAAAT TGAGTGAAAT 1140
 GAATATTTTA AATATAGCAT TATAGTTTGG ACTAAAAATT TACAAAACGG AAGGATGTAA 1200

	TCGAAGAAGC TAAAGCAAGC ATTAAACCAT TTATTCGTCG AACACCTCTA ATTAAATCAA	1320
	TGTATTTTAAG CCAAAGTATA ACTAAAGGGA ATGTATTTCT AAAATTAGAA AATATGCAAT	1380
5	TCACAGGATC TTTTAAATTT AGAGGCGCTA gCAATnAAAA TTAATCACTT AACAGATGAA	1440
	CAAAAAGAAA AAGGCATTAT CGCAGCATCT GCTGGGgAAC CATGCACAAG GTGTTGCTTT	1500
	AACAGCTAAA TTATTAGGCA TTGATGCAAC GATTGTAATG CCTGAAACAG CACCACAAGC	1560
10	GAAACAACAA GCAACAAAAG GCTATGGGGC AAAGGTTATT TTAAAAGGTA AAAACTTTAA	1620
	CGAAACTAGA CTTTATATGG AAGAATTAGC GAAAGAAAAT GGCATGACAA TCGTTCATCC	1680
	ATATGACGAT AAGTTTGTAA TGGCAGGCCA AGGAACAATT GGTTTAGAAA TTTTAGATGA	1740
15	TATTTGGAAT GTGAATACAG TCATCGTACC AGTTGGCGGT GGAGGATTAA TTGCAGGTAT	1800
	TGCCACCGCA TTAAATCAT TTAACCCTTC AATTCATATT ATCGGTGTTT AATCTGAGAA	1860
20	TGTTTCATGGT ATGGCTGAGT CTTTCTATAA GAGAGATTTA ACTGAACATC GAGTGGATAG	1920
	CACAATAGCA GATGGTTGTG ATGTAAAAGT TCCTGGTGAA CAAACATATG AAGTAGTTAA	1980
	ACATTTAGTA GATGAATTTA TTCTTGTTAC TGAAGAAGAA ATTGAACATG CTATGAAAGA	2040
25	TTTAATGCAG CGTGCCAAAA TTATTACTGA AGGTGCAGGC GCATTACCAA CAGCTGCAAT	2100
	TTTAAGTGGA AAAATAAACA ATAAATGGCT TGAAGATAAA AATGTTGTTG CATTAGTTTC	2160
	AGGCGGGAAT GTTGACTTAA CTAGAGTTTC AGGTGTCATT GAACATGGAC TGAATATTGC	2220
30	AGATACAAGC AAGGGTGTGG TAGGTTAAAA CATTTAATCT TAAAAATGAG GTGTAATTAT	2280
	GTCAAATGGT AAAGAATTAC AAAAAAATAT AGGTTTCTTC TCAGCGTTTG CTATTGTTAT	2340
	GGGGACAGTT ATTGGTTCAG GAGTATTCTT TAAAATATCA AACGTAACAG AAGTAACAGG	2400
35	AACAGCAGGA ATGGCCTTGT TTGTATGGTT CCTAGGCGGC ATCATTACCA TTTGTGCGGG	2460
	GTTAACAGCA GCAGAACTTG CTGCTGCAAT CCTGAAACA GGTGGCTTAA CGAAGTATAT	2520
	AGAATATACA TACGGTGATT TCTGGGGCTT CCTATCAGGT TGGGCGCAAT CATTATTTTA	2580
40	TTTTCCAGCT AACGTAGCAG CATTGTCTAT CGTATTTGCG ACACAGCTAA TTAATTTATT	2640
	CCATTTATCT ATAGGTTTCG TAATACCAAT AGCAATCGCA TCTGCGTTAT CTATTGTGTT	2700
45	GATAAATTTT CTAGGTTCAA AAGCAGGCGG AATTTTACAA TCAGTTACTT TAGTAATTAA	2760
	ACTGATTCCA ATCATCGTTA TTGTAATTTT TGGTATTTTT CAATCTGGAG ATATCACTTT	2820
	TTCAATTAATT CCAACTACAG GTAATTCaGG AAATGGCTTC TTACAGCAA TTGGTAGTGG	2880
50	TTTATTAGCA ACTATGTTTG CATATGATGG TTGGATTCAT GTAGGAAATG TTGCGGGGGA	2940
	ACTTAAAAAT CCTAACGCG ATTTACCTTT AGCGATTTCa GTTGGTATCG GTTGTATTAT	3000

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	TGGTAATTTA AATGCAGCTT CAGATACATC AAAAATATTA TTTGGTGAAA ATGGCGGTAA	3120
	GATTATTACA ATCGGTATAT TAATTTCTGT TTATGGTACG ATCAATGGCT ATACTATGAC	3180
5	TGGTATGCGC GTACCATATG CAATGGCTGA AAGAAAATTA TTGCCATTTA GCCATTTATT	3240
	CGCAAAATTA ACAAATCTG GCGCACCATG GTTTGGCGCA ATTATACAAC TTATAATCGC	3300
	TATCATCATG ATGTCAATGG GAGCATTTGA TACAATTACA AATATGTAA TCTTTGTTAT	3360
10	TTGGTTGTTT TATTGTATGT CATTGTGTC GGTAATAATT TTAAGAAAAC GTGAACCAA	3420
	TATGGAACGA CCATATAAAG TACCGTTATA TCCGATCATA CCTTTAATTG CTATTTTGGC	3480
	AGGATCATTT GTATTAATTA ATACACTGTT TACACAATTT ATATTAGCAA TCATTGGAAT	3540
15	TCTAATAACA GCACTTGGTA TACCAGTTTA TTACTATAAA AAGAAACAAA AAGCAGCATA	3600
	AGGTAAGATA ACTAGCATTG AGAATAAATG GATGGACTAC TAATAAATTT AAAGTTTTAC	3660
20	ACATTAAAAT CAAAAACCAT TCAATTATTC TATGGAACAG ACAAATTTCT GTTATGGAAT	3720
	TTGTCTGTTT TTCAAAAGTA TAGGGAGGCA AATAGAGATG GAAAAGCCGT CAAGAGAGGC	3780
	ATTTGAAGGC AATAATAAGT TGTTAATAGG AATTGTTCTA AGTGAATAA CGTTTTGGCT	3840
25	ATTTGCACAA TCATTGGTTA ATGTTGTACC AATACTTGAA GATAGTTTCA ATACAGATAT	3900
	TGGAACGGTT AATATCGCCG TTAGTATAAC TGCTTTATTT TCAGGAATGT TTGTAGTAGG	3960
	AGCAGGTGGT CTGCTGATA AATATGGCAG AATTAACTC ACGAACATTG GTATTATCTT	4020
30	AAATATATTA GGTTCAATTAT TAATCATTAT TTCAAATATT CCTTTATTAC TTATTATAGG	4080
	AAGATTAATT CAAGGACTTT CAGCAGCATG TATTATGCCT GCAACTTTGT CTATTATTAA	4140
	GTCATATTAC ATTGGGAAAG ATAGACAACG CGCTTTAAGT TATTGGTCAA TTGGCTCATG	4200
35	GGGCGGCTCT GGTGTTTGTT CATTTTTTGG AGGTGCAGTT GCAACGCTTT TAGGTTGGCG	4260
	TTGGATTTTC ATCCTATCAA TTATAATTTT ATTAATTGCA CTGTTTCTTA TTAAAGGCAC	4320
	ACCTGAAACT AAATCTAAAT CGATTTCTCT AAATAAATTT GACATTAAAG GTCTGGTTCT	4380
40	TTTAGTCATT ATGCTCCTCA GTTTAAATAT TTTAATTACT AAAGGATCAG AATTAGGTGT	4440
	AACCTCACTT CTTTTTATTA CTTTATTAGC TATTGCAATT GGATCTTTTA GTTTATTTAT	4500
45	AGTTCTTGAA AAGCGTGCTA CAAATCCTTT AATCGATTTT AAATTATTTA AAAATAAAGC	4560
	TTACACAGGT GCAACAGCTT CAACTTTTTT GTTAAATGGT GTTGCAGGAA CATTAAATAGT	4620
	AGCCAACACA TTTGTTCAAA GAGGTTTAGG ATATTCTTCA TTGCAAGCAG GAAGTTTATC	4680
50	AATCACTTAT TTAGTAATGG TACTAATTAT GATTCGTGTT GGTGAAAAGT TACTTCAAAC	4740
	ACTCGGATGC AAGAAACCAA TGTTAATTGG AACAGGAGTT CTTATTGTCTG GAGAATGTCT	4800

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	ATTCTTTGGT TTAGGACTAG GGATATATGC TACACCATCA ACAGATACAG CAATTGCAAA	4920
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5	TGGAGCATTT GGCCTCGCAT TGAGTGGTGC AGTATATGCA ATCGTATCAA ATATGaCAAA	5040
	CATTTATACA GGTGcAATGa TTGnCATTAT GGTtaAATGC AGGTATGGGa ATATTATCaT	5100
10	TCGTTATCAT TTTGtTACTT GTGcCTAAAC mAAACGACAC TCAATTATGA TAATTGAGAA	5160
	TTAAATTGAA ATCATACAAG TCGCTACAAT ATTAAACAAA AATATAAACC GATTCTTATG	5220
	TGTCATTATT TTAAATGAAC ATAGGGATTG GTTTTTTATT ACTCTTTTAC GCTACTTTAT	5280
15	TTATAATTAT TATAAATTGT CACAAATTCA ATTTACCTTA CAATATATTT TGTGTTATTA	5340
	TATTCTGGAG CATAAATAAA TTGTTCAACA CATAGTTGTA ATGTGTTTCA ATACTTTTTG	5400
	GATAGATTGC GAAATTGTAT TGAATCGTCA TCGTTTTAAA TTTTAAATG AGAATGGAAT	5460
20	GAGCATTACA ATACACAAGC AATCAAAAGT AAATACATTC ACAACACAAC AGAGACATAA	5520
	CAACAAGATA AGGAGTGAAC AATAGCTGTG AATTATCGTG ATAAATTCA AAAGTTTAGT	5580
	ATTCGTAAAT ATACAGTTGG TACATTTTCA ACTGTCATTG CGACATTGGT ATTTTTAGGA	5640
25	TTCAATACAT CACAAGCACA TGCTGCTGAA ACAATCAAC CAGCAAGCGT GGTTAAACAG	5700
	AAACAACAAA GTAATAATGA ACAGACTGAG AATCGAGAAT CTCAAGTACA AAATTCTCAA	5760
	AATTCACAAA ATGGTCAATC ATTATCTGCT ACTCATGAAA ATGAGCAACC AAATATTAGT	5820
30	CAAGCTAATT TAGTAGATCA AAAAGTAGCG CAATCATCTA CTACTAATGA TGAACAACCA	5880
	GCATCTCAAA ATGTAAATAC AAAGAAAGAT TCGGCAACGG CTGCGACAAC ACAACCAGAT	5940
35	AAAGAACAAA GTAAGCATAA ACAAAACGAA AGTCAATCTG CTAATAAAAA TGGAACGAC	6000
	AATAGAGCGG CTCATGTAGA AAATCATGAA GCAAATGTAG TAACAGCTTC AGATTCATCT	6060
	GATAATGGTA ACGTACAACA TGACCGAAAT GAATTACAAG CGTTTTTTGA TGCAAATTAT	6120
40	CATGATTATC GCTTTATTGA CCGTGAAAAT GCAGATTCTG GCACATTTAA CTATGTAAAA	6180
	GGCATTTTTG ATAAGATTAA TACGTTATTA GGCAGTAATG ATCCAATAAA CAATAAGAC	6240
	TTGCAACTTG CATACAAAGA ATTGGAACAA GCTGTTGCTT TAATTCGTAC AATGCCTCAA	6300
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	GCAGAGCCTA GATCAGTATC AGACTATCAA AATGCAAATT CATCATATTA TGTGAAAAT	6420
	GCTAATGATG GTTCGGGCTA TCCTGTTGGT ACATATATCa ATGCTTCTAG TAAAGGGGCG	6480
50	CCATATAATT TACCAACTAC ACCATGGAAT ACATTGAAGG CCTCTGACTC AAAGGAAATT	6540
	GCTCTTATGA CAGCGAAACA AACTGGAGAC GGGTACCAAT GGGTTATTAA GTTTAATAAA	6600

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5	CCTCATCGTT CACATGACTT TAAAATAAGA AATAGAAGTG GCCAAGTAAT ATATGACTGG	6840
	CCAACTGTCC ATATTTATTC TTTAGAAGAT TTATCTAGAG CGAGTGATTA TTTTAGTGAA	6900
	GCTGGAGCGA CACCTGCTAC TAAAGCTTTT GGTAGACAAA ATTTTGAATA TATTAATGGT	6960
10	CAAAAACCTG CTGAATCACC GGGTGTTCCT AAAGTTTATA CTTTCATCGG TCAAGGTGAT	7020
	GCAAGTTATA CAATTTCAAT TAAACACAA GGTCCAACCTG TTAATAAATT GTACTATGCA	7080
	GCAGGTGGGC GTGCTTTAGA GTACAATCAA TTATTTATGT ACAGTCAACT ATACGTCGAA	7140
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	ACGCCGAGTA ATAAAGTGTT AGGATTTTAT TCGAATAATG CAAATACTAA TGCTTTTAGA	7380
	CCGGGTGGAG CCCAACAATT AAATGAATAT CAATTAAGTC AATTATTTAC TGATCAAAAA	7440
25	TTACAAGAAG CAGCAAGAAC TAGAAACCCA ATAAGATTAA TGATTGGTTT CGACTATCCT	7500
	GATGCTTATG GTAATAGTGA ACTTTAGTTC CTGTAACTT AACGGTATTA CCTGAAATCC	7560
	AACATAATAT TAAATTCTTT AAAAATGACG ATACTCAAAA TATTGCTGAA AAACCATTTT	7620
30	CAAAACAAGC TGGGCATCCA GTTTTCTATG TATATGCAGG TAACCAAGGG AATGCTTCCG	7680
	TGAATTTAGG TGGTAGCGTA ACATCTATTC AACCATTACG TATTAATTTA ACAAGTAATG	7740
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35	ACTCGAÇAAA TAGACCTAAT AATGCCAGAG AACGCAATAT TGAACCTGTT GGTAACCTAT	7860
	TACCGGGGGA TTACTTTGGA ACGATACGTT TTGGACGTAA AGAACAATTA TTCGAAATTC	7920
	GTGTTAAACC ACATACACCA ACAATTACAA CGACAGCTGA GCAATTAAGA GGTACAGCAT	7980
40	TACAAAAAGT GCCTGTTAAT ATTTGCGGAA TACCGTTGGA TCCATCGGCA TTGGTTTATT	8040
	TAGTTGCACC AACAAATCAA ACTACGAATG GTGGTAGTGA GGCAGATCAA ATACCATCTG	8100
45	GTTATACGAT ACTTGCGACT GGTACACCTG ATGGGGTGCA TAATACAATT ACTATACGAC	8160
	CGCAAGATTA TGTTGTATTC ATACCACCTG TAGGTAAACA AATTAGAGCA GTAGTTTATT	8220
	ATAATAAAGT AGTTGCATCT AATATGAGTA ATGCTGTTAC TATTTTGCCA GATGACATTC	8280
50	CACCAACAAT CAATAATCCT GTTGGAATAA ATGCCAAATA CTATCGAGGC GACGAACCAA	8340
	CTTTACAATG GGTGTCTCTG ATAGACATTC TGGTATAAAA AATACAACCTA TTACGACATT	8400

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	TACAGGTAGA GTGAGTATGA ATCAGGCATT TAACAGTGAT ATTACATTTA AAGTGTGAGC	8520
	GACAGaCAAT GTCAATAATA CGACAAATGA TAGTCAATCT AAACATGTTT CAATTCATGT	8580
5	AGGTAAATT AGTGAAGATG CTCATCCGAT TGTATTAGGA AATACTGAGA AAGTTGTAGT	8640
	AGTCAATCCG ACTGCTGTAT CTAATGATGA AAAGCAAAGC ATAATTACTG CCTTTATGAA	8700
	TAAAAACCAA AATATAAGAG GATATTTAGC ATCAACTGAT CCAGTAACTG TCGATAATAA	8760
10	TGGTAATGTC ACATTACATT ACCGTGATGG CTCATCGACA ACGCTTGATG CTACAAATGT	8820
	GATGACATAC GAACCAGTTG TGAAACCTGA ATACCAAACT GTCAATGCTG CTAAAACAGC	8880
	AACGGTAACG ATTGCTAAAG GACAATCATT TAGTATTGGT GATATTAAAC AATATTTTAC	8940
15	TTTAAGTAAT GGACAACCTA TTCCAAGTGG CACATTTACA AATATTACAT CTGATAGAAC	9000
	TATTCCAAC TGCACAAGAAG TTAGTCAAAT GAACGCAGGC ACGCAGTTAT ACCATATAAC	9060
20	TGCTACAAAT GCGTATCATA AAGATAGTGA AGACTTCTAT ATTAGTTTGA AAATCATCGA	9120
	TGTGAAACAA CCAGAAGGCG ATCAACGTGT ATATCGTACA TCAACATATG ATTTAACTAC	9180
	TGATGAAATC TCAAAAGTAA AACAAGCATT TATTAAATGCA AATAGAGATG TAATTACGCT	9240
25	TGCCGAAGGT GATATTTTCA TTACAAATAC ACCTAATGGT GCTAATGTAA GTACTATTAC	9300
	AGTAAATATT AATAAAGGTC GATTAAACGAA ATCATTGCGG TCAAACCTAG CTAATATGAA	9360
	TTTCTTGCGT TGGGTTAATT TCCACAAGA TTATACAGTG ACATGGACGA ATGCAAAAAT	9420
30	TGCAACAGA CCAACAGATG GTGGTTTATC ATGGTCTGAT GACCATAAAT CTTTAATTTA	9480
	TCGTTATGAT GCTACATTAG GTACTCAAAT TACGACGAAT GATATTTTAA CAATGTTAAA	9540
	AGCAACAAC TACAGTGCCTG GATTGCGAAA TAACATTACT GGTAATGAAA AATCACAAGC	9600
35	AGAAGCTGGC GGAAGACCTA ACTTTAGAAC GACTGGTTAT TCACAATCAA ATGCGACAAC	9660
	TGATGGTCAA CGTCAATTTA CGTTGAATGG TCAAGTGATT CAAGTGTTAG ACATCATCAA	9720
	CCCTTCAAAC GGTATATGGTG GGCAACCTGT TACAAATTCA AATACTCGTG CAAACCATAG	9780
40	TAAC TCAACT GTTGTTAACG TAAACGAACC GGCAGCTAAT GGTGcTGCGC CATTTACAAT	9840
	TGACCACGTT GTAAAAAGTA ATTCTACACA TAATGCAAGT GATGCAGTTT ATAAAGCACA	9900
45	GTTATACTTA ACGCCATATG GTCCAAAACA ATATGTTGAA CATTTAAATC AAAATACAGG	9960
	AAATACTACT GACGCTATTA ACATTTATTT TGTACCAAGT GACTTAGTGA ATCCAACAAT	10020
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50	TACAGCGAAT GATAACTTTG GTGTGCAATC TGTAAGTGT CCAAATACAT CACAAATTAC	10140
	AGGTACTGTT GATAATAACC ATCAACATGT TTCTGCAACG GCACCAAATG TGACATCAGC	10200

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	GTTCAATGTA ACAGTGAAAC CTTTGCGTGA TAAATATCGA GTTGGTACTT CATCAACGGC	10320
	TGCTAATCCT GTGAGAATTG CCAATATTTC GAATAATGCG ACAGTATCAC AAGCTGATCA	10380
5	AACGACAATT ATTAATTCGT TAACGTTTAC TGAAACAGTA CCAAATAGAA GTTATGCAAG	10440
	AGCAAGTGCG AATGAAATCA CTAGTAAAC AGTTAGTAAT GTCAGTCGTA CTGGAAATAA	10500
	TGCCAATGTg CACAGTAACT GTTACTTATC AAGATGGAAC AACATCAACA GTGACTGTAC	10560
10	CTGTAAAGCA TGTCATTCCA GAAATCGTTG CACATTTCGCA TTACTGTGTA CAAGGCCAAG	10620
	ACTTCCCAGC AGGTAATGGT TCTAGTGCAT CAGATTACTT TAAGTTATCT AATGGTAGTG	10680
	ACATTGCAGA TGCAACTATT ACATGGGTAA GTGGACAAGC GCCAAATAAA GATAATACAC	10740
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20	CCAGAGGTGT TTTATACCCA GGTGTTTCAG ATATGTATGA TGCGAAACAA TATGTTAAGC	10920
	CAGTAAATAA TTCTTGGTCG ACAAATGCGC AACATATGAA TTTCCAATTT GTTGGAACAT	10980
	ATGGTCCTAA CAAAGATGTT GTAGGCATAT CTACTCGTCT TATTAGAGTG ACATATGATA	11040
25	ATAGACAAAC AGAAGATTTA ACTATTTTAT CTAAAGTTAA ACCTGACCCA CCTAGAATTG	11100
	ACGCAAATC TGTGACATAT AAAGCAGGTC TTACAAACCA AGAAATTAAA GTTAATAACG	11160
	TATTAAATAA CTCGTCAGTA AAATTATTTA AAGCAGATAA TACACCATT AATGTCACAA	11220
30	ATATTACTCA TGGTAGCGGT TTTAGTTCGG TTGTGACAGT AAGTGACGCG TTACCAAATG	11280
	GCGGAATTAA AGCAAAATCT TCAATTTCAA TGAACAATGT GACGTATACG ACGCAAGACG	11340
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	GCGACGGTTT TGATTTTCGGA CACGTAGAAA GATTATTCA AAACCCGCCA CATGGGGCAA	11520
	CGGTTGCATG GCATGATAGT CCAGATACAT GGAAGAATAC AGTCGGTAAC ACTCATAAAA	11580
40	CTGCGGTTGT AACATTACCT AATGGTCAAG GTACGCGTAA TGTGAAGTT CCAGTCAAAG	11640
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	CTGCAGCATG GGCAAATAGA CAACAACCAA ATAACCAACA AGCAGGCGTG CAACATTTAA	11820
	ATGTCGATGT CACATATCCA GGTATTTTCAG CTGCTAAACG AGTTCCTGTT ACTGTTAATG	11880
50	TATATCAATT TGAATTCCT CAAACTACTT ATACGACAAC GGTGGAGGC ACTTTAGCAA	11940
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	TGAATAAACC GAATGTGGCT AAAGTCGTTA ACGCAAATA TGACGTCATC TATAACGGAC	12120
	ATACTTTTGC AACATCTTTA CCAGCGAAAT TTGTAGTAA AGATGTGCAA CCAGCGAAAC	12180
5	CAACTGTGAC TGAAACAGCG GCAGGAGCGA TTACAATTGC ACCTGGAGCA AACCAAACAG	12240
	TGAATACACA TGCCGGTAAC GTAACGACAT ACGCTGATAA ATTAGTTATT AAACGTAATG	12300
10	GTAACGTTGT GACGACATTT ACACGTCGCA ATAATACGAG TCCATGGGTG AAAGAAGCAT	12360
	CTGCAGCAAC TGTAGCAGGT ATTGCTGGAA CTAATAATGG TATTACTGTT GCAGCAGGTA	12420
	CTTTCAACCC TGCTGATACA ATTCAAGTTG TTGCAACGCA AGGAAGCGGA GAGACAGTGA	12480
15	GTGATGAGCA ACGTAGTGAT GATTTTCACAG TTGTGCGACC ACAACCGAAC CAAGCGACTA	12540
	CTAAGATTG GCAAAATGGT CATATTGATA TCACGCCTAA TAATCCATCA GGACATTTAA	12600
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25	ATCCAAGTAC ATTAAGTCA CCGGCAGCTC ATACTGTCAA CACAAGTAA ATTGTGAAAG	12900
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	GTACTGCAAC GATTAAAAAT GGCACAGCAA TGCCTACTAA TTTAGCTGGT GGTAGCACAA	13020
30	CGACGATTCC TGTGACAGTA ACTTACAATG ATGGTAGTAC TGAAGAAGTA CAAGAGTCCA	13080
	TTTTCACAAA AGCGGATAAA CGTGAGTTAA TCACAGCTAA AAATCATTTA GATGATCCAG	13140
	TAAGCACTGA AGGTAAAAAG CCAGGTACAA TTACGCAGTA CAATAATGCA ATGCATAATG	13200
35	CGCAACAACA AATCAATACT GCGAAAACAG AAGCACAACA AGTGATTAAAT AATGAGCGTG	13260
	CAACACCACA ACAAGTTTCT GACGCACTAA CTAAAGTTCG TGCAGCACAA ACTAAGATTG	13320
40	ATCAAGCTAA AGCATTACTT CAAAATAAAG AAGATAATAG CCAATTAGTA ACGTCTAAAA	13380
	ATAACTTACA AAGTTCGTG AACCAAGTAC CATCAACTGC TGGTATGACG CAACAAAGTA	13440
	TTGATAACTA TAATGCGAAG AAGCGTGAAG CAGAACTGA AATAACTGCA GCTCAACGTG	13500
45	TTATTGACAA TGGCGATGCA ACTGCACAAC AAATTCAGA TGAAAAACAT CGTGTGCGATA	13560
	ACGCATTAAC AGCATTAAC CAAGCGAAAC ATGATTTAAC TGCAGATACA CATGCCTTAG	13620
	AGCAAGCAGT GCAACAATTG AATCGCACAG GTACAACGAC TGGTAAGAAG CCGGCAAGTA	13680
50	TTACTGCTTA CAATAATTCG ATTCGTGCAC TTCAAAGTGA CTTAACAAGT GCTAAAAATA	13740
	GCGCTAATGC TATTATTCAA AAGCCAATAA GAACAGTACA AGAAGTGCAA TCTGCGTTAA	13800

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	CTGATAATAG	TGCTTTAAAA	ACTGCTAAGA	CGAAACTTGA	TGAAGAAATC	AATAAATCAG	13920
	TAACTACTGA	TGGTATGACA	CAATCATCAA	TCCAAGCATA	TGAAAATGCT	AAACGTGCGG	13980
5	GTCAAACAGA	ATCAACAAAT	GCACAAAATG	TTATTAACAA	TGGTGATGCG	ACTGACCAAC	14040
	AAATTGCCGC	AGAAAAAACA	AAAGTAGAAG	AAAAATATAA	TAGCTTAAAA	CAAGCAATTG	14100
	CTGGATTAAAC	TCCAGACTTG	GCACCATTAC	AAACTGCAAA	AACTCAGTTG	CAAAATGATA	14160
10	TTGATCAGCC	AACGAGTACG	ACTGGTATGA	CAAGCGCATC	TATTGCAGCA	TTAATGAAA	14220
	AACTTTCAGC	AGCTAGAACT	AAAATTCAAG	AAATTGATCG	TGTATTAGCC	TCACATCCAG	14280
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	ATTTAGATCA	TGCACGTCAA	GCTTTAACAC	CAGATAAAGC	GCCGCTTCAA	ACTGCGAAAA	14640
25	CGCAATTAGA	ACAAAGCATT	AATCAACCAA	CGGATACAAC	AGGTATGACG	ACCGCTTCGT	14700
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	TGTTGAATGG	CAACCCAAC	GTCCAAAATA	TCAATGATAA	AGTGACAGAG	GCAAACCAAG	14820
30	CTAAGGATCA	ATTAAATACA	GCACGTCAAG	GTTTAACATT	AGATAGACAG	CCAGCGTTAA	14880
	CAACATTACA	TGGTGCATCT	AACTTAAACC	AAGCACAACA	AAATAATTTT	ACGCAACAAA	14940
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35	ATACTGCGAT	GACGAAATTA	AAAGACAGTG	TTGCGGATAA	TAATACAATT	AAATCAGATC	15060
	AAAATTACAC	TGACGCAACA	CCAGCTAATA	AACAAGCGTA	TGATAATGCA	GTTAATGCGG	15120
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40	AAGCAGCATC	TGTTAAATCG	ACGAAAGATG	CTTTAGATGG	TCAACAAAAC	TTACAACGTG	15240
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	AAACGACTCA	AAGCTTAAAT	ACTGCTATGA	CAGGTTTAAA	ACGTGGCGTT	GCTAATCATA	15420
	ACCAAGTCGT	ACAAAGTGAT	AATTATGTCA	ACGCAGATAC	TAATAAGAAA	AATGATTACA	15480
50	ACAATGCATA	CAACCATGCG	AATGACATT	TTAATGGTAA	TGCACAACAT	CCAGTTATAA	15540
	CACCAAGTGA	TGTTAACAAT	GCTTTATCAA	ATGTCACAAG	TAAAGAACAT	GCATTGAATG	15600

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	ATTAAATAA	TGCACAACGT	CAAACTTAC	AATCGCAAAT	TAATGGTGCG	CATCAAATTG	15720
	ATGCAGTTAA	TACAATTAAG	CAAAATGCAA	CAAACTTGAA	TAGTGCAATG	GGTAACTTAA	15780
5	GACAAGCTGT	TGCAGATAAA	GATCAAGTGA	AACGTACAGA	AGATTATGCG	GATGCAGATA	15840
	CAGCTAAACA	AAATGCATAT	AACAGTGCAG	TTTCAAGTGC	CGAAACAATC	ATTAATCAAA	15900
	CAACAAATCC	AACGATGTCT	GTTGATGATG	TTAATCGTGC	AACTTCAGCT	GTTACTTCTA	15960
10	ATAAAATGC	ATTAAATGGT	TATGAAAAAT	TAGCACAATC	TAAACAGAT	GCTGCAAGAG	16020
	CAATTGATGC	ATTACCACAT	TTAAATAATG	CACAAAAAGC	AGATGTTAAA	TCTAAAATTA	16080
	ATGCTGCATC	AAATATTGCT	GGCGTAAATA	CTGTTAAACA	ACAAGGTACA	GATTTAAATA	16140
15	CAKCGATGGg	TAAGTTGCAA	GGTGCAATCA	ATGATGAACA	AACGACGCTT	AATAGTCAAA	16200
	ACTATCAAGA	TGCGACACCT	AGTAAGAAAA	CAGCATACAC	AAATGCGGTA	CAAGCTGCCA	16260
20	AAGATATTTT	AAATAAATCA	AATGGTCAAA	ATAAAACGAA	AGATCAAGTT	ACTGAAGCGA	16320
	TGAATCAAGT	GAATTCTGCT	AAAAATAACT	TAGATGGTAC	GCGTTTATTA	GATCAAGCGA	16380
	nCAAaCAGCA	AAACAGCAGT	TAAATAATAT	GACGCATTTA	ACAACTGCAC	AAAAAACGAA	16440
25	TTTAACAAAC	CAAATTAATA	GTGGTACTAC	TGTCGCTGGT	GTTCAAACGG	TTCAATCAAA	16500
	TGCCAATACA	TTAGATCAAG	CCATGAATAC	GTTAAGACAA	AGTATTGCCA	ACAAAGATGC	16560
	GACTAAAGCA	AGTGAAGATT	ACGTAGATGC	TAATAATGAT	AAGCAAACAG	CATATAACAA	16620
30	CGCAGTAGCT	GCTGCTGAAA	CGATTATTAA	TGCTAATAGT	AATCCAGAAA	TGAATCCAAG	16680
	TACGATTACA	CAAAAAGCAG	AGCAAGTGAA	TAGTTCTAAA	ACGGCACTTA	ACGGTGATGA	16740
	AAACTTAGCT	GCTGCAAAAC	AAAATGCGAA	AACGTACTTA	AACACATTGA	CAAGTATTAC	16800
35	AGATGCTCAA	AAGAACAATT	TGATTAGTCA	AATTACTAGT	GCGACAAGAG	TGAGTGGTGT	16860
	TGATACTGTA	AAACAAAATG	CGCAACATCT	AGACCAAGCT	ATGGCTAGCT	TACAGAATGG	16920
	TATTAACAAC	GAATCTCAAG	TGAAATCATC	TGAGAAATAT	CGTGATGCTG	ATACAAATAA	16980
40	ACAACAAGAG	TATGATAATG	CTATTACTGC	AGCGAAAGCG	ATTTTAAATA	AATCGACAGG	17040
	TCCAAACACT	GCGCAAAATG	CAGTTGAAGC	AGCATTACAA	CGTGTTAATA	ATGCGAAAGA	17100
45	TGCATTGAAT	GGTGATGCAA	AATTAATTGC	AGCTCAAAAC	GCAGCGAAAC	AACATTTAGG	17160
	TACTTTAACG	CATATCACTA	CAGCTCAACG	TAATGATTTA	ACAAATCAAA	TTTCACAAGC	17220
	TACAACTTA	GCTGGTGTG	AATCTGTTAA	ACAAAATGCG	AATAGTTTAG	ATGGTGCTAT	17280
50	GGGTAACCTA	CAAACGGCTA	TCAACGATAA	GTCAGGAACA	TTAGCGAGCC	AAAACCTCTT	17340
	GGATGCTGAT	GAGCAAAAAC	GTAATGCATA	CAATCAAGCT	GTATCAGCAG	CCGAAACCAT	17400

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	TGTTAATAAT GCGAAACATG CATTAAATGG TACGCAAAAC TTAAACAATG CGAAACAAGC	17520
	AGCGATTACA GCAATCAATG GCGCATCTGA TTAAATCAA AAACAAAAG ATGCATTAAA	17580
5	AGCACAAGCT AATGGTGCTC AACGCGTATC TAATGCACAA GATGTACAGC ACAATGCGAC	17640
	TGAACTGAAC ACGGCAATGG GCACATTAAA ACATGCCATC GCAGATAAGA CGAATACGTT	17700
	AGCAAGCAGT AAATATGTTA ATGCCGATAG CACTAAACAA AATGCTTACA CAACTAAAGT	17760
10	TACCAATGCT GAACATATTA TTAGCGGTAC GCCAACGGTT GTTACGACAC CTTCAGAAGT	17820
	AACAGCTGCA GCTAATCAAG TAAACAGCGC GAAACAAGAA TTAAATGGTG ACGAAAGATT	17880
	ACGTGAAGCA AAACAAAACG CCAATACTGC TATTGATGCA TTAACACAAT TAAATACACC	17940
15	TCAAAAAGCT AAATTAAAAG AACAAAGTGGG ACAAGCCAAT AGATTAGAAG ACGTACAAAC	18000
	TGTTCAAACA AATGGACAAG CATTGAACAA TGCAATGAAA GGCTTAAGAG ATAGTATTGC	18060
20	TAACGAAACA ACAGTCAAAA CAAGTCAAAA CTATACAGAC GCAAGTCCGA ATAACCAATC	18120
	AACATATAAT AGCGCTGTGT CAAATGCGAA AGGTATCATT AATCAAATA ACAATCCGAC	18180
	TATGGATACT AGTGCGATTA CCCAAGCTAC AACACAAGTG AATAATGCTA AAAATGGTTT	18240
25	AAACGGTGCT GAAAACCTAA GAAATGCACA AAACACTGCT AAGCAAACT TAAATACATT	18300
	ATCACACTTA ACAAATAACC AAAAACTGC CATCTCATCA CAAATTGATC GTGCAGGTCA	18360
	TGTGAGTGAG GTAAC TGCTA CTA AAAATGC AGCAACTGAG TTGAATACGC AAATGGGTAA	18420
30	CTTGGAACAA GCTATCCATG ATCAAAACAC AGTTAAACAA AGTGTTAAAT TTAATGATGC	18480
	AGATAAGCT AAACGTGATG CGTATACAAA TGCGGTAAAGC AGAGCTGAAG CAATTCTGAA	18540
	TAAACGCAA GGTGCAAATA CGTCTAAACA AGATGTTGAA GCGGCTATTC AAAATGTTTC	18600
35	AAGTGCTAAA AATGCATTGA ATGGTGATCA AAACGTTACA AATGCGAAGA ATGCAGCTAA	18660
	AAATGCATTA AATAACTTAA CGTCAATTAA TAATGCACAA AAACGTGACT TAACAACTAA	18720
	AATTGATCAA GCAACAAC TGCTGGTGT TGAAGCTGTA TCTAATACGA GTACACAATT	18780
40	GAATACAGCG ATGGCTAACT TGCAAAATGG TATTAATGAT AAAACAAATA CACTAGCAAG	18840
	TGAAAACATAT CATGATGCTG ATTCAGATAA GAAAAC TGCT TATACTCAAG CCGTTACGAA	18900
45	CGCAGAAAAT ATTTTAAATA AAAATAGTGG ATCAAATTTA GACAAAAC TG CCGTTGAAAA	18960
	CGCGTTGTCA CAAGTTGCTA ATGCGAAAGG TGCCCTAAAT GGTAACCATA ATTTAGAGCA	19020
	AGCTAAATCA AATGCAAACA CTACTATAAA CGGACTTCAA CATTTAACAA CTGCTCAAAA	19080
50	AGATAAATTG AAACAACAAG TGCAACAAGC ACAAATGTT GCAGGTGTAG ATACTGTTAA	19140
	ATCAAGTGCC AACACATTAA ATGGTGCTAT GGGTACGTTA AGAAATAGCA TACAAGATAA	19200

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	TAACAATGCT GTTGATAGTG CTAATGGTGT CATTAAATGCA ACAAGCAATC CAAATATGGA	19320
	TGCTAATGCA ATTAACCAAA TCGCTACACA AGTGACATCA ACGAAAAATG CATTAGATGG	19380
5	TACACATAAT TTAACGCAAG CGAAACAAAC AGCAACAAAT GCCATCGATG GTGCTACTAA	19440
	CTTAAATAAA GCGCAAAAAG ATGCGTTAAA AGCACAAAGTT ACAAGTGCGC AACGTGTTGC	19500
	AAATGTAACA AGTATCCAAC AAACGTGAAA TGAACCTAAT ACAGCTATGG GTCAATTACA	19560
10	ACATGGTATT GATGATGAAA ATGCAACAAA ACAAACTCAA AAATATCGTG ACGcTGAACA	19620
	AAGTAAGAAA ACTGCTTATG ATCAAGCTGT AGCTGCTGCG AAAGCAATTT TAAATAAACA	19680
	AACAGGTTCA AATTCAGATA AAGCAGCAGT TGACCGTGCA TTACAACAAG TAACAAGTAC	19740
15	GAAAGATGCA TTGAATGGTG ATGCAAAACT GGCAGAAGCG AAAGCGGCAG CTAAACAAAA	19800
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20	TCAAGCGACG ACTGTTGATG GCGTTAATAC TGTA AAAACA AATGCCAATA CATTAGACGG	19920
	CGCAATGAAT AGCTTACAAG GTTCAATCAA TGATAAAGAT GCGACATTAA GAAATCAAAA	19980
	TTATCTTGAT GCGGATGAAT CAAAACGAAA TGCATATACG CAAGCTGTCA CAGCGGCTGA	20040
25	AGGCATTTTA AATAACAAA CTGGTGGTAA CACATCTAAA GCAGACGTTG ATAATGCATT	20100
	AAATGCAGTT ACAAGAGCGA AAGcGgCTTT AAATGGTGCT GACAACTTAA GAAATGCGAA	20160
	AACTTCAGCA ACAAAATACGA TTGATGGTTT ACCTAACTTA ACACAATTAC AAAAAACAA	20220
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	AGGTAATACG TTAAATACTG CCATGGGTGC ATTACGTACA AGTATCCAAA ATGATAATAC	20340
	GACGAAAACA AGTCAAAATT ATCTTGATGC ATCTGACAGC AACAAAAATA ATTACAATAC	20400
35	TGCTGTAAAT AATGCAAATG GTGTTATTAA TGCAACGAAC AATCCAAATA TGGATGCTAA	20460
	TGCGATTAAAT GGCATGGCAA ATCAAGTCAA TACAACAAA GCAGCGTTAA ATGGTGCACA	20520
40	AAACTTAGCT CAAGCTAAAA CAAATGCGAC GAACACAATT AACACGCAC ATGACTTAAA	20580
	CCAAAAACAA AAAGATGCAT TAAAAACACA AGTTAACAAT GCACAACGTG TATcTGATGC	20640
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45	TATTGCTGAT AAAGAAAGAA CAAAAGCAAG CGGTAATTAT GTCAATGCTG ATCAAGAAAA	20760
	ACGTCAAGCG TATGATTCAA AAGTGACTAA CGCTGAAAAT ATCATTAGTG GTACACCGAA	20820
	TGCGACATTA ACAGTCAATG ACGTAAATAG TGCGGCATCA CAAGTCAATG CGGCTAAAAC	20880
50	AGCATTAAAT GGTGATAACA ACTTACGTGT AGCGAAAGAG CATGCCAACA ATACAATTGA	20940
	CGGCTTAGCA CAATTGAATA ATGCACAAAA AGCAAAATTA AAAGAACAAG TTCAAAGTGC	21000

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	GAAAGGCTTA AGAGATAGTA TTGCGAATGA AGCAACAATT AAAGCAGGTC AAAACTACAC	21120
	TGACGCAAGT CCAAATAATC GTAACGAGTA CGACAGTGCA GTTACTGCAG CAAAAGCAAT	21180
5	CATTAATCAA ACATCGAACC CAACGATGGA ACCAAATACT ATTACGCAAG TAACATCACA	21240
	AGTGACAACCT AAAGAACAGG CATTAAATGG TGCGCGAAAC TTAGCTCAAG CTAAGACAAC	21300
	TGCGAAAAAC AACTTGAATA ACTTAACATC AATTAACAAT GCACAAAAAG ATGCGTTAAC	21360
10	GCGTAgcATT GATGGTGCAA CAACAGTAGC TGGTGTAAT CAAGAACTG CAAAAGCAAC	21420
	AGAATTAAAT AACGCAATGC ATAGTTTACA AAATGGTATC AATGATGAGA CACAAACAAA	21480
	ACAACTCAG AAATACCTAG ATGCAGAGCC AAGTAAGAAA TCAGCTTATG ATCAAGCAGT	21540
15	AAATGCAGCG AAAGCAATTT TAACAAAAGC TAGTGGTCAA AATGTAGACA AAGCAGCAGT	21600
	TGAACAAGCA TTGCAAAATG TGAACAGTAC GAAGACGGCG TTGAACGGTG ATGCGAAATT	21660
20	AAATGAAGCT AAAGCAGCTG CGAAACAAAC GTTAGGTACA TTAACACACA TTAATAATGC	21720
	ACAACGTACA GCGTTAGACA ATGAAATTAC ACAAGCAACA AATGTTGAAG GTGTTAATAC	21780
	AGTTAAAGCC AAAGCGCAAC AATTAGATGG TGCTATGGGT CAATTAGAAA CATCAATTCG	21840
25	TGATAAAGAC ACGACGTTAC AAAGTCAAAA TTATCAAGAT GCTGATGATG CTAAACGAAC	21900
	TGCTTATTCT CAAGCAGTAA ATGCAGCAGC AACTATTTTA AATAAAACAg CTGGCGGTAA	21960
	TACACCTAAA GCAGATGTTG AAAGAGCAAT GCAAGCTGTT ACACAAGCAA ATACTGcATT	22020
30	AAACGGTATT CAmAACTTAG ATCGTGCGAA ACaGCTGCT AACACAGCGA TTACAAATGC	22080
	TTCGGACTTA AATACAAAAC mAAAAGAAGC ATTAAAAgCA CAAGTAACAA GTGCAGGACG	22140
	TGTATCTGCA GCAAATGGTG TTGAACATAC TGCGACTGAA TTAAATACTG CGATGACAGC	22200
35	TTTAAAGCGT GCCATTGCTG ATAAAGCTGA GACAAAAGCT AGTGGTAACT ATGTCAATGC	22260
	TGATGCGAAT AAACGTCAAG CATATGATGA AAAAGTTACA GCTGCCGAAA ATATCGTTAG	22320
	TGGTACACCA ACACCAACGT TAACACCAGC AGATGTTACA AATGCAGCAA CGCAAGTAAC	22380
40	GAATGCTAAG ACGCAGTTAA ACGGTAATCA TAATTTAGAA GTAGCGAAAC AAAATGCTAA	22440
	CACTGCAATT GATGGTTTAA CTTCTTTTAAA TGGTCCGCAA AAAGCAAAAC TTAAAGAACA	22500
45	AGTGGGTCAA GCGACGACGT TGCCAAATGT TCAAAGTGT CGTGATAATG CACAAACATT	22560
	AAACACTGCA ATGAAAGGTC TACGAGATAG CATTGCGAAT GAAGCAACGA TTAAAGCAGG	22620
	TCAAACTAC ACAGATGCAA GTCAAAACAA ACAAACTGAC TACAACAGTG CAGTCACTGC	22680
50	AGCAAAAGCA ATCATTGGTC AAACAAC TAGTCCATCAATG AATGCGCAAG AAATTAATCA	22740
	AGCGAAAGAC CAAGTGACAG CTAAACAACA AGCGTTAAAC GGTCAAGAAA ACTTAAGAAC	22800

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	AGATGCAGTG AAACGTCAAA TCGAAGGTGC AACGCATGTT AATGAAGTAA CACAAGCACA	22920
	AAATAATGCG GATGCATTAA ATACAGCTAT GACGAACTTG AAAAATGGTA TTCAAGATCA	22980
5	GAATACGATT AAGCAAGGTG TTAAC TTCAC TGATGCCGAC GAAGCGAAAC GTAATGCATA	23040
	TACAAATGCA GTGACGCAAG CTGAACAAAT TTTAAATAAA GCACAAGGTC CAAATACTTC	23100
	AAAAGACGGT GTCGAAACTG CGTTAGAAA TGTACAACGT GCTAAAAACG AATTGAACGG	23160
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	AATTAATAAT GCACAAAAAG AAGCATTGAA ATCACAATT GAAGGTGCGA CAACAGTTGC	23280
	AGGTGTAAAT CAAGTGCTA CAACGGCATC TGAATTAAAT ACAGCAATGA GCAACTTACA	23340
15	AAATGGTATT AATGATGAAG CAGCTACAAA AGCAGCGCTT AATGGTACTC AAAACCTTGA	23400
	AAAAGCTAAA CAACACGCAA ATACAGCAAT TGACGGTTTA AGCCATTTAA CAAATGCACA	23460
20	AAAAGAGGCA TTAACAAT TGGTACAACA ATCGACTACT GTTGAGAAG CACAAGGTAA	23520
	TGAGCAAAAA GCAACAATG TTGATGCAGC AATGGACAAA TTACGTCAA GTATTGCAGA	23580
	TAATGCGACA ACAAACAAA ACCAAAATTA TACTGATGCA AGTCAGAATA AAAAGGATGC	23640
25	GTACAATAAT GCTGTCACAA CTGCACAAGG TATTATTGAT CAACTACAA GTCCAACCTT	23700
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	TGGTAATGAA AACCTAGAGG CAGCGAAACA ACAAGCGTCA CAATCATTAG GTTCATTAGA	23820
30	TAACCTAAAT AATGCGCAA AACAAACAGT TACTGATCAA ATTAATGGCG CGCATACTGT	23880
	TGATGAAGCA AATCAAATTA AGCAAAATGC GCAAACTTA AATACAGCGA TGGGTAACCT	23940
	GAAACAAGCG ATAGCTGACA AAGATGCTAC GAAAGCGACA GTTAACCTCA CTGATGCAGA	24000
35	TCAAGCAAAA CAACAAGCAT ATAACA CTGC TGTACAAAT GCTGAAAATA TCATTTCAAA	24060
	AGCTAATGGC GGCAATGCAA CACAAGCTGA AGTTGAACAA GCAATCAAAC AAGTTAATGC	24120
	TGCAAAACAA GCATTAAATG GTAATGCCAA CGTTCAACAT GCAAAAGACG AAGCAACAGC	24180
40	ATTAATTAAT AGCTCTAATG ACCTTAACCA AGCACA AAAA GACGCATTAA AACAACAAGT	24240
	TCAAAATGCA ACTACTGTAG CTGGTGTA AA CAATGTTAAA CAAACAGCAC AAGAGTTAAA	24300
45	CAATGCTATG ACACAATTAA AACAAGGCAT TGCAGATAAA GAACAAACAA AAGCTGATGG	24360
	TAACCTTGTC AATGCAGATC CTGATAAGCA AAATGCATAT AATCAAGCAG TAGCGAAAGC	24420
	TGAAGCATT ATTAGTGCTA CGCCTGATGT TGTCGTTACA CCTAGCGAAA TTA CTGCAGC	24480
50	GTAAATAAA GTTACGCAAG CTAAAAATGA TTAAATGGT AATACAACT TAGCAACGGC	24540
	GAAACAAAAT GTTCAACATG CTATTGATCA ATTGCCAAAC TTAAACCAAG CGCAACGTGA	24600

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	AGCGGCGACA ACGCTTAATG ACGCGATGAC ACAATTGAAA CAAGGTATTG CGAATAAAGC	24720
	ACAAATTAAA GGTAGCGAGA ACTATCACGA TGCTGATACT GACAAGCAAA CAGCATATGA	24780
5	TAATGCAGTA ACAAAGCAG AAGAATTGTT AAAACAAACA ACAAATCCAA CAATGGATCC	24840
	AAATACAATT CAACAAGCAT TAACTAAAGT GAATGACACA AATCAAGCAC TTAACGGTAA	24900
	TCAAAAATTA GCTGATGCCA AACAAGATGC TAAGACAACA CTTGGTACAC TAGATCATTT	24960
10	AAATGATGCT CAAAAACAAG CGCTAACAAAC TCAAGTTGAA CAAGCACCAG ATATTGCAAC	25020
	AGTTAATAAT GTTAAGCAAA ATGCTCAAAA TCTGAATAAT GCTATGACTA ACTTAAACAA	25080
	TGCATTACAA GATAAACTG AGACATTAAA TAGCATTAAAC TTTACTGATG CAGATCAAGC	25140
15	TAAGAAAGAT GCTTATACTA ATGCGGTTTC ACATGCAGAA GGTATTTTAT CTAAAGCAAA	25200
	TGGCAGCAAT GCAAGTCAAA CTGAAGTGGA ACAAGCGATG CAACGTGTGA ACGAAGCGAA	25260
20	ACAAGCATTG AATGGTAATG ACAATGTACA ACGTGCAAAA GATGCAGCGA AACAAAGTGAT	25320
	TACAAATGCA AATGATTTAA ATCAAGCAAT GACACAATTG AAACAAGGTA TTGCAGATAA	25380
	AGACCAAACCT AAAGCAAATG GTAACCTTGT CAATGCTGAT ACTGATAAGC AAAATGCTTA	25440
25	CAACAATGCG GTAGCACATG CTGAACAAAT AATTAGTGGT ACACCAAATG CAAACGTGGA	25500
	TCCACAACAA GTGGCTCAAG CGTTACAACA AGTGAATCaA GCTAAGGGTG ATTTAAACGG	25560
	TAACCATAAC TTACAAGTTG CTAAAGACAA TGCAAATACA GCCATTGATC AGTTACCAAA	25620
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	ACAACAAATT CAAGCGAACA GTCAAGTACC ACAGTCAGTT GACTTTACAC AAGCGGATCA	25800
35	AGACAAACAA CAAGCATATA ACAATGCGGC TAACCAAGCG CAACAAATCG CAAATGGCAT	25860
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	GAAAGATGCA TTAAACGGTG ATGAAAAATT AGCACAAGCG AAACAAGAAG CTTTAGCAAA	25980
40	TCTTGATACG TTACGCGATT TAAATCAACC ACAACGTGAT GCATTACGTA ACCAAATCAA	26040
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45	aGCaATGAGT AACTTGAAAC aAGGTATTGC aAACAAAGAT ACTGTCAAAG CAAGTGAGAA	26160
	CTATCATGAT GCTGATGCCG ATAAGCAAAC AGCATATACA AATGCAGTGT CTCAAGCGGA	26220
	AGGTATTATC AATCAAACGA CAAATCCAAC GCTTAACCCA GATGAAATAA CACGTGCATT	26280
50	AACTCAAGTG ACTGATGCTA AAAATGGCTT AAACGGTGAA GCTAAATTGG CAACTGAAAA	26340
	GCAAAATGCT AAAGATGCCG TAAGTGGGAT GACGCATTTA AACGATGCTC AAAAAACAAGC	26400

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	AGCAACGAGC CTAGATCAAG CAATGGATCA ATTATCACAA GCTATTAATG ATAAAGCTCA	26520
	AACATTAGCG GACGGTAATT ACTTAAATGC AGATCCTGAC AAACAAAATG CGTATAAACA	26580
5	GGCAGTAGCA AAAGCTGAAG CATTATTGAA TAAACAAAGT GGTACTAATG AAGTACAAGC	26640
	ACAAGTTGAA AGCATCACTA ATGAAGTGAA CGCAGCGAAA CAAGCATTAA ATGGTAATGA	26700
	CAATTTGGCA AATGCAAAAC AACAAGCAAA ACAACAATTG GCGAACTTAA CACACTTAAA	26760
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	CACTACGATT AATCAAAAAG CACAAACGTT AGATCATGCG ATGGAATTAT TAAGAAATAG	26880
	TGTTGCGGAT AATCAAACGA CATTAGCGTC TGAAGATTAT CATGATGCAA CTGCGCAAAG	26940
15	ACAAAATGAC TATAACCAAG CTGTAACAGC TGCTAATAAT ATAATTAATC AAACCTACATC	27000
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	TCAATTAGAT CATTTGAATA ATGCGCAAAA GCAACAGTTA CAATCACAAA TTACGCAATC	27180
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25	GGGTAACCTTA ATTAATGCGA TTGCAGATCA TCAAGCCGTT GAACAACGTG GTAACCTCAT	27300
	CAATGCTGAT ACTGATAAAC AAACCTGCTTA TAATACAGCG GTAAATGAAG CAGCAGCAAT	27360
	GATTAACAAA CAACTGGTC AAAATGCGAA CCAAACAGAA GTAGAACAAG CTATTACTAA	27420
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	TGCGACGCAA GCAATTGATG CTTTAAACAAG CTTAAATGAT CCTCAAAAAA CAGCATTAAA	27540
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35	TACGCTTAAC CAAGCAATGC ATGGTTTAAG ACAGAGCATT CAAGATAACG CAGCAACTAA	27660
	AGCAAATAGC AAATATATCA ACGAAGATCA ACCAGAGCAA CAAAACCTATG ATCAAGCTGT	27720
40	TCAAGCCGCA AATAATATTA TCAATGAACA AACTGCAACA TTAGATAATA ATGCGATTAA	27780
	TCAAGCAGCG ACAACTGTGA ATACAACGAA AGCAGCATT AATGGTGATG TGAAGTTACA	27840
	AAATGATAAA GATCATGCTA AGCAAACGGT TAGTCAATTA GCACATCTAA ACAATGCACA	27900
45	AAAACATATG GAAGATACGT TAATTGATAG TGAAACAAC TTAAGCAAGA	27960
	TTTGAAGTAA GCACAAGCAT TAGATCAACT TATGGATGCA TTACAACAAA GTATTGCTGA	28020
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	CAATAAAGGT AATGTATCAA GTGCGACTCA AGCAGTAATA TCATCTAAAA ATGCATTAGA	28200

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	TCAATTAACA CCAGCTCAAC AACAAAGCGCT AGAAAAATCAA ATTAATAATG CAACAACCTCG	28320
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10	TGCTAAAAAC AATTTACATG GTGATCAAAA ACTAGCTCAA GATAAGCAAC GTGCAACAGA	28620
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	CAAGTTTATC AATGAAGATA AaCCaCmAAA AGrTGCTTAC CAAGCAGCAG TTCAAATGC	28860
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	GACACAAGCT GTTAACCAAG CTAAAGATAA CCTACACGGT GATCAAAAAC TTGCAGACGA	28980
	TAAACAACAT GCGGTTACTG ATTTAAATCA ATTAAATGGT TTGAATAATC CGCAACGTCA	29040
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	TGAAGCAAAA GCGCTTGATC AAGCAATGCA AGCATTACGT AATAGTATTC AAGATCAACA	29160
	ACAAACAGAA TCTGGTAGCA AGTTTATCAA TGAAGATAAA CCGCAAAAAG ATGCTTACCA	29220
30	AGCAGCAGTT CAAAATGCAA AAGATTTAAT TAACCAAACA GGTAATCCAA CACTCGACAA	29280
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	TCAAAAACCTT GCTCGTGATC AACACAAGC AGTAACAACCT GTAAATGCAT TGCCAAAACCT	29400
35	AAATCATGCA CAACAACAAG CATTAACTGA TGCTATAAAT GCAGCGCCTA CAAGAACAGA	29460
	GGTTGCACAA CATGTTCAAA CTGCTACTGA ACTTGATCAC GCGATGGAAA CATTGAAAAA	29520
40	TAAAGTTGAT CAAGTGAATA CAGATAAGGC TCAACCAAAT TACACTGAAG CGTCAACTGA	29580
	TAAAAAAGAA GCAGTAGATC AAGCGTTACA AGCTGCAGAA AGCATTACAG ATCCAACTAA	29640
	TGGTTCAAAT GCGAATAAAG ACGCTGTAGA CCAAGTATTA ACTAAGCTTC AAGAAAAAGA	29700
45	AAATGAGTTA AATGGTAATG AGAGAGTCGC TGAAGCTAAA ACACAAGCGA AACAACTAT	29760
	TGACCAATTA ACACATTTAA ATGCTGATCA AATTGCAACT GCTAAACAAA ACATTGATCA	29820
	AGCGACGAAA CTTCAACCAA TTGCTGAATT AGTAGATCAA GCAACGCAAT TGAATCAATC	29880
50	TATGGATCAA TTACAACAAG CAGTTAATGA ACATGCTAAC GTTGAGCAAA CTGTAGATTA	29940
	CACACAAGCA GATTCAGATA AACAAAATGC TTATAAACAA GCTATTGCTG ATGCTGAAAA	30000

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TGCAAAACAA GCATTAAATG GTGATGAACG TGTAGCACTT GCTAAAACAA ATGGTAAACA 30120
 TGACATCGAC CAATTGAATG CATTAAACAA TGCTCAACAA GATGGATTTA AAGGTCGCAT 30180
 5 CGATCAATCA AACGATTTAA ATCAAATCCA ACAAATTGTA GATGAGGCTA AGGCACTTAA 30240
 TCGTGCAATG GATCAATTGT CACAAGAAAT CACTGACAAT GAAGGACGCA CGAAAGGTAG 30300
 CACGAACTAT GTCAATGCAG ATACACAAGT CAAACAAGTA TATGATGAAA CGGTTGATAA 30360
 10 AGCGAAACAA GCACTTGATA AATCGACTGG TCAAACTTA ACTGCAAAAC AAGTTATCAA 30420
 ATTAAATGAT GCAGTCACTG CAGCTAAGAA AGCATTAAAT GGTGAAGAAA GACTTAATAA 30480
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 15 ACAATTAGCA ATCCAACAAA TTAATAATGC TGAAACGCTA AATAAAGCAT CTCGAGCAAT 30600
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 20 GCACCTTGGT GTTATCAGCA GCACAAATTA CATCAATGCA GATGACAATT TGAAAGCAAA 30720
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 TGCaaaAGCT GAAGCAGAGC AATTGAAACA AAATATTATC GATGCTCAAA ATGCATTAAA 30840
 25 TGGAGACCAA AACCTTGCAA ATGCCAAAGA TAAAGCAAAT GCGTTTGTTA ATTCGTTAAA 30900
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 30 GAAACATTTA GTTGACAATG AAATTCCAAA TGCAGAGCAA ACTGTCAATT ACCAAAACGC 31080
 TGACGATAAT GCTAAA 31096

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

45 ATGACAGAAT GGGAGCGAGG ACTTAGAATG TTTCCTAAAT CAGGTTTATT AAATTTTGAG 60
 TTAGCGATAG mAAATCGTTC ATTAAATGAT GATGAAAAAG CATTAAAATA TGTGCGTAAA 120
 GCATTAAATG CAGACCCTAA AAATACAGAT TATATTAAGT TAGAAAAAGA GTTGACTAAA 180
 50 TCAAATGAGT CGAAAAATAA ATAACCTTTA TGATGTACAA CAGTTATTGA AAAGTTACGG 240
 ATTTCTAATA TATTTTAAAA ATCCAGAAGA TATGTACGAA ATGATTCAAC AGGAGATTTC 300

	TAATCAGAGA AGGAATGAAC AGAAATGACA AAAATTATTT TAGCAGCTGA TGTAGGCGGG	420
	ACGACTTGTA AATTAGGTAT TTTCACACCT GAATTAGAAC AATTACATAA ATGGTCTATT	480
5	CACACTGATA CATCTGATAG TACAGGATAT ACACTTTTGA AAGGAATTTA TGATTTCGTTT	540
	GTTGAAAAAG TAAATGAAAA TAATTATAAT TTTTCAAATG TACTTGCCGT AGGTATTGGT	600
	GTACCAGGTC CTGTTGACTT TGAAAAAGGT ACAGTAAATG GAGCAGTAAA CTTATATTGG	660
10	CCAGAAAAAG TTAATGTACG TGAGATTTT GAACAATTCG TTGATTGTCC AGTGATGTGA	720
	GATAATGATG CTAACATAGC TGCTTTAGGG GaGAAACACA AAGGTGCTGG TGAAGGTGCC	780
	GATGATGTTG TTGCCATCAC ACTTGGTACA GGTCTAGGTG GAGGAATTAT TTCCAAATGG	840
15	TGAAATCGTA CATGGTCATA ATGGCTCtGG CGCAGAAATA GGTCAATTTA GAgCAGACTT	900
	CgATCAACGA TTTaAATGTA ATTGTGGTCG TTCTGGATGT ATTGAAACAG TTGCTTCaGC	960
20	GACAGGCGTT GTTAACTTAG TTAACCTCtA CTATCCGAAG TTGACGTTTA GATCTTCTAT	1020
	ATTAGAATTG ATTAAAGAAA ATAAGGTtAC aGCAAAAGCT GTTTTTGATG CGGCAAAAGC	1080
	TGGTGACCAA TTCTGTATTT TCATTACTGA AAAGGTTGCA AACTATATTG GATATTTATG	1140
25	TAGTATTATT AGTGTTACAA GTAATCCGAA ATATATCGTT CTAGGTGGAG GAATGTCTAC	1200
	TGCAGGACCT ATTTTAATTG AAAATATTAA AACAGAATAT CATAATTTAA CATTTGCACC	1260
	TGCTCAATTT GAAACTGAAA TTGTACAAGC GAAATTAGGT AATGATGCAG GTATTACAGG	1320
30	AGCAGCAGGA TTAATCAAGA CCTATGTATT AGATAAAGAG GGGGTAAAAT AATGGCTATT	1380
	GTTGATGTGG TTGTTATTCC AGTTGGAACG GAAGGTCCGA GTGTTAGTAA ATATATTGCA	1440
	GATATTCAGA AAAAaCTTCA AGAATATAAA GCAATGGGTA AAATTGATTT TCAATTAACA	1500
35	CCAATGAATA CTCTAATTGA AGGTGAATTA AGCGATGTAT TAGAAGTTGT GCAAGTGATA	1560
	CATGAATTAC CTTTTGATAA AGGTTTAAGT AGAGTTTGTA CAAATATCCG TATTGATGAC	1620
	CGACGAGACA AATCTAGAAA AATGAATGAT AAACTAACAT CAGTACAAAA ACATTTAGAA	1680
40	AATAGTGGTG AAAACCTATG AGGATTTCAA GCTTAACTTT AGGCTTAGTT GATACTAATA	1740
	CGTATTTTCA CGAAAATGAC AAAGCTGTTA TTCTGATTGA CCCTTCAGGT GAAAGTGAAA	1800
45	AAATTATTAA AAAATTAAAC CAAATAAATA AACCGTTAAA AGCTATTTTA TTAACACATG	1860
	CACACTTTGA TCATATCGGA GCAGTCGATG ATATAGTTGA TCGATTCGAT GTCCCGGTTT	1920
	ATATGCATGA AGCAGAGTTT GATTTTCTAA AAGATCCCGT TAAAAATGGG GCAGATAAAT	1980
50	TTAAGCAATA TGGATTACCA ATTATTACAA GTAAGGTAAC TCCTGAAAAG TTAAmCGAAG	2040
	GTAGCACAGA AATAGAAGGA TTTAAGTTnT nAyrTGTaCA CACACCTGGA CATTACCAG	2100

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GAATCGGACG TACAGATTTA TATAAAGGTG ATTATGAAAC GCTAGTTGAT TCTATTCAAG 2220
 ATAAAATATT TGAATTAGAA GGC 2243

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8009 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

TTGGnATCAT tyAcgGTAAA AAGAATAAaG CAAGATTtAT TTCATTAGTA CTAATTTGTG 60
 CAATGTTTGC AATTTGTTGG GTTGCATATA TTCAATGGGA GTCTACAATC GCTTCATTTA 120
 CACAATCTAT TAATATTTCa ATGGCACAAT ATAGTGTTTT ATGGACAATT AACGGAATAA 180
 TGATTTTAGT AGCACAAACCA TTAATTAAAC CGATTCTCTA TCTGTTAAAA GGAAACTTAA 240
 AGAAGCAAAT GTTTGTCCGC ATCATCATTT TTATGTTGTC GTTCTTTGTC ACGAGTTTTG 300
 CCGAAAACCTT TACAATATTT GTTGTCCGTA TGATTATTTT AACTTTTGGG GAAATGTTTG 360
 TATGGCCAGC AGTTCCAACCT ATAGCCAATC AGTTAGCGCC AGATGGTAAG CAAGGACAGT 420
 ACCAAGGTTT TGTGAATTCA GCTGCTACAG TAGGAAAAGC ATTTGGTCCA TTTCTTGGTG 480
 GTGTATTAGT TGATGCGTTT AATATGCGCA TGATGTTTAT CCGTATGATG CTACTACTTG 540
 TATTTGCATT AATATTATTA ATGGTTTTCa AGGAGAATAA TACGCAACCT AAAAAAATAG 600
 ATGCATAATG AGTAAATAGA ATTAACGTTA TAGACTTGAA ATAAATGTCG TTATAACATA 660
 ATATTAAATTT GTATAATTTA ATTTTCGTTTG GAGCTTTTCT ACAGAAAGCT AGTGATGCTG 720
 AGAGCTAGTG TTAAGGACTA AATGTAAATC GTATTAAATTT TAAATTGAAT GAATGACATC 780
 TCTTACTATT AAAATGAGTG CACAATTTTT GTGAAATAGG GTGGTAACGC GGCAAATGTC 840
 GTCCCTATGT AAATAGAATA GTTAGAGGTG TCTTTTTTAT TGAATAGGAG GAAATGTGTT 900
 GAATTACAAC CACAATCAAA TTGAAAAGAA ATGGcAAGAC TATTGGGACG AAAATAAAAC 960
 ATTTAAAACA AATGATAACT TAGGTCAAAA GAAATTTTAT GCTTTAGACA TGTTTCCATA 1020
 TCCATCAGGT GCTGGTTTAC ATGTTGGACA TCCTGAGGGc TATACAGCAA CAGATATCAT 1080
 TTCAAGATAT AAAAGAATGC AAGGATATAA TGTATTACAT CCGATGGGGT GGGATGCATT 1140
 CGGATTACCA GCAGAGCAAT ATGCTTTAGA CACTGGCAAC GACCCACGTG AATTTACAAA 1200
 GAAAAATATC CAAACTTTTA AACGACAAAT TAAAGAATTA GGGTTCAGTT ATGATTGGGA 1260

	GTTATATAAC AAAGGTTTAG CATACGTTGA TGAAGTTGCA GTTAACTGGT GTCCAGCATT	1380
	AGGCACTGTT TTATCTAACG AAGAAGTGAT TGATGGTGTC TCTGAACGTG GTGGACATCC	1440
5	AGTTTATCGT AAGCCGATGA AACAATGGGT ACTTAAATC ACAGAATATG CAGATCAATT	1500
	ATTAGCAGAT TTAGATGATT TAGATTGGCC TGAGTCTTTA AAAGATATGC AGCGCAATTG	1560
	GATTGGACGT TCTGAAGGGG CCAAAGTTTC ATTTGATGTA GATAATACGG AAGGAAAAGT	1620
10	AGAAGTATTT ACGACTAGAC CAGATACAAT CTATGGTGCA TCATTCTTAG TCTTAAGTCC	1680
	TGAACATGCA TTAGTTAATT CAATTACAAC AGATGAATAT AAAGAAAAAG TAAAAGCTTA	1740
	TCAAACAGAA GCTTCTAAAA AGTCAGATTT AGAACGTACA GATTTAGCAA AAGATAAATC	1800
15	AGGTGTATTT ACTGGTGCAT ATGCAACTAA TCCTTTATCT GGTGAAAAAG TACAAATTTG	1860
	GATTGCTGAT TATGTATTAT CAACATATGG TACTGGAGCA ATTATGGCAG TACCAGCGCA	1920
20	TGATGACAGA GATTATGAAT TTGCTAAAAA GTTTGATTG CCAATCATTG AAGTCATCGA	1980
	AGGTGGAAT GTTGAAGAAG CAGCATACAC TGGTGAAGGT AAACATATTA ATTCTGGTGA	2040
	ACTTGATGGT TTAGAAAAATG AAGCGGCAAT TACTAAAGCT ATTCAATTAT TAGAGCAAAA	2100
25	AGGTGCTGGC GAAAAGAAAG TTAATTACAA ATTAAGAGAT TGGTTATTCA GTCGTCAGCG	2160
	TTATTGGGGC GAACCAATTC CTGTCATTCA TTGGGAAGAT GGAACAATGA CAACTGTTCC	2220
	TGAAGAAGAG CTACCATTGT TGTTACCTGA AACAGATGAA ATCAAGCCAT CAGGGACTGG	2280
30	TGAGTCTCCA CTAGCTAATA TTGATTCATT TGTAATGTT GTAGATGAAA AAACAGGTAT	2340
	GAAAGGACGT CGTGAAACAA ATACAATGCC ACAATGGGCA GGTAGTTGTT GGTATTATTT	2400
	ACGTTACATC GATCCTAAAA ATGAAAATAT GTTAGCAGAT CCTGAAAAAT TAAAACATTG	2460
35	GTTACCTGTT GATTTATATA TCGGTGGAGT AGAACATGCG GTTCTTCACT TATTATATGC	2520
	AAGATTTTGG CATAAAGTCC TTATGATTT GGCTATCGTA CCTACTAAAG AACCTTTCCA	2580
	AAAATTATTT AACCAAGGTA TGATTTTAGG AGAAGGTAAT GAGAAGATGA GTAAATCTAA	2640
40	AGGAAATGTA ATCAATCCTG ATGATATAGT ACAGTCTCAT GGTGCAGATA CTTGCGTCT	2700
	TTACGAAATG TTTATGGGAC CTTTAGATGC TGCAATTGCA TGGAGTGAAA AAGGATTAGA	2760
45	TGGGTCTCGT CGATTCTTAG ATCGCGTATG GCGTTTAATG GTAAATGAAG ATGGGACATT	2820
	GAGTTCAAAA ATTGTAAC TAATAATAA ATCTTTAGAT AAAGTTTATA ACCAACTGT	2880
	TAAAAAGGTA ACAGAAGACT TTGAAACATT AGGATTTAAT ACTGCTATTA GTCAATTAAT	2940
50	GGTATTTATT AATGAGTGTT ATAAAGTTGA TGAAGTTTAT AAACCTTACA TTGAAGGCTT	3000
	CGTTAAAAATG TTAGCACCTA TTGCACCACA TATCGGTGAA GAATTATGGT CAAAATTAGG	3060

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	TGATGAAGTA GAAATCGTTG TTCAAGTGAA TGGTAAATTG AGAGCTAAAA TTAAAATTGC	3180
	TAAAGATACA TCAAAAGAAG AAATGCAAGA AATTGCCTTA TCTAATGACA ATGTTAAAGC	3240
5	GAGTATTGAA GGTAAAGACA TCATGAAAGT CATCGCTGTT CCTCAAAAAT TAGTCAATAT	3300
	TGTAGCTAAA TAATGTTTTA AGGAGGACTT TGAAATGAAG TCAATTACTA CAGATGAATT	3360
	AAAAAATAAA CTTT TAGAAT CTAAACCAGT TCAAATTGTT GATGTTCGTA CTGATGAAGA	3420
10	AACAGCAATG GGATATATTC CTAATGCAAA GTTAATTCCA ATGGATACCA TTCCGGATAA	3480
	TTTAAATTCA TTTAATAAAA ATGAAATATA TTATATTGTA TGTGCTGGTG GAGTTCGAAG	3540
	CGCTAAAGTT GTAGAATATT TAGAGGCAAA TGGCATTGAT GCCGTAAATG TCGAAGGCGG	3600
15	CATGCACGCA TGGGGCGATG AAGGTTTGGA AATAAAAAGT ATTTAAAGTA GTGACATAAT	3660
	TTAAATAAT ATTACATTTG TAATGACACC AAGTAACGTT TCGGTTGCTT GGTGTTTTTT	3720
20	GGTATGAATT ACTTTCTGTT ACAAACAAT CTAAAGCGTT CTGTTATGT TTTATTAAGA	3780
	TTTTAATTAC AAAACGGAAA CTAAATTGTA ATAAATAAAA ACTTTATTTT ATAAATGAT	3840
	GATGATAAAA TTGAGTGAAC TTAAATATT GTACAAAATA ATATAGCTAT AAATATAATA	3900
25	TAGCTATAAA TATAATATGA GGGAGCGTAT ATTTT TAGCA TAATTCTTAA CAACACAGCA	3960
	GAGAACAGAC AACCAGGAGG AAAATGAAAT GAATTTGTTA AAGAAAAATA AATATAGTAT	4020
	TAGGAAGTAT AAAGTAGGCA TATTCTCTAC TTTAATCGGA ACAGTTTTAT TACTTTCAA	4080
30	CCCAAATGGT GCACAAGCCT TAACTACGGA TAATAATGTA CAAAGCGATA CTAATCAAGC	4140
	AACACCTGTA AATTCACAAG ATAAAGATGT TGCTAATAAT AGAGGTTTAG CAAATAGTGC	4200
	GCAGAATACA CCTAATCAAT CTGCAACAAC CAATCAAGCA ACGAATCAAG CATTGGTTAA	4260
35	TCATAATAAT GGTAGTATAG TAAATCAAGC TACGCCAACA TCAGTGCAAT CAAGTACGCC	4320
	TTCAACACAA AACAATAATC ATACAGATGG CAATACAACA GCAACTGAGA CAGTGTCAAA	4380
40	CGCTAATAAT AATGATGTAG TGTCGAATAA TACCGCATT AATGTACCAA CTAAAACAAA	4440
	TGAAAATGGT TCAGGAGGAC ATCTAACTTT AAAGGAAATT CAAGAAGATG TTCGTCATTC	4500
	TTCAAATAAA CCAGAGCTAG TTGCAATTGC TGAACCAGCA TCTAATAGAC CGAAAAAGAG	4560
45	AAGTAGACGT GCGGCACCGG CAGATCCTAA TGCAACTCCA GCAGATCCAG CGGCTGCAGC	4620
	GGTAGGAAAC GGTGGTGAC CAGTTGCAAT TACAGCGCCA TATACGCCAA CAACTGATCC	4680
	TAATGCCAAT AATGCAGGAC AAAATGCACC TAACGAAGTG CTGTCAATTG ATGACAATGG	4740
50	TATTAGACCA AGTACCAACC GTTCTGTGCC AACAGTAAAC GTTGTTAATA ACTTGCCGGG	4800
	CTTCACACTA ATCAATGGTG GCAAAGTAGG GGTGTTTAGT CATGCAATGG TAAGAACGAG	4860

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	TCGTATACAT	GGAAGTACATA	CGAATGACCA	TGGCGATTTT	AATGGTATCG	AGAAAGCATT	4980
	AACAGTAAAT	CCGAATTCTG	AATTAATCTT	TGAATTTAAT	ACAATGACTA	CTAAAAACGG	5040
5	TCAAGGCGCA	ACAAATGTTA	TTATCAAAAA	TGCTGATACT	AATGATACGA	TTGCTGAAAA	5100
	GACTGTTGAA	GGCGGTCCAA	CTTTGCGTTT	ATTTAAAGTA	CCTGATAATG	TGAGAAATCT	5160
	CAAAATTCAA	TTTGTAACCTA	AAAATGACGC	AATAACAGAT	GCGCGTGGCA	TTTATCAACT	5220
10	AAAAGATGGT	TACAAATACT	ATAGCTTTGT	TGACTCTATC	GGACTTCATT	CTGGGTCACA	5280
	TGTTTTTGTT	GAAAGACGAA	CAATGGATCC	AACAGCAACA	AATAATAAAG	AGTTTACTGT	5340
	AACAACATCA	TTAAAGAATA	ATGGTAATTC	TGGTGCTTCT	CTAGATACAA	ATGACTTTGT	5400
15	ATATCAAGTT	CAATTACCTG	AAGGTGTTGA	ATATGTGAAC	AATTCATTGA	CTAAAGATTT	5460
	TCCAAGTAAC	AATTCAGGCG	TTGATGTTAA	TGATATGAAT	GTTACATATG	ATGCAGCAAA	5520
20	TCGTGTGATA	ACAATTAAAA	GTACTGGAGG	AGGTACAGCA	AACTCTCCGG	CACGACTTAT	5580
	GCCTGATAAA	ATACTCGATT	TAAGATATAA	ATTACGTGTA	AATAATGTGC	CGACACCAAG	5640
	AACAGTAACA	TTTAACGAGA	CATTAACGTA	TAAAACATAT	ACACAAGATT	TCATTAATTC	5700
25	AGCTGCAGAA	AGTCATACTG	TAAGTACAAA	TCCATATACT	ATCGATATCA	TCATGAATAA	5760
	AGATGCATTA	CAAGCCGAAG	TTGACAGACG	TATTCAACAA	GCTGATTATA	CATTTGCGTC	5820
	ATTAGATATC	TTTAATGGTC	TGAAACGACG	CGCACAAACG	ATTTTAGATG	AAAATCGTAA	5880
30	CAATGTACCA	TTAAATAAAA	GAGTTTCTCA	AGCATATATT	GATTCATTAA	CTAATCAAAT	5940
	GCAACATACG	TTAATTCGAA	GTGTTGATGC	TGAAAATGCA	GTTAATAAAA	AAGTTGACCA	6000
	AATGGAAGAT	TTAGTTAATC	AAAATGATGA	ATTGACAGAT	GAAGAAAAAC	AAGCAGCAAT	6060
35	ACAAGTTATC	GAGGAACATA	AAAATGAAAT	AATTGGTAAT	ATTGGTGACC	AAACGACTGA	6120
	TGATGCGGTT	ACTAGAATCA	AAGATCAAGG	TATACAGACC	TTAAGTGGGG	ATACTGCAAC	6180
	ACCGGTTGTT	AAACCAAATG	CTAAAAAAGC	AATACGTGAT	AAAGCAACGA	AACAAAGGGA	6240
40	AATTATCAAT	GCAACACCAG	ATGCTACTGA	AGACGAGATT	CAAGATGCAC	TAAATCAATT	6300
	AGCTACGGAT	GAAACAGATG	CTATTGATAA	TGTTACGAAT	GCTACTACAA	ATGCTGACGT	6360
45	TGAAACAGCT	AAAAATAATG	GCATCAATAC	TATTGGAGCA	GTTGTTCTCT	AAGTAACTCA	6420
	TAAAAAAGCT	GCAAGAGATG	CAATTAACCA	AGCAACAGCA	ACGAAAAGAC	AACAAATAAA	6480
	TAGTAATAGA	GAAGCAACTC	AGGAAGAGAA	AAATGCAGCA	TTGAACGAAT	TAECTCAAGC	6540
50	AACCAACCAT	GCTTTAGAAC	AAATCAATCA	AGCAACAACA	AATGCTAATG	TTGATAACGC	6600
	CAAAGGAGAT	GGTCTAAATG	CCATTAATCC	AATTGCTCCT	GTAAGTGTG	TTAAGCAAGC	6660

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TGATGCGACT CAAGAAGAAA GACAAGCAGC AATTGACAAA GTGAATGCTG CTGTAAGTGC 6780
 AGCAAACACA AACATTTTAA ACGCTAATAC CAATGCTGAT GTTGAACAAG TAAAGACAAA 6840
 5 TGCGATTCAA GGAATACAAG CAATTACACC AGCTACAAAA GTAAAAACAG ATGCAAAAAA 6900
 TGCCATCGAT AAAAGTGCGG AAACGCAACA TAATACGATA TTTAATAATA ATGATGCGAC 6960
 GCTCGAAGAA CAACAAGCAG CACAACAATT ACTTGATCAA GCTGTAGCCA CAGCGAAGCA 7020
 10 AAATATTAAT GCAGCAGATA CGAATCAAGA AGTTGCACAA GCAAAAGATC AGGGCACACA 7080
 AAATATAGTA GTGATTCAAC CGGCAACACA AGTTAAAACG GATACTCGCA ATGTTGTAAA 7140
 TGATAAAGCG CGAGAGGCGA TAACAAATAT CAATGCTACA ACTGGCGCGA CTCGAGAAGA 7200
 15 GAAACAAGAA GCGATAAATC GTGTCAATAC ACTTAAAAAT AGAGCATTAA CTGATATTGG 7260
 TGTGACGTCT ACTACTGCGA TGGTCAATAG TATTAGAGAC GATGCAGTCA ATCAAATCGG 7320
 CGCAGTTCAA CCGCATGTAA CGAAGAAACA AACTGCTACA GGTGTATTAA ATGATTTAGC 7380
 20 AACTGCTAAA AAGCAAGAAA TTAATCAAAA CACAAATGCA ACAACTGAAG AAAAGCAAGT 7440
 GGCTTTAAAT CAAGTGATC AAGAGTTAGC AACGGCAATT AATMATATAA ATCAAGCTGA 7500
 25 TACAAATGCG GAAGTAGATC AAGCGCAACA ATTAGGTACA AAAGCAATTA ATGCGATTCA 7560
 GCCAAATATT GTTAAAAAAC CTGCAGCATT AGCACAAATC AATCAGCATT ATAATGCTAA 7620
 ATTAGCTGAA ATCAATGCTA CACCAGATGC AACGAATGAT GAGAAAAATG CTGCGATCAA 7680
 30 TACTTTAAAT CAAGACAGAC AACAAAGCTAT TGAAAGTATT AAACAAGCTA ACACAAATGC 7740
 AGAAGTAGAC CAAGCTGCGA CAGTAGCAGA GAATAATATC GATGCTGTTT AAGTTGATGT 7800
 AGTAAAAAAA CAAGCAGCGC GAGATAAAAT CACTGCTGAA GTGGcGAacG TATTGaAGCG 7860
 35 GTTAAACAAA CACCTAATGC AACTGACGAA GAAAAGCAGG CTGCTGTTAA TCAAATCCAA 7920
 TCAACTTTAA AGATTCAAGC AATTTAATCC AAATTTAATC CAAAACCCAA ACAAATGGAT 7980
 TCAGGGTAGG ACACCACTTA CAAATCCAA 8009

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10953 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

ACCCACCCn TGGGGATAnT TTACCTGGTG GGGCCTTCGA TTGCCTTTAG GTGAAACCaG 60

	AGATGAATGC TAACCATATT CATTCTGCTA AAGATGGTCG TGTTACTGCG ACAGCTGAAA	180
	TTATTCATCG AGGTAAGTCG ACACATGTAT GGGATATAAA AATTAAGAAT GACAAAGAAC	240
5	AATTAATTAC AGTTATGCGT GGTACAGTTG CTATTAAACC TTTAAAATAA AAGAACTGCT	300
	AGCTGAAATG TTATGAGATA TTCATACTA CGGCTAGCAG TTTTTTTATG CGCTATATTG	360
	TTGTAGTTTT AGAAATGCTT GTTCAATGCG TTCGGCAGCT TTACGGCCAC CCATAACATT	420
10	TCTACCAAAT GGTCTTAATT CTAAGTCTGC AAAGCATCCT GCGACAAATA GATTTGGTAT	480
	CCATTCTAAT TTTTCGGAAA TAACAGGGTA ATTACATTCG TTGATAGGTG CATCATAATT	540
	TTGTATTAAT TGCTTAATAA GTGGTTGTGA CATAAAATCT TGTTCAAAAC CAGTTGCAAC	600
15	CATAATCTGT TGATATGGAA CAGAATCATT TTCAGTGTTA ATTACACCAC CACTAATTTG	660
	AGTGATAGGT GTTTTATGCa CATTITATACG ACCATTTTTTA ATATGTTTTT TAAGGCGTAA	720
20	GTACAGTTCG TGAGGCATTG ATCCTTTATG ACGTTCGCGT TGTACAATGG CATTTCTTTC	780
	AGGCATGCTT TTAGTACTTA AAAATGAAGA CATATTTTTT GGACCTAACC AACCAGGATC	840
	AGCATCAAAG TCATGTATTT CAATATCTTT ATTTAGCCAT AAATGAATCT TTTTATCGTT	900
25	ATCATGATTT AACAATTTAA GTGCAAGATG TGCAGCAGTa ATGCCGCTAC CAACGATATG	960
	ATCGGTCTTA TCATATACTA CTTGATCAAG TTCTTTCTCG AAGATATGAT TTACATTCTG	1020
	TTTGTCTTTT AAAATGTCAG GCATAAACGG AATATTTGTA CTGCCTATTG CAATAACGAC	1080
30	GCAATCTGTA GTGATAATTT GTCCATCTTC TAACTTGATA TGCCATTTGT CTTCTTGTTT	1140
	ATCTAAAGTT TGAACATAAC CTTGAACCAA GCAATCCTCT AATTGATATT GTTTAGAAGC	1200
	ATGTGCAATA TGATCCATAA ACATTGTCAA TTCAGGTCGT TGATAAGGAC CATAAAAAGC	1260
35	ATTTGTATAT TGGTGCTGTT TAGCGAATTG TTTTAGATGG AACGGTTGTG GATGTACGTG	1320
	ATGTACAATC GGTGATCTTA AATAAGGCAT TTCTATTCTGA TTTGTATATG AGTTAAACCT	1380
	TTGGCAAAAA GTTTCGTGTG GGTCAATGAT TGTTAATCGG TCTGTTGTTA ATCCGCTTGA	1440
40	TAATAGTTTT TGTGCGATTG CAGTTCCCTG TATGCCACCG CCGATAATTG TCCAATGCAT	1500
	AATAAACCT CTCTCTTTTT AAAACGTAAT AGTTACGATT TATAATTATT ATTATCATAA	1560
45	TACATAACGA CATGAAAGGC AATTAAATTA AAGAGATATA TGTAGATAGG GCGAATCTGT	1620
	AGTCAAAGAA AAAATCATTG AAAAAGAGGT AACAAATGTCA AAAGAWACA GCAGTAAAAT	1680
	CATTCCTAAT TTGGAATCAT CTTACTGCTG TTTGTTGTG ATTTATATTC ATGATTTTGT	1740
50	TATATAATCT ACAATTTTGT GTCTTTTAAG TCTCCGAAA TTTCATCGAC TTTAGTCTTT	1800
	TTAGTATAAG GCGTTTTAAT ATTATATGCT GCTTTCATAA TCATATGACT TGAAAGAGGA	1860

	GCAATAAAAT ATAAAAACGT ACCAAATAGT AATGACATTG CACCTAATGT TGATGCTTTT	1980
	CCGGCAGCAT GTGCACGTGA ATATACATCT TCAAGTCTCA ATAATCCTAT AGCTGCTAGG	2040
5	GCGCTAATTA AAGCACCGAT GATAACAAAG ATAAGTGCAA GACTAATCAG TATGATTTTG	2100
	ATCATGTTCA ATCACCTTAC CTTTGTCCAT AAATTTAGAG AATACTGCAG TACCTAAAAA	2160
	AGCTAATATA CCAATCATCA TAATAACGAC AATCATGTAT TTAATATTTA ATAAAATACT	2220
10	GAATAATGCT ATAACTGCCA TTAATTGAAG ACCAATCGCA TCTAATGCGA CAACACGATC	2280
	GGCAAGTGAT GGGCCTAGCA CAACGCGAAT GAGCATAGCT AACATAGAAA TGACAACTAT	2340
	GATTAATGCA ATAACGATAA TAACATTATG ATTCAATATA TTTCGCCCAC CTCTCTTACA	2400
15	ATTTTCTCTA ATGATGTTTT AATACTTTCT ACTTCTTGCT CTTTAGTTGA AAAATCTATG	2460
	GCATGAATAT AAATTTTTGT ACGATCGTCA CTTACACCAA GCACTACAGT ACCAGGTGTT	2520
20	AATGTAATTA AATTAGACAG CAAGACAATT TGCCAATCTT TTTTAAATC TGTGTGATAA	2580
	ACAAAGAATC CTGGTTCATT TTTAATCGAA GGTTTAATAA TAATTTTCAA AACATCAAAA	2640
	TTAGCTTTAA TCAGTTCGAT TAAGAAAATA ATAACATAAT TAATAATACG ATATAGCGTG	2700
25	ATGACATAAA ATCTACCTGG TAACACTCTG TGTAAGAGGT AAACAAGAAC TAGGCCAAAG	2760
	ATGAAACCTA ACACAAAGTT ATTTGTTGTG TAACTATTTG TCACAAACAA CCAAAACACT	2820
	GCGATAATAA AGTTTAATAC TAATTGTACA GCCATGTTAT TTACCTCCTA ATACAGCTTT	2880
30	AACGTAGGTT GATGGATTGT AGAATGTTTC TGCACCAGCT TTTACCATTG GATATAAGTA	2940
	ATCTGCTGAC AATCCATATA AAACAGTTAT CACAAC TGCA ACGATTGCAA TCGTAGTTAA	3000
	ATATTTGACG TCGACTTTGT TATTAAGATC ATATCCTTTT GGTGACCGA AAAAGCCTTG	3060
35	TAGGAATATG CGAATGACAG AATATAATAC GACTAACTT GATAATAAGA CGATGACACC	3120
	ACTTAAATAA AATCCTCTTT CAAATGTTGA TTGGACAATA AAAAAATTTTC CATAAAAGCC	3180
	ACTGAGTGGG GGAATGCCAG CTAAACTTAA TGCTGCGATA AAGAATGACC AACCAGTAC	3240
40	AGGATATCGT TTAATTAAGC CACCAAATTG TCTTAAATCA GCAGTGCCTG TAATTTTAAT	3300
	CATAATTCCG ATAAGCAAGA ATAATGCAAG TTTTACTAAC ATGTCGTGCA ATGTATAGTA	3360
45	AATAGCCCCA ATCATACCTG ACTCTGTCAT CATTGCAACG CCGACTAAGA TCACACCTAC	3420
	AGCAATCATG ACATTGTATA GGATGATTTT TTTAATGTTG GCATATGCAA CAGCACCGAC	3480
	ACAACCAAAG ATGATCGTTA ATAGTGCTAA GAATAAAATG ACATAATGTG AAAAGCTTAC	3540
50	ATTATCACTA AAGAATAGGC TCAATGTTCT AGCGATTGCA TAAACACCAA CTTTGTGTTAA	3600
	CAAAGCACCA AAGAATGCAA TGATTGGAAT TGGTGGCAT AGTATGCACT AGGTAACCAA	3660

	ATATTGACTA AGCCACTGTC ATGCGCTGAA AGGTTAGCTA ATTTATTGCT TATATCTGCT	3780
	AGATTCAATG TTCCTACTAC TGAATATAAA ATCGCTACAC CCATTACGAA GAAGGATGAC	3840
5	GATACAACGT TAACAAGAAC ATATTTTATT GTTTCTTGTA GTTGAATTTT TGTAGAACCA	3900
	ATTACTAATA AGAAATAAGA TGACATTAAA AATACTTCGA AAAATACGAA TAGGTTGAAA	3960
	ATGTCACCAG TTGTGAATGC ACCAATGATA CCTATTAAAC TAAATAGTAC TGAAAAATAA	4020
10	TAATAATATC TTTCACGTTC AATACCAATT GTTTGGTATG AATATAAAAT CACAATAGCT	4080
	GTAATAATAA TACTAGTAAT TATTAGTAGG GCACTGAATA TGTCTAATAC AAAGACAATA	4140
	CTGTATGGTG CTTTCCATGA ACCTAGCTCT ACGCGTATTG GTCCATGTTT AACAAACATTT	4200
15	GCTAAATTGA TAATTGCCGC GACCAAGGTT AATAATGTAC CGCCTAGTGC GACATAACGC	4260
	TTTATAATAG GACGCTTTCC AATAAAGACA AGTAATATGG CTGTAATTAC TGGAATAACT	4320
20	AGCGTTAACA CAAGCATATT ACTTTCAATC ATCTTCTGGA ACTCCTTTCA TACTCTCAAC	4380
	GTTATCTGTG CCTAATTCTT TATATGTTCT AAATGCTAAT ACTAAGAAAA AGGCTGTTGT	4440
	CGCAAGGCGA TAACGATTGC TGTAAAAATA AGTGCTTGCG GGaTAGGaTC AACATAGCTT	4500
25	TTTACGTTCG CTTCATAAAT TGGAACAGTA CCATGTTTAA GTCCGCCCCAT AGTTATTAAA	4560
	AATAAATTTG CTGCATGTGT TAATAGTGTA GTTCCCATAA CAATTCGTAT CAGACTTTTA	4620
	GACAAAACGA GATAGACACT AATTGCTGTG AGAATACCAC TAACAAAAAT CATAATAATT	4680
30	TCCACTATTC GTTCTCTCCA ATCGAAATAA TAATTGTCAT GACAGTACCA ACTACTGCAC	4740
	ATAAAACACC GAAATCAAAG AATACTGCTG TTGTCAATG AACAGGTTCT AATATAAATA	4800
	ACGGTATATC AAATGTGACA TGCCTAAAGA AATTTTTGCC TAAAAACCAA CTTGCGATAG	4860
35	GCGTCGCAAT ACAAAAAACT AATCCGATAC CTATCAAGAT TTTAAATCT AATGGGAAAA	4920
	TTTTACGCAT TGTTTCTATA TCAAATGCAA TCGTAATGAT AACAAGTGAA CTTGCGAATA	4980
40	ATAATCCGCC GACGAAACCG CCACCAGGTG TATAATGTCC TGCTAAGAAA AGTGAAAAAC	5040
	CAAAGACCAT TACCATGAAA AAGATAATAA CTGCAGCAAA TTGCAAAATT AGATCATTTT	5100
	GTTGTCTATT CATGATTTTT CACCTCGTTA CCTTGCCTTT GACGCTTTTT ACGTAATTTA	5160
45	ATCATTGTAT ATACAGCTAA TCCTGCGATA CCAAGCACAG ATGACTCGAA TAAAGTATCC	5220
	ATACCACGGA AATCAACAAG TATGACGTTT ACCATGTTTT TACCGTGAGC tAAATCATAA	5280
	ACGTGCTCTT GATAAACTT AGATATCGAT TCAAAATGTC TATTTCCGTA TGCAATTAAA	5340
50	CCGATAATAA TGACGGACAA ACCAACACCA CCAGCAATTA AAGCATTAGT AAGCTGGAAT	5400
	GAGCGCTTTT CATTATAACG ATTTAAATTT GGTAAGTGGT AGAAGCATAA TAAGAACAAT	5460

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	ATAACAATA CAGACACAGC ATATCCAAC T GCACTTAACA TAATGATGCT AAATAATCTT	5580
	GATTTAGCGA AAAGAATTAA AAAGGCAGCA CTTAATAATA AAATTACGAT ACAAACCTTCG	5640
5	AAAATTCTAA TCGGACTAAC GTCTTTAAAA TTAATGTTGA AAGGTACTGA GAATATAGTG	5700
	ACAAATGTTA ATAAAATTAA TGCACCAAAA ATGATAACTA AATTATTACG TGAATAATCG	5760
	GTAACATAGC TATTCGTCAT CTTTTTCAGAG TAGTTTGGAA TAACATTTGC ACTTCTGTTG	5820
10	TACCAATAAT TGAATGTTAG TTTACCAGGT TGTCGTTGCA ACAATTTTCAC CCAATAACTA	5880
	AATGTCACAA TTAGTAAGAT ACCTAAAATA TAAATCACTA ATGTTGATAA AAAGGCAGGC	5940
	GTTAATCCAT GGAACATATG GAATTCAACA TCATCAATTA CCGTATGATT AATCGAAGag	6000
15	TnAGCTGGTT CAATAATCGA ATTAGTTAAA ATGCCAGGGA ATAAACCAAA TACAATTACT	6060
	AATGTAGCTA AAATAGCTGG TGATAAAAGC ATTAATATTG ATACTTCGTG TGCTTTTTTA	6120
20	GGTAATTGTT CAGGTTTATA TTGTCCGAAA AATATATGCA TTATAAATTT AATTGAATAT	6180
	ACAAATGTGA AGACACTGCC CACTATACCA ATGATTGGGA ATAGGTAGCC TAATGTATCA	6240
	ACACTGAATA AATTTGCTTG GCTTGCTGTA AATGTTGTTT CTAAAAATGA TTCTTTTGAT	6300
25	AAGAAACCAT TGAACGGTGG TACACCAGCg CATACTTAAT GCTGTAATAA CAGTGATTGT	6360
	AAATGAAATA GGCATAATTG TTAGTAAGCC ACCTAATTC TTAACATCAC GTGTACCAGT	6420
	AGAATGATCC ACTGCACCTG TAATCATAAA TAGGGCACCT TTAAATGTTG CATGGTTGAT	6480
30	TAAATGGAAT ATTGCAGCCG TAAATGCAGC AGCATATATT TTGCTATCAT CGCCTTGATA	6540
	GTGATAACTA ATGGCACCGA TTCCAAGCAT CGCCATAATC ATACCTAATT GGGATACTGT	6600
	TGAAAATGCC AGTATACCTT TCAAGTCTTG TTGTTTGTGTT GCGTTTAGCG AAgCCCAGAA	6660
35	TAATGTAATT AAACCAACGA GTGTGACAGT CCATACCCAA CCTTGCGATG CTGCGAAGAT	6720
	TGGTGTCAAT CGAGCGATTA AATATAACCC TGCTTTAACC ATTGTTGCTG AATGAAGATA	6780
40	AGCACTGACT GGTGTAGGTG CTTCCATTGC ATCTGGTAGC CAAATATAAA ATGGAAACTG	6840
	AGCAGATTTT GTAAAAGCAC CAATCATGAT TAAAATCATC GCAAAAATGA AGAATGGGCT	6900
	ATTTTGAATT TCAGAAGCAT GTTGAATCAT GTACTGAATG CTAAATGATT GTGTTGGTAT	6960
45	AGCGAGTAAG ATGATACCAC CTAATAATGA TAGACCACCA AATACTGTGA TTATGAGCGA	7020
	TTTTTGAGCA CCATATATAG ATGCTTGTCG TTCGCGCCAG AATGAAATAA GTAAAAAACT	7080
	AGAAAATGAC GTTAGCTCCC AGAATAAATA TAGAATAATA ACATTATCTG AAAGTACGAC	7140
50	ACCTAACATT GCACCCATAA ATAGTAATAA ATAACAATAA AAATTCCCTA GTTGTCTCTGA	7200
	CTTACTTAAG TAGCCGATTG AATATAATAC TACTAACTG CCGATTCCCTG AAATAAGCAA	7260

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	CCAATTTAAG GTTTTCATTA CAGTATTACC TGACATCGTC GTTTTAATTA ATGTAAGCAT	7380
	ATAAATAAAT ATGACGATAG GGACAGGTAA TACGAACCAT CCTAAATGTA TACGTTTAAA	7440
5	AAATCTATAC AGGATAGGAA TAATGAGTGC GAATATTAAC GGTAATATCA CCGCAATATG	7500
	TAACAAACTC ACTATGTTGT CCTCCTTTAA AAAATATTTA TGTATTTCAT TATACATGAA	7560
	TGATATAGTT CTGAAAAACG TACACACTCC TTGTGTGCT TTATTTTCAG AaGTATTTAA	7620
10	ATAAGAAGAA ACACGTCATT TTTTATTTAA AATTTTCTTT GTATTGAAGT GAATAATCTT	7680
	CTTTTAAGCG TGCTAAACTA GCTAAAGACA TTTCAGCATG TTTTGTTTGC TGAGCTTTAA	7740
	GTTTAGTTTC TAAATCTGTA ATTGCTTGTT GAAGTGAATC TTCATAGCGC AATACATCAA	7800
15	CATTGAAGTC GCGTAATTGT GAACGTTTCG TATAGCGTTT TTCAAATGG CTTAATGCTT	7860
	TGCGGTCATG GAAAAATACA CCTTCAGTTT CAGTAGGGTT ATGTAAATCA CCTGTGTTTCG	7920
20	GGTGTGTTGAT AACTTGTTCA ACTTTAACAA GGACATCGTC TCCATTTTCT TCAACAATCG	7980
	TGACACCATA GCTACCTGTT TTGTGTGAAA ATCGATATAG CTTTCATGCTA TTTTCCTCCC	8040
	TTAAAAGTAT GTTAATATAT ATGTATCATA ACATGAATGG AGAATATAAA TGGCTAACTA	8100
25	TCCACAGTTA AACAAAGAAG TACAACAAGG TGAAATCAAA GTGGTTATGC ACACAAATAA	8160
	AGGTGACATG ACATTCAAAT TATTTCCAAA TATTGCACCA AAAACAGTTG AAAATTTTGT	8220
	GACACATGCA AAAAATGGTT ATTATGATGG AATCACATTC CACCGTGTCA TTAATGACTT	8280
30	CATGATTCAA GGTGGCGATC CAACAGCTAC TGGTATGGGT GGCgAAAGTA TTTATGGCGG	8340
	TGCTTTTGAA GATGAATTTT CATTAAATGC ATTAACTTA TATGGCGCAT TATCAATGGC	8400
	TAActCAGGA CCTAATACTA ATGGTTCACA ATTTTTCATT GTTCAAATGA AAGAAGTACC	8460
35	TCAAATATG TTAAGTCAAC TTGCAGATGG TGGCTGGCCT CAACCAATCG TTGATGCATA	8520
	TGGCGAAAAG GGTGGTACAC CATGGTTAGA TCAAAAACAT ACAGTATTCG GTCAAATCAT	8580
	TGATGGTGAA aCTACATTAG AAGATATTGC AAATACAAA GTGGGACCAC AAGATAAACC	8640
40	ACTTCATGAT GTTGTAATTG AATCTATTGA TGTGAAGAA TAATATCTAA ACATAATTAA	8700
	CTACCAACAT TTTAACTCG GATAAAGCTA ATTTATGAAT GGATTAGTAT ATATTCCAAC	8760
45	gAAAATAAAT AAActAATAT GATGAGCAAT CTCAATATAT TTATCaAGAA AGCACAGTTT	8820
	TTAAATAGAT GTGTATTTTA AAGATAATAG TTGAGGTTGC TTTTATGTT TTTACAGAGA	8880
	ATTGCTATTC AAATAGTAAA TAAATTGAAA ACAAAGTAGC TGGATATCAT ATTGATTTAG	8940
50	ATAGGAATTT GTTGCTAATT TTATTTGTAA ATCCAAGTTT GTAGAATTCT TATTCATTTA	9000
	TAAAATAATA TTCGTATGAT TTGATTTTTT AATTAGTCCA CCATTTTCGAT TTGTGCTATG	9060

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AACATATCAA GGTGCGTGTA CTGGTATTCA ACCATACGGT GCGTTTGTTG AGACCCCTAA 9180
TCATACTGAA GGACTGATTC ATATATCAGA AATTATGGAT GACTACGTTT ATAATTTGAA 9240
5 GAAATTTCTA TCAGAAGGCC AAATTGTTAA AGCTAAAATT TTGTCTATAG ATGATGAAGG 9300
AAAGCTTAAT CTATCATTAAGGATAATGA TTACTTCAAA AATTATGAGC GTAAGAAGGA 9360
AAAACAATCA GTATTAGATG AAATCAGAGA AACAGAAAAA TATGGGTTTC AAACACTTAA 9420
10 AGAACGCTTA CCAATCTGGA TAAAACAGTC AAAGCGAGCA ATTCGAAACG ACTAAAGGAA 9480
CAGATAAATC GTACCGAAAA TCATACAAAG GGTCTGAAAT GAAAGTTTCT TAGACTATAA 9540
AAGAGATTAG TATCTATTAA ATTTTATTAG ATACTAATCT CTTTTTGTCT ACGATAACGT 9600
15 AATATGATTG ATTCTATTTA CACGTACAAA TGGTTTAAGG TGACATATCC ATTATCTTTG 9660
TTAGATAGAA TCGTTGATTT GCaATATTGT ATGTGGATTT GTTTTTTTTA TTTATTTTAG 9720
AAATGAGAAC TACAACTTAA AGTATTAAAC GAATTGCAAC TATATAAACA GATAATTGGA 9780
20 GAATGAAAAA ATTACATGTT ATAGTCAACT CAATAATTTT AAGGAGGAAT TAAGTAATGA 9840
AAAGTAAATA CGAACCATTG TTTGATAAAG TAGAATTACC AAATGGAGTA GAGTTGAGAA 9900
25 ATCGATTTGT GTTAGCCCCCT TTAACACATA TTTCTTCAAA TGATGATGGT ACTATTTTCAAG 9960
ATGTAGAACT TCCTTATATT GAAAAGCGTT CACAAGATGT TGGTATTACA ATTAATGCTG 10020
CGAGTAATGT GAGTGATGTC GGAAAAGCAT TTCCAGGACA GCCATCAATC GCGCATGACA 10080
30 GTAATATTGA AGGACTAAAA CGATTAGCTA CAGCAATGAA GAAAAACGGT GCCAAAGCAC 10140
TCGTACAAAT ACATCATGGC GGTGCACAAG CATTCGCTGA ATTAACACCT GATGGAGACG 10200
TCGTAGCACC AAGTCCAATT TCTTTAAAAA GTTTTGGTCA GAAACAAGAA CATAGTGCTA 10260
35 GAGAAATGAC GAATGAAGAG ATTGAACAAG CAATCAAGGA TTTTGGTGAA GCAACGCGAC 10320
GTGCAATTGA AGCAGGGTTT GATGGTGTTG AAATACATGG CGCGAATCAT TACTTAATTC 10380
ATCAATTTGT ATCACCATAC TATAATAGAA GAAATGATGT ATGGGCAAAT CAATATAAAT 10440
40 TCCCGGTCGC TGTGATTGAA GAAGTACTTA AAGCGAAAGA AGCGTATGGC AATAAAGACT 10500
TTATAGTTGG ATACAGATTA TCTCCAGAGG AAGCGGAGTC TCCAGGAATC ACAATGGAAA 10560
45 TTACAGAGGA ACTCGTTAAT AAAATTAGCC ATATGCCAAT CGACTATATT CATGTTTCAA 10620
TGATGGATAC GCATGCAACG ACACGTGAAG GTAAATACGC TGGACAAGAA AGACTGCCTT 10680
TAATTCACAA ATGGATAAAT GGTCTGATGC CACTTATCGG TATTGGTTCA ATTTTCACAG 10740
50 CTGACGAAGC TTTAGATGCA GTTGAAAATG TTGGTGTTGA CTTAGTAGCC ATTGGTAGAG 10800
AGCTACTACT GGATTATCAA TTTGTTGAAA AAATTAAAGA TGGACGGGAA GATGAAATTA 10860

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AATTTAATGA AGGGTTTTAT CCATTACCAC GTA

10953

(2) INFORMATION FOR SEQ ID NO: 63:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8155 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

15	TTTGATAnAA AACTGAATHa ATTAAATGTA TCGATTCAAC CTAATGAAGT GAATTTACAA	60
	GTAAAGTAG AGCCTTTTtag CanAAAGGTT AAAGTAAATG TTAAACAGAA AGGTAGTTTA	120
	GCAGATGATA AAGAGTTAAG TTCGATTGAT TTAGAAGATA AAGAAATTGA AATCTTCGGT	180
20	AGTCGAGATG ACTTACAAA TATAAGCGAA GTTGATGCAG AAGTAGATTT AGATGGTATT	240
	TCAGAATCAA CTGAAAAGAC TGTAAAAATC AATTTwCCAG AACATGTCAC TAAAGCACAA	300
	CCAAGTGAAA CGmAGGCTTA TATAAATGTA AAATAAATAG CTAAATTAAA GGAGAGTAAA	360
25	CAATGGGAAA ATATTTTGGT ACAGACGGag TAAGAGGTGT CGCAAACCA GAACTAACAC	420
	CTGAATTGGC ATTTAAAITA GGAAGATACG GTGGCTATGT TCTAGCaCAT AATAAAGGTG	480
	AAAAACACCC ACGTGTACTT GTAGGTCGCG ATACTAGAGT TTCAGGTGAA ATGTTAGAAT	540
30	CAGCATTAAT AGCTGGTTTG ATTTCAATTG GTGCAGAAGT GATGCGATTA GGTATTATTT	600
	CAACACCAGG TGTTGCATAT TTAACACGCG ATATGGGTGC AGAGTTAGGT GTAATGATTT	660
	CAGCCTCTCA TAATCCAGTT GCAGATAATG GTATTAAATT CTTGGATCA GATGGTTTTA	720
35	AACTATCAGA TGAACAAGAA AATGAAATTG AAGCATTATT GGATCAAGAA AACCCAGAAT	780
	TACCAAGACC AGTTGGCAAT GATATTGTAC ATTATTCAGA TTACTTTGAA GGGGCACAAA	840
	AATATTTGAG CTATTTAAAA TCAACAGTAG ATGTTAACTT TGAAGGTTTG AAAATTGCTT	900
40	TAGATGGTGC AAATGGTTCA ACATCATCAC TAGCGCCATT CTTATTTGGT GACTTAGAAG	960
	CAGATACTGA AACAATTGGA TGTAGTCCTG ATGGATATAA TATCAATGAG AAATGTGGCT	1020
45	CTACACATCC TGAAAAATTA GCTGAAAAAG TAGTTGAAAC TGAAAGTGAT TTTGGGTTAG	1080
	CATTTGACGG CGATGGAGAC AGAATCATAG CAGTAGATGA GAATGGTCAA ATCGTTGACG	1140
	GTGACCAAAT TATGTTTATT ATTGGTCAAG AAATGCATAA AAATCAAGAA TTGAATAATG	1200
50	ACATGATTGT TTCTACTGTT ATGAGTAATT TAGGTTTTTA CAAAGCGCTT GAACAAGAAG	1260
	GAATTAAATC TAATAAAACT AAAGTTGGCG ACAGATATGT AGTAGAAGAA ATGCGTCGCG	1320

	CTGGTGATGG TTTATTAACT GGTATTCAAT TAGCTTCTGT AATAAAAATG ACTGGTAAAT	1440
	CACTAAGTGA ATTAGCTGGA CAAATGAAAA AATATCCACA ATCATTAAAT AACGTACGCG	1500
5	TAACAGATAA ATATCGTGTT GAAGAAAATG TTGACGTAA AGAAGTTATG ACTAAAGTAG	1560
	AAGTAGAAAT GAATGGAGAA GGTCGAATTT TAGTAAGACC TTCTGGAACA aACCATTAGT	1620
	TCGTGTCATG GTTGAAGCAG CAACTGATGA AGATGCTGAA aGATTTGCAC AACAAATAGC	1680
10	TGATGTGGTT CAAGATAAAA TGGGATTAGA TAAATAAATA CTGTATTACA AATGAGCCGA	1740
	TGCGTATGcA nTcgtTTTTT GTGTTTGTAG AAATAATTTA TAGTACAAAC GTAAAAATGAT	1800
	ATAAACAAAA TAAAAACAAA GTAATCAATA TGTAATATAA AATACACTGG TACTCAATAT	1860
15	ATAATGATGA TAAAATTAAT TTAAATTAGA TAGAGTTGCT TTGTGTTTTT AACGCAGATG	1920
	CTACTACTTA TCTTAACAGT TGATTAAGTG AAATCATTTA ACAGCGAGAA TAATCAACCA	1980
20	GGAGGATGAC TTAATGAATT TATTCAGACA ACAAAAATTT AGTATCAGAA AATTTAATGT	2040
	CGGTATTTTT TCAGCTTTAA TTGCCACTGT TACTTTTATA TCTACTAACC CGACAACAGC	2100
	GTCTGCAGCA GAGCAAAATC AGCCTGCACA AAATCAACCA GCACAACCAG CTGATGCCAA	2160
25	TACACAGCCT AACGCAAATG CTGGTGCTCA AGCTAATCCT ACAGCACAGC CAGCTGCACC	2220
	TGCCAACCAA GGACAACCAG CAGTACAACC AGCAAACCAA GGTGGACAGG CTAATCCAGC	2280
	AGGAGGAGCA GCACAACCAA ATACACAACC AGCTGGACAA GGTGATCAAG CTGATCCGAA	2340
30	TAACGCTGCA CAAGCACAAC CTGGAAATCA AGCAACACCG GCAAACCAAG CAGGTCAAGG	2400
	AAATAACCAA GCAACACCTA ATAATAATGC AACACCGGCA AATCAAACAC AGCCAGCGAA	2460
	TGCTCCAGCA GCAGCGCAAC CAGCAGCACC TGTAGCAGCA AACGCACAAA CTCAAGATCC	2520
35	AAATGCTAGC AATACTGGTG AAGGCAGTAT TAATACGACA TTAACATTTG ATGATCCTGC	2580
	CATATCAACA GATGAGAATA GACAGGATCC AACTGTAACT GTTACAGATA AAGTAAATGG	2640
40	TTATTCAATTA ATTAACAACG GTAAGATTGG TTTCGTTAAC TCAGAATTAA GACGAAGCGA	2700
	TATGTTTGAT AAGAATAACC CTCAAAACTA TCAAGCTAAA GGAAACGTGG CTGCATTAGG	2760
	TCGTGTGAAT GCAAATGATT CTACAGATCA TGGTAACTTT AACGGTATTT CAAAACTGT	2820
45	AAATGTAAAA CCAGATTCAG AATTAATTAT TAACTTTACT ACTATGCAAA CGAATAGTAA	2880
	GCAAGGTGCA ACAAATTTAG TTATTAAAGA TGCTAAGAAA AATACTGAAT TAGCAACTGT	2940
	AAATGTTGCT AAGACTGGTA CTGCACATTT ATTTAAAGTA CCAACTGATG CTGATCGTTT	3000
50	AGATTTACAA TTTATTCTCG ACAATACAGC AGTTGCTGAT GCTTCAAGAA TTACAACAAA	3060
	TAAAGATGGT TATAAATACT ATTCATTCAT TGATAATGTA GGTCTATTCT CAGGATCACA	3120

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	TAATACTGAA ATCGGTAACA ATGGTAATTT TGGTGCTTCA TTAAAAGCAG ATCAATTTAA	3240
	ATATGAAGTA ACATTACCAC AAGGTGTAAC TTACGTTAAT AATTCATTAA CTACAACATT	3300
5	CCCTAATGGT AATGAAGACA GTACAGTATT GAAAAATATG ACTGTTAATT ATGATCAAAA	3360
	TGCAAAATAAA GTTACATTTA CAAGCCAAGG TGTGACAACG GCACGTGGTA CACACACTAA	3420
	AGAAGTTTTA TTCCCAGATA AATCTTTAAA ATTATCATAT AAAGTTAATG TTGCGAATAT	3480
10	CGATACACCT AAAAATATTG ATTTTAATGA AAAATTAACA TATCGTACTG CTTCAGATGT	3540
	TGTAATTAAT AATGCGCAAC CAGAAGTaCA CTAAGTGCAG ATCCATTTTC AGTAGCGGTT	3600
	GAAATGAACA AAGATGCGTT GCAACAACAA GTAAACTCAC AAGTTGATAA TAGTCATTAC	3660
15	ACAACAGCAT CAATTGCAGA ATACAATAAA CTAAACAAC AAGCAGATAC TATTTTAAAT	3720
	GAAGATGCGA ATCATGTTAA AACTGCAAAT CGTGCATCTC AAGCGGATAT TGATGGTTTA	3780
20	GTAAGTAAAT TACAAGCTGC ATTAATTGAT AATCAAGCAG CAATTGCTGA ATTAGATACT	3840
	AAAGCTCAAG AAAAGGTTAC AGCAGCACAA CAAAGTAAAA AAGTTACGCA AGATGAAGTT	3900
	GCAGCACTTG TAACTAAAAT TAACAATGAT AAAAATAATG CAATCGCAGA AATTAATAAA	3960
25	CAAAGTACAG CACAAGGTGT CACAAGTCAA AAAGATAATG GTATCGCAGT GTTAGAACAA	4020
	GATGTGATTA CACCAACAGT TAAACCTCAA GCGAAACAAG ATATTATCCA AGCAGTTACA	4080
	ACTCGTAAAC AACAAATTAA AAAGTCAAAT GCATCATTAC AAGATGAAAA AGATGTAGCA	4140
30	AATGATAAAA TTGGTAAAAT TGAAACAAAG GCAATTAAAG ATATTGATGC AGCAACAACA	4200
	AATGCACAAG TAGAAGCCAT TAAACAAAA GCAATCAATG ATATTAATCA AACTACACCT	4260
	GCTACAACAG CTAAAGCAGC AGCTCTTGAA GAATTTGACC AAGTTGTTCA AGCACAAATT	4320
35	GATCAAGCAC CTTTAAATCC TGATACAACA AATGAAGAAG TAGCGGAAGC TATTGAACGT	4380
	ATTAATGCAG CTAAAGTTTC TGGTGTAAAA GCAATTGAAG CGACAACGAC TGCACAAGAT	4440
	TTAGAAAGAG TTA AAAACGA AGAAATCTCA AAAATTGAAA ATATTACTGA CTCTACGCAA	4500
40	ACAAAAATGG ATGCCTATAA TGAAGTTAAA CAAGCTGCAA CAGCTAGAAA AGCTCAAAAT	4560
	GCTACAGTTT CAAATGCAAC AAATGAAGAA GTAGCAGAAG CTGATGCAGC AGTAGATGCA	4620
45	GCTCAAAAGC AAGGTTTACA TGACATCCAA GTTGTTAAAT CAAAACAGGA AGTTGCTGAT	4680
	ACAAAATCAA AAGTATTAGA TAAATCAAT GCAATTCAAA CACAAGCAA AGTTAAACCT	4740
	GCAGCTGATA CGGAAGTAGA AAACGCATAT AATACACGTA AACAGAAAT TCAAAATAGC	4800
50	AATGCTTCAA CTACAGAAGA AAAACAAGCT GCATATACAG AATTAGATAC TAAAAAGCAA	4860
	GAAGCAAGAA CAAATCTTGA TGCTGCAAAT ACAAACAGTG ATGTAACAAC AGCTAAAGAC	4920

	GCGGAAATCG CTCAAAAAGC AAGTGAACGT AAAACAGCAA TTGAAGCAAT GAATGATTCTG	5040
	ACTACTGAAG AACACAAGC AGCGAAAGAC AAAGTGGATC AAGCAGTAGT TACTGCAAAC	5100
5	GCTGATATAG ATAATGCTGC AGCAAACAAT GATGTGGATA ATGCAAAAAC TACAAATGAA	5160
	GCTACAATCG CAGCCATTAC ACCTGATGCA AATGTTAAAC CAGCAGCAAA ACAAGCAATT	5220
	GCAGATAAAG TACAAGCTCA AGAAACAGCA ATTGATGGAA ATAACGGCTC AACAACTGAA	5280
10	GAAAAAGCAG CTGCTAAACA ACAAGTTCAA ACTGAAAAAA CAACAGCTGA TGCCGCAATA	5340
	GATGCAGCAC ATACAAATGC GGAAGTTGAA GCGGCTAAAA AAGCAGCAAT TGCTAAAATT	5400
	GAAGCGATTG AGCCAGCAAC AACAACTAAA GATAATGCGA AAGAAGCAAT TGCTACGAAA	5460
15	GCGAATGAAC GTAAACAGC AATCGCTCAA ACGCAAGACA TTACTGCTGA AGAAATTGCA	5520
	GCGGCTAATG CGGACGTAGA TAATGCTGTG ACACAAGCAA ATAGCAACAT TGAAGCTGCT	5580
20	AATAGTCAAA ATGATGTAGA CCAAGCGAAA ACGACAGGTG AAAATAGTAT TGATCAAGTA	5640
	ACACCAACAG TTAATAAAAA AGCAACTGCA CGTAATGAAA TCACAGCAAT TTTAAATAAC	5700
	AAATTGCAAG AGATTCAAGC TACGCCAGAT GCAACAGATG AAGAAAAACA AGCAGCTGAT	5760
25	GCTGAAGCAA ATACTGAAAA TGGTAAAGCA AATCAAGCCA TTTCAGCAGC AACTACTAAC	5820
	GCACAAGTTG ATGAAGCTAA AGCAAATGCA GAAGCAGCGA TTAATGCGGT AACACCAAAA	5880
	GTTGTGAAGA AACAGCGGC TAAAGATGAA ATTGATCAAT TACAAGCAAC GCAAACAAAT	5940
30	GTTATCAATA ATGATCAGAA CGCTACAACA GAAGAAAAAG AAGCAGCTAT TCAACAATTA	6000
	GCAACAGCAG TTACAGACGC GAAAAATAAT ATTACAGCTG CAACTGATGA TAATGGTGTA	6060
	GATCAGGCGA AAGACGCTGG AAAGAATTCA ATTCAAAGCA CGCAACCAGC AACAGCGGTT	6120
35	AAATCAAATG CTAAAAATGA TGTGATCAA GCTGTGACAA CTCAAAAATCA AGCAATTGAT	6180
	AATAEAACTG GTGCTACAAC TGAAGAGAAA AATGCAGCAA AAGATTTAGT TTTAAAAGCT	6240
	AAAGAAAAAG CGTATCAAGA TATCTTAAAT GCACAAACAA CTAATGATGT TACGCAAATT	6300
40	AAAGATCAAG CAGTTGCTGA TATTCAAGGT ATTACTGCAG ATACAACAAT TAAAGATGTT	6360
	GCGAAAGATG AATTAGCAAC AAAAGCAAAC GAACAAAAAG CGCTTATTGC ACAAAGTGCA	6420
45	GATGCGACTA CTGAAGAAAA AGAACAAGCA AATCAACAAG TAGACGCACA ATTAACACAA	6480
	GGTAATCAAA ATATTGAAAA TGCACAGTCA ATCGATGATG TAAACACTGC AAAAGATAAT	6540
	GCAATTCAAG CAATTGACCC AATTCAAGCA TCAACAGATG TTA AACGAA TGCAAGAGCG	6600
50	GAATTGCTAA CTGAAATGCA AAATAAAATA ACTGAAATAC TTAATAATAA TGAGACTACT	6660
	AATGAAGAAA AAGGTAACGA TATTGGACCA GTTAGAGCAG CATATGAAGA AGGTTTAAAT	6720

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	AAAGTTCAAC AACTTCATGC AAATCCTGTT AAGAAACCAG CAGGTAAAAA AGAATTAGAT	6840
	CAAGCTGCAG CTGATAAGAA AACACAAATA GAACAAACAC CAAATGCATC ACAACAAGAA	6900
5	ATTAATGATG CAAAACAAGA AGTTGATACT GAATTAAATC AAGCGAAAAC AAATGTCGAT	6960
	CAATCATCAA CAAATGAATA TGTGATAAT GCAGTTAAAG AAGGAAAAGC TAAAATTAAT	7020
	GCAGTTAAAA CATTTAGTGA GTACAAAAAA GATGCTTTAG CTAAAATTGA AGATGCATAT	7080
10	AATGCTAAAG TAAACGAAGC GGATAACTCT AACGCATCGA CTTCAAGTGA AATTGCTGAA	7140
	GCGAAACAAA AACTTGCTGA ATTAAAACAA ACTGCGGATC AAAATGTTAA TCAAGCTACT	7200
	TCTAAAGATG ACATTGAAGT TCAAATTCAT AATGACTTAG ATAATATTAA CGATTACACA	7260
15	ATTCCAACAG GTAAAAAGA ATCAGCTACA ACAGATTTAT ATGCTTATGC AGATCAGAAG	7320
	AAAAATAATA TTTCAGCTGA CACTAATGCA ACACAAGATG AAAAGCAACA AGCAATTAAG	7380
	CAAGTTGACC AAAATGTTCA AACTGCATTA GAAAGCATT AATATGGTGT GGATAATGGT	7440
20	GACGTTGATG ATGCATTAAC ACAAGGTAAA GCAGCAATTG ATGCTATTCA AGTAGATGCT	7500
	ACTGTTAAAC CTAAAGCGAA CCAAGCTATT GAAGTTAAAG CAGAAGATAC GAAAGAATCT	7560
25	ATTGATCAAA GTGACCAGTT AACTGCTGAA GAAAAAAGT AAGCATTAGC AATGATTAAA	7620
	CAAATTACAG ATCAAGCTAA ACAAGGTATT ACTGATGCAA CAACAACTGC TGAAGTTGAA	7680
	AAAGCGAAAg cTcAAGGACT TGAAGCATTT GATAACATTC AAATCGACTC AACAGAAAAA	7740
30	CAAAAAGCTA TCGAAGAATT AGAAACTGCA CTAGACCAGA TTGAAGCAGG TGTAAATGTC	7800
	AACGCTGATG CTACAACTGA AGAAAAAGAA GCGTTTACGA ATGCTTTAGA AGACATTTTA	7860
	TCAAAAGCAA CTGaAGATAT TTCTGATCAA ACTACAAATG CAGAAATCGC TACTGTCAAA	7920
35	AATAGTGCAG TTGAACAACT TAAAGCACAA CGTATTAATC CTGAAGTTAA GAAAAATGCT	7980
	TTGGAAGCAA TCAGAGAAGT GGTTAACAAG CAAATAGGAA tAATTAAAAA TGCAGATGCA	8040
	GATGCATCGG CGGAAAGAnA TTGCACGTAC GGGATTTAGG TAGATATTTT GGACCGATTT	8100
40	GCTGGATAAA TTTAGGGTnA AACCCCAACC AATGCCGAAG TTGCCTGAAT TACCA	8155

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

CTGTTTTATT TGCAGCACCC ATACTGGAAA TCACTTTAAT CCCTCGGTCA AGACACTCTT 120
 TCATTAAGTG TACTTTGTAC ATTATTGTAT CACTTGCATC TACAAAATAA TCTATATCGT 180
 5 AGTTATCGAA AATTTCTTCA TATGTCTCTT CTGTATAAAA CATATGTAAG GCGGTGACTT 240
 TACAATCTGG ATTAATTAAT TTAATACGTT CTTCCATCAA AGAAACTTTA CTTTGTCTTA 300
 CCGTTGTAGT TAAAGCGTGT AATTGTCTGT TTACATTGT AATATCAACA TCATCTTTAT 360
 10 CTATTAATAT AATATGACCA ATATTCGTTT TTGCTAATGC TTCAGCAGCA AATGAACCAA 420
 CACCTCCAAC GCCAAGTATG ACAACAGTTT GTTGCTTCAA TAAATCTAAA CTTGTGTGTC 480
 CAATCGCTAG TTCATTTCTT GAAAATTGAT GTTTCATTAT TTTACCTCTT TCACTGATTT 540
 15 ATACATAAGT ACATAGTAAC TTAAATTTT ATATTTAGCA TTATCACTTT GATTATTTTC 600
 CCAAATTC ACGAGGAAAC ATTTATTAAA CGCTATAAAA CCCAACTAAT TCTTTATTAA 660
 20 AAACTTAAAG AAACGCATAA AAATACGCAA GACAAAGTCT TGCATATCGA TAGAGTCCGT 720
 ATTGCCGTAG TTATAATAGC TTGATCATTG GGCCTGTTAT ATACAGGTGG GTGCCCTGTT 780
 TCTTGTTTTG TACGTCCTTC ATATAAGGCG TGTACGCTGC AAGAAAACCC ATTGGGCTCC 840
 25 CTTGATCAAA GAGTGTTAGG CCCAAATTAA AAAGCAAAC TACGAACAAC TCAGATGACT 900
 ATCTTATGAT GTTATATTAC CACATAATTA AAATTAATGA AATTATAACA AACCAGTT 960
 TATTGATTTT TTAAATTTA GTGACGAATT CGCAAAGAAA GTTCTTCTAA TTGTTTATCA 1020
 30 GAAACTTCAC TAGGCGCATT CGTTAATAAA CATGTAGCAG ATGCTGTTTT AGGGAATGCG 1080
 ATTGTATCTC TCAAGTTTGT TCTATTAGTC AATAACATGA CTAATCGGTC TAATCCTAAT 1140
 GCAATACCGC CATGTGGTGG TGCACCATAT TTAATGCAT CTAGTaAGAA GCCGAACGT 1200
 35 TCCTGTGCTT GTTCTTTAGT AAATCCAAGA ACTTCGAACA TTTTCTCTG TAACTCACCA 1260
 TCATGAATTC TGATTGAACC GCCACCTAAT TCATAACCAT TTAATACTAT GTCATAAGCA 1320
 TTTGCCTCAG CTTCTCTGG CGCAGTGCCA AGCTTAGCAA TATCAGCTTC TTTTGGAGAT 1380
 40 GTAAATGGAT GATGTGCTGC AACGTAACGT TTCGCATCTT CATCATATTC TAATAATGGC 1440
 CAATCTGTCA CCCATAAGAA GTTTAATTTT GTTTCATCGA TTAAACCTAA TTCTTTAGCT 1500
 45 AATTTGACAC GTAATGCACC TAACTTTGT GCAACGACAT TTGGTtGTC TGCAACAAAC 1560
 ATTACTAAGT CACCAGCTTC AGCACCAGTT AATGTAAGTA ATGTTTCAAC ATTTTCTGTT 1620
 CAAAGAAACG 1630

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 732 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

5	CAATTGGACA TCTTGTATGA AAAGGACAAC CTGCGGCGG ATTACTTGGC GAAGGTAATT	60
10	CTCCTTTTAA TATAATTCTA TTGTTATTAT GTTTATCAAT TTGTGGTATT GATGAAATCA	120
	ACGCTTTTGT ATATGGATGT TTGGGATTTT CATAAATTTT TTTATCAGAT GCGATTTCAA	180
	CTATATGACC TAAATACATA ACTCCAATGA CATCACTTAT ATGTTTACT ACACTTAAAT	240
15	CATGTGCGAT AAATAAATAG CTTAAGTTAA ATTGTTCTTG TAAATCTTTT AATAAATTCA	300
	GTACTTGAGA TTGAACAGAT ACATCTAATG CACTTACAGG CTCATCAGCA ACAATTAAAC	360
	TCGGACGCAA AGCCAATGCT CTTGCAATTC CCACTCTTTG TCTCTGTCCA CCTGAAAATT	420
20	CATGTGCATA TTtATAATAT GCATCTTCAC TTAGGCCAAC ACATTTTAAT AAATATAGTA	480
	CTTCTTTTTT TATTTCTTCT TTTGGCAATT TTTTATAATT TAAATAGGT TCTGAAATGA	540
25	TATCTCCAAC CATTTGCATC GGATTCAATG ATGCATACGG ATCTTGAAAT ATCATCTGAT	600
	ATTGTTGTCTG TGATTTTCTG AGTTTTTTC CTTGTAATCT TGTATATCT TCACCATTAA	660
	CAATTATTGA GCCTGAAGTT GCATCTTCAA GCCTGATAAT CACTTTACCT AACGTTGACT	720
30	TACCACAACC CG	732

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5838 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

40	AATATATTCA TATGTTTCAT CAACAATATT AGCTGCTTTT TGAATTAAAG CAATTTTCGTC	60
45	AGCATCTTTG ACGTCTCTAA TTTTATCTAC AGTATTAGAA ATGCTTATTA ATGATATACG	120
	GCTTTTATTT AATTCAAGGT ATGTATCATA ACTTACATGA TGCCCCCTCAA AACCTACATT	180
	TTCAAAATTT TCTTGGTGTA GCAATTCTTT AATCTCACCA ATAATAGTAG ATTTACGATT	240
50	AATAATTTCA TAATTTGGCG CCTGCTTAGT TGCTTGATCA ATATATCTAA AGTCTGTTAT	300
	CAAATATTGT TTATCTTTAG ATATGATAAG TGCTCCACTG GTACCAGTAA AACCTGATAA	360
55	ATATCTTCTA TTGTAATCCG AAAGAATGaT AATCGCATCT AAATGTTTTT GTTCTAAAT	420

	CAACTTTATA CATTAAAATA ATATCATAAT AAGGATAAAA AATAATAGAT ATTGATTTTA	540
	GGGAGATAGT AATGAAAAAA TTGGTTTCAA TTGTTGGCGC AACATTATTG TTAGCTGGAT	600
5	GTGGATCACA AAATTTAGCA CCATTAGAAG AAAAAACAAC AGATTTAAGA GAAGATAATC	660
	ATCAACTCAA ACTAGATATT CAAGAACTTA ATCAACAAAT TAGTGATTCT AAATCTAAAA	720
	TTAAAGGGCT TGAAAAGGAT AAAGAAAACA GTAAAAAAC TGCATCTAAT AATACGAAAA	780
10	TTAAATTGAT GAATGTTACA TCAACATACT ACGACAAAGT TGCTAAAGCT TTGAAATCCT	840
	ATAACGATAT TGAGAAAGAT GTAAGTAAAA ACAAAGGCGA TAAGAATGTT CAATCGAAAT	900
15	TAAATCAAAT TTCTAATGAT ATTCAAAGTG CTCACACTTC ATACAAAGAT GCTATCGATG	960
	GTTTATCACT TAGTGATGAT GATAAAAAAA CGTCTAAAAA TATCGATAAA TTAAACTCTG	1020
	ATTTGAATCA TGCATTTGAT GATATTAAAA ATGGCTATCA AAATAAAGAT AAAAAACAAC	1080
20	TTACAAAAGG ACAACAAGCG TTGTCAAAT TAACTTAAA TGCAAATCA TGATAGGAGT	1140
	CTTTTAATGC GTAATATAAT ATTTTATCTT GTACTTATTA TTGCTGCGAT TGGATTAGTA	1200
	ATGAATCTAG ATGCCTTTAT TTTTCAATC GTCAGAATGT TAATCAGCTT TGcGTAAaTAG	1260
25	CTGGTATTAT TTATCTGATT TATTATTTCT TCATCTTAAC TGAAGACCAA CGCAAATATC	1320
	GCAAAGCAAT GCgTrAaGTA TAAAAGAAAT CAAAGAAGAA AATAGATAAA AAAACGGAAG	1380
	CACITGTAGG TAAAATAGTC TACGTGCTTC CATTTTAT TCTAAAACT ACTTTCTAAA	1440
30	CATCCATTCA TCTGAACGAT ATTTTTCAGT TAATCTTCC ACTTCTGCCA ATTGAGCTTC	1500
	TGcTAATTCA AGTGGCTTTA ATTCTATATT TAAACCTTTC TTAAACCTT TCTCGAAAGC	1560
	TTCTTCATT TGAATAATAG TAATGTGTTT ATCTGAAATA TCATTGATGG CAACTGCTTT	1620
35	TTCAACGAAT GCCTCTTCA TTTTAAATTT TAATCTTCA TTTTATAAA TrAACATATC	1680
	AAACAGTTCA TCAATATCAA TATCTTGTA AATCGAACCG TGTTGGAGGA TTACGCCCTT	1740
40	TTGTCTCGTT TGAGCACTCC CAGCAATCTT ACGGCCTTCA ACAACTAGCT CATACCAACT	1800
	TGGTGCATCA AAACACACTG AACTTCGAGG TTGTTTTAAT TTTTGACGCT CTTCAGGCGT	1860
	TTTAGGTACC GCAAAATAAG TATCAAATCC TAAGTTTTTA AATCCTTCTA ATAATCCTTG	1920
45	TGAAATCACT CTGTACGCTT CTGTAAGTGT AGAAGGCATA TTCGGATGCG ATTCAGGCAC	1980
	AATCACACTG TAAGTTAACT CTTTATCATG TAGCACCCCA CGGCCACCAG TTTGACGCCT	2040
	TACGAGACCA AAACCTTCT CTTTAACCTT ATCAATATCA ATTTCTTTT GTAGCCTTG	2100
50	GAAATACCCT ATTGATAATG TTGCAGGATT CCATGTGTAA AAACGTATAA CTGGATCAAT	2160
	TTACCTCTA GAGACAAAAT TTAATAACGC TTCATCCATT GCCATATTAT AATATGGGTC	2220

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	AAATGTATAA	TATTTGATTG	GCTAATTAAT	CAATTTAACT	AAATGAATAA	TAATTGCAAT	2340
	TCTTTAGTGA	AATATTTTGA	TAATTTGACC	TAACAGTCTT	ATAATTATAT	TATCGTTTAA	2400
5	TTAGGGAGGA	TGCAAGATGA	GTGCTAGTTT	GTACATCGCA	ATAATTTTAG	TTATAGCAAT	2460
	TATTGCTTAT	ATGATTGTTG	AACAAATTCT	TAACAAGCGA	GCTGTTAAAG	AATTAGATCA	2520
	AAATGAATTC	CATAATGGGA	TTAGAAAAGC	TCAAGTCATC	GATGTTAGAG	AGAAAGTTGA	2580
10	CTATGACTAC	GGTCACATTA	ATGGGTCTCG	CAATATTCCT	ATGACAATGT	TCAGGCAACG	2640
	ATTCCAAGGA	TTAAGAAAAG	ATCAACCGGT	ATACTTATGT	GATGCCAATG	GGATTGCTAG	2700
	CTATAGAGCC	GCTCGTATTT	TGAAAAAGAA	TGGATATACA	GATATCTATA	TGTTAAAAGG	2760
15	CGGCTATAAA	AAATGGACTG	GAAAAATAAA	GTCTAAAAAA	TAGTTTTTGT	AAATTTAATA	2820
	TACGATTTAA	TAAAATCTGA	GTGTTAATTG	ATCATCAATA	ACAATACTCA	GATTTTAATT	2880
20	TTTTAACAAA	GTCTGTTACT	ATATTTCTCT	AGCTTCACTG	ATCATTAAAC	TTAGTTTCAG	2940
	CATAATAAAG	AAAGTTCAGC	TCATTTTCAA	TACGATTCAA	TTACCGCAAT	CTAAAAAATG	3000
	AAAAGACAAT	TTCTATGAAA	GAATAATACC	AAACCCTAAG	AGTTATTACT	TCGGTTTAGT	3060
25	TTTCTTGTTT	AAATAGAAAT	TGTCITTTTC	AATTGATTTT	GAAACCATTA	TCCTTAAATC	3120
	TTCATACAAA	GTTAGAATAA	TAATTCCTCG	AATATGTGTT	TAATACTTTA	TTTTTCCTGT	3180
	TTAAGATTTT	CAAACITTTA	TATTGGTTTA	CGAGCAGCTG	TAGCTTCGTC	TAATCGATCA	3240
30	ATCACAGTTG	TATGTGGTGC	TTCTAGCaCT	TTATCAGGAT	CATTTTTAGC	TTCTTCAGCA	3300
	ATACTAATTA	ATGTATCGAT	AAAATAATCA	AGTGTTTCTT	TAGACTCTGT	CTCAGTCGGT	3360
	TCAATCATCA	TACCTTCTTC	AACATTTAAT	GGGAAGTATA	TTGTTGGTGG	ATGTACACCG	3420
35	AAATCTAATA	ATCGCTTAGC	CATGTCTAAA	GTACGTACAC	CAAATTCTTT	TTGACGCACA	3480
	CCACTTAACA	CAAACCTCGT	TTTACAATAT	TGTTTATAAG	GTATTTCAAA	GTGTTTAGAT	3540
40	AAACGTGCTT	TAATATAATT	CGCATTAAAG	ACCGCTGCTT	CAGAAACCTC	TTAAGTCCA	3600
	GTTGCTCCCA	TAGTTTGAAT	ATACGTATAA	GCTCTTAAGT	AAATACCAAA	GTTACCATAA	3660
	AATGGTTTTA	CACGTCCGAT	AGAATTTTTA	ATGTCATTAT	CATATTTAAA	TTTGTGCGCA	3720
45	TCTTTAATAA	CCATTGGCTT	TGTAAGTAA	CTTGCTAGTT	CTTTTACTAC	ACCGACTGGA	3780
	CCTGAACCAG	GACCGCCACC	ACCATGTGGA	CCAGTAAATG	TTTTATGCAA	GTTTAAATGA	3840
	ACAGCATCAA	ATCCCATATC	TCCTGGGCGA	ACTTTGTCCA	TAATAGCGTT	TAAATTCGCA	3900
50	CCATCATAAT	ATAATAGACC	ACCAGCATTG	TGGACGATTT	CACGGATTTC	CATAATATTT	3960
	TTTTCGAAAA	TACCTAAAGT	GTTTGGATTA	GTAAACATAA	TAGCTGCTGT	ATTTTCATTT	4020

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	GATTTAAATC CTGCAAATGa AGCTGAGGCT GGaTTCGTAC CATGCGCAGA ATCTGGcACA	4140
	ATGACTTCAT CACGATGACC TTCACCATTA TTCTCATGGT AAGCTTTAAA TATCATCAAT	4200
5	GCAGTCCAAT CACCATGTGC GCCAGCAGCT GGTGTGAATG TCACCTCATC CATACCAGTA	4260
	ATTTCTTTTA ATTCTTCTTG CAAACTATAA ATAATTTCTA ATGAACCTTG AACTTGATCT	4320
	TCATCTTGTA ATGGATGTGA TTCACTAAAT CCTGGTATTC TAGCAACCTT TTCATTAATT	4380
10	TTAGGGTTAT ACTTCATCGT ACATGAACCC AATGGATAAA ATCCGTTGTC TACACCGAAA	4440
	TTTTTATTTG AAAGTTCAGT ATAATGACGT ACTAAGTCTA GTTCAGCAAC TTCAGGAAAC	4500
	TCCGCTTTGT TTTTACGAAT AAATTTATCA TCTAACAATG ACTCAACAGA ATTTGTTTTA	4560
15	ATATCACTTT TTGGTAATGA ATATGCATAT CTGCCTTCAC GAGATCTTTC AAAAATTAAT	4620
	GGACTTGATT TACTAGTCAT TTAACCTACC AGCCTTTTCT ACAAATGTAT CGATTTTCATC	4680
20	TTTTGTTCTT AATTCAGTTA CAGCTATTAA CATGTGATTT TTAAAGTCGT CTGAAACAAC	4740
	ACCTAAATCA AAACCACCGA TAATATTGTA CTTCACTAAT TCCTCGTTAA CTTGTTGAAT	4800
	TGGTTTGTCA AATTTGACTA CAAACTCATT GmNAAGnTGT ACCATCTAAT ACTTCAAAAC	4860
25	CTTTTTTAAT AAATTGTTGT TTAGCATAGT TAGCATGTTT TATATTTTGA ACTGCAATAT	4920
	CATAGATACC TTGTTTACCA AGTGCTGACA TTGCAATTGA TGaCGcTAAA GCATTTAATG	4980
	CTTGTTTAGA ACAAATATTA GATGTCGCTT TATCGCGTCG AATATGTTGT TCACGTGCTT	5040
30	GTAATGTAA TACAAAGCCA CGATTACCTT CATCATCTTG TGTGTTGACCG ACTAATCTAC	5100
	CTGGCACTTT ACGCATTAACT TTTTCGTCG TTGCAAAATA TCCACAATGT GGCCCAACCGA	5160
	ATTGAGCAGG AATTCGAAT GGCTGAGTAT CACCTACAAC AATATCTGCA CCAAATGAAC	5220
35	CTGGAGGTGT AAGTAATCCC AATGCTAATG GATTTGCATA TACGATAAAT AATGCTTTTT	5280
	TATCTTCAAT AAAGCTATGA ATCTTTTCAA GATCTTCAAT TGAACCGTAA AAGTTTGGAT	5340
40	ATTGTACTGC AACAGCTGCT GTTTCATCAT CCACTGCTGC TTCTAATTTT TTCAAATCTG	5400
	TAACAGTGCC ATCTAAATCG ATTTCCACTA CTTCGAATTC CTTACGCGTC TTAGCATAAG	5460
	TATGAAGTAC TTGTAATGCT TGATAATGTA AACCTTTTGA GACTACAATT TTATTTTTCT	5520
45	TTGTTTGAAT AAATGCTAAG ATACATGCTT CAGCAAAGCT AGTCATCCCA TCATACATAG	5580
	AAGAATTTGC TACATCCATA TCTGTTAATT CACAAATTAA AGTTTGGAAC TCAAAAATGG	5640
	CTTGTAATTC ACCTTGAGAA ATTTCCGCTT GATATGGCGT ATATGCTGTG TAAAAATTCTG	5700
50	ATCTTGAAAT CATAGCATCC ACAACTGATG GCGCGTAATG ATCATAAACA CCAGCACCCA	5760
	rAAATGATGT ATGCGTTTCT TTAGTGATAT tCTTGCTkGC AATGGGGATT TAAACnTCTA	5820

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(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18355 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

	ATrATAATTG GCTTTGCTAA TAATTACTTC CCTGAATTAC aAGTATTAGC AAACGAAATA	60
15	AAATCTGATA TGGCTAGTTC ATTAAAACAA TGATATTTTT ATTTAAATTT TTaAAGCTTT	120
	GTACGAAATT GTACAAAGCT TTTTGGTGC GTATTGTATG GGCAACAAC TACGATGAA	180
	AATCCGTTAC AGGATTGGTA ATAGGAAATG TTAGCGAAAG ACAAGGGTAT CCATTGTAGA	240
20	TTAACAAAAG GACGTTTCCA CAAGTGTGGG TTATTCTCAC TAAAGCAATA CGCAGAGACA	300
	ACTTACGTAA AATTTGAAC TGACTAGAAC GGAACCTCTA CTCAATTATT GATAAAAATT	360
	TTCAAAAAGA CTGGAATGTG CTGAGAATAC GAAGTTTATG GAAGGATTAT CAAAATATAA	420
25	ATGTGCATTC ATTTACAACC TTTATTGACA ATGATTCTCA ACTAATATAG TATATAATCA	480
	AATCGTAATA GTTACGATTT GTTTCTGCA ACTTTTTTGA AGTTTTAGTT GAGGTGAAAA	540
	CAATAAAGC ATCTAAGTGA ATGTAGTTAA CGGACAAC TG CATTGCTTG TAGAGCCACA	600
30	AGAAGCAACT TTAAATAAGG TTTACGGTTG CATTTTGATA CAACAACCGA TTACTAAGTC	660
	ATGCTTTCCA CTTTGCGGGT TAGCATGACT TACCTAATAG ATAGAGCTAT TAGGTTTCAGC	720
	TTCTAAAAAA TTACAGTTTT AGAGGAATAC AGTTGCTTGC tTCGCAACAA CTGCATAAGA	780
35	GCCATGGTTT TCGCTTTTGC GAATTAGCAT GACTTACCTA CTAGATAGAG CTATTAGGTT	840
	CATCTTCTAA AAAATTACAG GTTTAGAGGA ATACAGTTGT TTGCTTCGCA ACAACTGCAT	900
40	AAGAGCCTCT AGTAATTAAA ATTACAGAGG CTCTAAAAAT ACATCTAAAG GAGTGTGCGTA	960
	TGAATCGGCA GGTATAGAA TTTTCTAAGT ATAATCCTTC GGGGAATATG ACGATACTTG	1020
	TTCATTCAAA ACATGATGCT AGTGAATATG CATCTATCGC CAATCAGTTG ATGGCCGCAA	1080
45	CACATGTATG CTGTGAACAG GTAGGCTTTA TAGrATCAAC ACAAATGAT GATGGTAATG	1140
	ATTTTCACTT AGTTATGAGC GGTAATGAAT TTTGCGGTAA TGCGACGATG TCATATATAC	1200
	ATCATTTGCA GGAAAGTCAT TTGCTTAAAG ACCAACAGTT TAAGGTGAAG GTGTCTGGCT	1260
50	GTTGCGATTT AGTGCAATGC GCAATTCATG ATTGCCAATA CTATGAAGTT CAAATGCCAC	1320
	AAGCCCATCG TGTGTGCCA ACAACAATTA ATATGGGTAA TCATTTCATGG AAAGCAATAG	1380

	TTCAACATTT	GGTTGAAGCG	TTTGTGCGTG	AgcAACAAATG	GAGTCACAAA	TATAAAACAG	1500
	TAGGTATGAT	GCTTTTTGAT	GAACAACGTC	AATTTTTTACA	GCCATTAATC	TATATACCAG	1560
5	AAATTCAAAG	TTTAATTTGG	GAAAATAGCT	GTGGTTCTGG	TACAgcATCA	ATTGGGGTTT	1620
	TTAATAATTA	TCAACGTAAT	GACGCATGCA	AAGATTTTAC	AGTACATCAG	CCAGGGGGCA	1680
	GTATTTTAGT	GACATCAAAG	CGATGTCATC	AATTGGGATA	TCAAAC TTCA	ATTAAAGGAC	1740
10	AGGTTACAAC	TGTAGCTACA	GGaAAAGCAT	ATATAGAATA	AGGAGCCTAC	AATGAATAAC	1800
	TTTAATAATG	AAATCAAATT	GATATTACAA	CAATATTTAG	AAAAGTTTGA	AGCGCATTAC	1860
	GAGCGTGTAT	TACAAGACGA	TCAATATATC	GAAGCATTAG	AAACATTGAT	GGATGACTAT	1920
15	AGTGAATTTA	TTTTAAATCC	TATTTATGAA	CAACAATTTA	ATGCTTGGCG	TGACGTTGAA	1980
	GAAAAAGCAC	AATTaATAAA	ATCACTGCAA	TATATTACAG	CGCAGTGTGT	TAAACAAGTG	2040
20	GAAGTCATTA	GAGCGAGACG	TCTATTAGAC	GGACAGGCGT	CTACCACAGG	TTACTTTGAC	2100
	AATATAGAAC	ATTGTATTGA	TGAAGAGTTT	GGACAAATGA	GTATAGCTAG	CAATGACAAA	2160
	TTATTGTTAG	TTGGTTCAGG	TGCATATCCA	ATGACGTTAA	TTCAAGTAGC	AAAAGAAACA	2220
25	GGTGCTTCAG	TTATCGGTAT	TGATATTGAT	CCACAAGCCG	TTGACCTAGG	GCGCAGAATC	2280
	GTTAACGTCT	TAGCACCAAA	TGAAGATATA	ACAATTACGG	ATCAAAAGGT	ATCTGAACTT	2340
	AAAGATATCA	AAGATGTGAC	GCATATCATA	TTCAGCTCGA	CAATTCCTTT	AAAGTACAGC	2400
30	ATTTTAGAAG	AATTATATGA	TTTAACAAAT	GAAAATGTG	TAGTTGCAAT	GCGCTTTGGT	2460
	GATGGCATCA	AAGCAATATT	TAATTATCCG	TCACAAGAAA	CAGCGGAAGA	TAAGTGGCAA	2520
	TGTGTGAATA	AACATATGAG	ACCACAGCAA	ATTTTGTGATA	TAGCACTTTA	TAAAAAAGCA	2580
35	GCTATAAAGG	TAGGTATTAC	GGATGTCTAA	ATTATTAATG	ATAGGCACTG	GTCCgGTCCG	2640
	AATGCAATTA	GCGAATATTT	GCTATTTAAA	ATCAGATTAT	GAGATTGATA	TGGTTGGACG	2700
	TGCCTCAACA	TCAGAAAAAT	CAAAACGCTT	ATATCAAGCG	TATAAAAAAG	AGAAACAATT	2760
40	TGAAGTCAAA	ATACAAAACG	AGGCGCATCA	ACATCTGGAA	GGTAAGTTTG	AAATTAATCG	2820
	TTTGTATAAA	GATGTTAAAA	ACGTTAAGGG	TGAATACGAA	ACGGTTGTCA	TGGCATGCAC	2880
45	AGCAGATGCT	TATTATGACA	CACTACAGCA	ATTGTCGTTA	GAAACTTTGC	AAAGTGTCAA	2940
	ACATGTCATT	TTAATATCAC	CGACATTTGG	TTCGCAAATG	ATTGTCGAAC	AATTTATGTC	3000
	TAAATTTAAT	AAAGATATCG	AAGTGATTTC	ATTCTCAACT	TATCTTGGCG	ATACACGTAT	3060
50	TGTTGATAAA	GAAGCGCCTA	ATCATGTGTT	GACAACAGGT	GTAAAAAAGA	AATTGTACAT	3120
	GGGATCGACA	CATTCAAAC	CAACAATGTG	TCAACGAATC	TCTGCTTTAG	CTGAGCAATT	3180

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	TTATGTGCAC CCACCACTAT TTATGAATGA CTTTTCATTG AAAGCCATTT TCGAAGGAAC	3300
	AGATGTACCG GTTTATGTGT ATAAGTTATT TCCTGAAGGA CCGATAACGA TGACACTAAT	3360
5	CCGTGAAATG CGTTTAATGT GGAAGGAAAT GATGGTTATT TTACAAGCAT TTAGAGTGCC	3420
	GTCAGTCAAC CTGCTTCAAT TTATGGTGAA GGAAAATTAT CCAGTACGTC CTGAAACTTT	3480
10	GGATGAAGGT GATATTGAGC ATTTGCGAAAT CTTGCCAGAT ATCTTACAAG AATATCTGCT	3540
	TTATGTGAAGA TATACCGCAA TCCTCATTGA TCCATTTTCA CAGCCAGACG AAAACGGACA	3600
	TTACTTTGAT TTTTCAGCTG TACCATTTAA GCAAGTCTAT AAAAATGAAC AGGATGTTGT	3660
15	TCAAATTCCA AGAATGCCAA GTGAAGATTA TTACAGAACG GCGATGATTC AGCATATTGG	3720
	GAAAATGCTA GGTATCAAAA CGCCAATGAT TGATCAGTTC CTAAGTCTGCT ATGAAGCAAG	3780
	TTGCCAGGCG TACAAGGATA TGCATCAAGA TCAACACTTA TCTTCTCAAT TTAATACAAA	3840
20	TCTATTTGAA GGAGATAAAG CACTCGTCAC AAAATTTTTG GAAATCAATA GAACGCTTTC	3900
	ATAATAAGGG TTTGAAGTTT TATAATAGAA AAAAATTATT GAATTATGTT TGACATTTAC	3960
	ATAAAAATAA GCAATAATT GAGAAAAATA ATCATTACGA TTTGATTAAG TAATGCAACT	4020
25	TATCAATTTA GAAAGAGGAA AAGCAAATGA GAAAACTAAC TAAAATGAGT GCAATGTTAC	4080
	TTGCATCAGG GCTAATTTTA ACTGGTTGTG GCGGTAATAA AGGTTTAGAG GAGAAAAAAG	4140
	AAAACAAGCA ATTAACGTAT ACGACGGTTA AAGATATCGG TGATATGAAT CCGCATGTTT	4200
30	ACGGTGGATC AATGCTGCT GAAAGTATGA TATACGAGCC GCTTGTACGT AACACGAAAG	4260
	ATGGTATTAA GCCTTTACTA GCTAAAAAGT GGGATGTGTC TGAAGATGGG AAGACATACA	4320
35	CGTTCCATTT GAGAGATGAC GTTAAATTCC ATGATGGTAC GCCATTTGca TGctGACGCA	4380
	GTTAAGAAAA ATATTGACGC AgTTCAAGAA AACAAAAAAT TGCATTCTTG GTTAAAGATT	4440
	TCGACATTAA TTGACAATGT TAAAGTTAAA GATAAGTACA CGGTTGAATT GAATTTGAAA	4500
40	GAAGCATATC AACCTGCATT GGCTGAATTA GCGATGCCTC GTCCATATGT ATTTGTGTCT	4560
	CCAAAAGACT TTaaaaACGG TACAacAAAA GATGGCGTTA AAAAGTTCGA TGGTACTGGT	4620
	CCATTTAAAT TAGGTGAACA CAAAAAGAT GAGTCTGCAG ACTTTAACAA AAATGATCAA	4680
45	TACTGGGGCG AAAAGTCTAA ACTTAACAAA GTACAAGCAA AAGTAATGCC TGCTGGTGAA	4740
	ACAGCATTCC TATCAATGAA AAAAGGTGAA ACGAACTTTG CCTTCACAGA TGATAGAGGT	4800
	ACAGATAGCT TAGACAAAGA CTCTTTAAAA CAATTGAAAG ATACAGGTGA CTATCAAGTT	4860
50	AAGCGTAGTC AACCTATGAA TACGAAAATG TTAGTTGTCA ATTCTGGTAA AAAAGATAAC	4920
	GCTGTGAGTG ACAAACAGT CAGACAAGCG ATTGGTCATA TGGTAAACAG AGATAAAATT	4980

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	ACAGACATTA ATTTTCGATAT GCCAACACGT AAGTATGACC TTAAAAAAGC AGAATCATT	5100
	TTAGATGAAG CTGGTTGGAA GAAAGGTAAA GACAGCGATG TTCGTCAAAA AGATGGTAAA	5160
5	AACCTTGAAA TGGCAATGTA CTATGACAAA GGTTCTTCAA GTCAAAAAGA ACAAGCAGAA	5220
	TACTTACAAG CAGAATTTAA GAAAATGGGT ATTAAGTTAA ACATCAATGG CGAAACATCA	5280
	GATAAAATTG CTGAACGTCG TACTTCTGGT GATTATGACT TAATGTTCAA CCAAACCTGG	5340
10	GGATTATTGT ACGATCCACA AAGTACTATT GCAGCATTTA AAGAGAAAAA TGGTTATGAA	5400
	AGTGCAACAT CAGGCATTGA GAACAAAGAT AAAATATACA ACAGCATTGA TGACGCATT	5460
	AAAATCCAAA ACGGTAAAGA GCGTTCAGAC GCTTATAAAA ACATTTTGAA ACAAATTGAT	5520
15	GATGAAGGTA TCTTTATCCC TATTTACAC GGTAGTATGA CAGTTGTTGC ACCaAAAGAT	5580
	TTAGAAAAAG TATCATTAC ACAATCACAG TATGAATTAC CATTCAATGA AATGCAGTAT	5640
20	AAATAAAGGA GCAATTAGAT GTTCAAATTT ATCTTAAAAC GTATTGCGCT CATGTTTCCA	5700
	TTGATGATTG TAGTAAGTTT TATGACATTT CTATTGACGT ATATTACAAA TGAAAATCCA	5760
	GCTGTGACAA TTTTACATGC ACAAGGGACG CCAATGTAA CACCAGAGTT GATTGCAGAA	5820
25	ACGAATGAGA AGTACGGTTT CAATGATCCA TTATTAATTC AATATAAAAA TTGGTTACTT	5880
	GAAGCGATGC AATTTAATTT TGGTACAAGC TACATTACAG GTGACCCAGT TGCTGAACGT	5940
	ATTGGTCCAG CATTATGAA TACATTGAAA TTAACAATAA TTTCAAGTGT TATGGTGATG	6000
30	ATTACATCAA TTATTTTAGG TGAGTTAGT GCATTAAAAA GAGGAAAGTT CACTGATCGT	6060
	GCGATACGTT CAGTGGCTTT CTTTCTAACT GCATTACCAT CATATTGGAT AGCTTCAATA	6120
	CTTATTATTT ACGTTTCAGT GAAGTTAAAC ATATTGCCGA CTTCTGGATT AACAGGTCCA	6180
35	GAAAGTTACA TATTGCCAGT GATCGTTATT ACGATTGCCT ATGCTGGTAT TTACTTTAGA	6240
	AATGTTAGAC GCTCGATGGT GGAACAATTA AATGAAGATT ATGTACTTTA TTAAAGAGCA	6300
40	AGCGGTGTGA AATCTATCAC ATTAATGTTG CATGTGTTGC GTAATGCTTT ACAAGTTGCG	6360
	GTATCAATCT TTTGTATGTC TATACCAATG ATAATGGGTG GACTAGTTGT TATCGAGTAT	6420
	ATCTTTGCAT GGCCTGGACT AGGTCAATTA AGTTTAAAAG CAATACTTGA ACACGATTTT	6480
45	CCAGTCATTC AAGCATATGT ATTAATTGTA GCGGTATTAT TTATTGTATT TAATACATTA	6540
	GCAGATATCA TTAATGCGCT ATTAAATCCA AGATTAAGGG aGGGCGCACG ATGATAATTT	6600
	TAAAmCGATT ATTMCArGwT AAAGGTGCAG TAATTGCTTT AGGCATTATT GTATTATATG	6660
50	TCTTTTTAGG ATTAGCAGCA CCACTTGTGA CATTTTATGA TCCTAACCAT ATCGATACAG	6720
	CAACAAATT TGCTGGCATG AGTTTTCAAC ATCTACTAGG TACTGACCAT TTAGGTAGAG	6780

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	TATTTGTTTC TGTACTTATT GGATCTATTT TAGGATTCTT ATCAGGATAT TTCCAAGGGT	6900
	TTGTTGACGC CTTAATCATG CGTGCGTGTG ATGTTATGTT GGCATTCCCA AGTTATGTTG	6960
5	TAACGTTAGC ATTAATTGCA TTGTTTGGAA TGGGTGCCGA AAATATTATC ATGGCATTTA	7020
	TTTTGACGCG TTGGGCATGG TTCTGTCGTG TTATACGTAC AAGTGTTATG CAGTACACTG	7080
	CTTCTGACCA TGTAAGATTT GCTAAAACAA TCGGTATGAA TGATATGAAA ATTATTCACA	7140
10	AACATATTAT GCCATTAACA TTAGCAGATA TTGCTATCAT CTCTAGTAGC TCGATGTGTT	7200
	CAATGATCTT GCAAATATCT GGCTTTTCAT TTTTAGGATT AGGTGTCAAA GCGCCTACTG	7260
	CAGAGTGGGG CATGATGCTT AACGAaGCTA GAAAAGTGAT GTTTACACAT CCTGAAATGA	7320
15	TGTTTGCGCC AGGTATTGCC ATAGTGATTA TAGTGATGGC ATTTAACTTC TTATCCGATG	7380
	CTTTACAAAT TGCTATTGAT CCCC GCATCT CTTCTAAAGA TAAACTTCGT TCTGTGAAAA	7440
	AAGGAGTGGT GCAATCATGA CATTGTTAAC AGTTAAACAT TTGACGATTA CAGATACCTG	7500
20	GACAGATCAA CCACTCGTGA GTGATGTGAA TTTTACATTA ACTAAGGGTG AAaCTTTAGG	7560
	CGTTATTGGA GAAAGTGGTA GTGGTAAATC AATCACTTGT AAATCGATTA TTGGTTTGAA	7620
25	TCCCGAACGA CTCGGGGTGA CAGGTGAAAT TATCTTTGAT GGTACaCAA TGTTGTcATT	7680
	ATCTGAATCG CAATTGAAAA AGTACCGTGG TAAAGACATT GCGATGGTCA TGCAACAAGG	7740
	TAGTCGTGCC TTTGACCCAT CAACTACTGT CGGTAAACAA ATGTTTGAGA CTATGAAAGT	7800
30	ACATACGTCA ATGTCTACAC AAGAAATTGA AAAGACATTG ATTGAATATA TGGATTATTT	7860
	AAGTTTGAAA GATCCTAAAC GTATATTAAA ATCATACCCT TACATGTTAT CAGGAGGAAT	7920
	GTTACAGCGA TTGATGATTG CTTTAGCGTT AgcTTTgAAA CCAAAGTTAA TCATTGCTGA	7980
35	TGAGCCGACA ACGGCTTTAG ATACAATTAC ACAATATGAT GTACTGGAAG CATTTATAGA	8040
	TATTAAAAAA CACTTTGACT GTGCGATGAT TTTcATTtCA CATGATTtAA CGGTTATTAA	8100
	CAAGATTGCA GACCGTGTG TTGTGATGAA AAATGGTCAG CTTATTGAAC AAGGGACACG	8160
40	TGAATCAGTC TTGCATCATC CAGAACATGT TTATACGArt ATTKtATTAT CAACGAAGAA	8220
	GAAGATTAAT GATCATTTTA AACATGTGAT GAGGGGTGAT GTACATGATT AAAATTAAAG	8280
45	ATGTTGAAAA GTCATATCAA AGCGCACATG TTTTTAAGCG TCGTCGAACA CCTATCGTGA	8340
	AAGGTGTGTC ATTTGAGTGT CCAATCGGTG CGACGATTGC GATTATCGGA GAAAGTGGTA	8400
	GCGGTAAATC GACGTTGAGT CktATGATAT TAGGTATTGA GAAACCGGAT AAAGGTTGTG	8460
50	TAACCTTAAA TGATCAACCG ATGCATAAGA AGAAAGTGAG ACGTCATCAA ATTGGTGCTG	8520
	TATTTCAAGA TTATACGTCA TCATTACATC CATTTcAGAC TGTTAGAGAA ATCTTATTTG	8580

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	TGTTGGAAGA	AGTCGGTCTA	TCTAAGGCAT	ACATGGATAA	ATATCCTAAT	ATGTTATCAG	8700
	GTGGAGAGGC	GCAACGTGTT	GCGATTGCGC	GTGCAATATG	TATTAACCCT	AAATATATTT	8760
5	TGTTTGATGA	AGCCATTAGT	TCACTCGACA	TGTCAATTCA	AACACAAATA	TTAGATTTAT	8820
	TGATTCATTT	ACGTGAAACG	CGTCAGTTGA	GTTATATTTT	TATCACACAT	GATATTCAAG	8880
	CTGCCACGTA	TTTATGTGAT	CAATTAATTA	TTTTTAAAAA	CGGAAAAATA	GAAGAACAAA	8940
10	TTCCGACAAG	CGCATTGCAT	AAAAGTGACA	ATGCTTATAC	AAGAGAATTA	ATAGAAAAAC	9000
	AACTATCATT	CTAAGGAGTG	AGATAATGAA	AGGTGCAATG	GCTTGGCCCT	TTTTGAGATT	9060
	ATATATATTA	ACATTGATGT	TCTTLAGTGC	CAATGCAATC	TTAAACGTGT	TTATACCTTT	9120
15	ACGAGGGCAT	GATTTAGGCG	CAACGAATAC	GGTTATCGGT	ATCGTTATGG	GGGCATACAT	9180
	GTTAACAGCA	ATGGTATTTT	GACCATGGGC	AGGACAAATT	ATTGCTCGTG	TCGGTCCCAT	9240
20	TAAAGTATTA	AGAATTATTT	TGATTATCAA	TGCCATAGCT	TTAATTATTT	ATGGTTTTAC	9300
	TGGCTTAGAA	GGTATTTTCG	TAGCACGTGT	TATGCAAGGT	GTGTGTACGG	CATTCTTTTC	9360
	TATGTCTTTA	CAGCTAGGTA	TTATTGATGC	ATTACCAGAG	GAACATCGTT	CTGAAGGTGT	9420
25	ATCATTGTAC	TCGCTATTTT	CAACGATTCC	AAACTTAATC	GGACCATTAG	TTGCCGTAGG	9480
	TATTTGGAAT	GCAAATAATA	TTTCACTATT	TGCAATTGTC	ATTATCTTTA	TCGCATTAAC	9540
	AACAACATTC	TTTGsTATCG	CGTGACCTTT	GCTGAACAGG	AACCCGATAC	GTCAGATAAG	9600
30	ATTGAAAAAA	TGCCGTTTAA	CGCTGTAACT	GTTTTTGCGC	AATTTTTCAA	AAATAAAGAG	9660
	TTGTTGAACA	GTGGTATTAT	CATGATTGTT	GCATCGATTG	TATTTGGTGC	AGTTAGTACA	9720
	TTTGTACCGT	TATACACAGT	GAGTTTAGGA	TTCCGGAATG	CGGGAATCTT	TTTGACAATA	9780
35	CAGGCCATCG	CAGTTGTTGC	GGCAAGATTT	TACTTAAGGA	AATACATTCC	GTCAGATGGT	9840
	ATGIGGCATC	CTAAATATAT	GGTATCTGTA	CTATCATTAT	TAGTAATCGC	GTCATTTGTA	9900
	GTGGCATTTG	GTCCGCAAGT	AGGTGCAATT	ATTTTCTATG	GTAGTGCGAT	ATTAATAGGA	9960
40	ATGACGCAAG	CAATGGTGTA	CCCAACATTA	ACATCATACT	TAAGCTTCGT	CTTACCAAAA	10020
	GTAGGTCGTA	ATATGTTGTT	AGGTTTATTT	ATTGCTGTG	CAGACTTAGG	TATATCGTTA	10080
45	GGTGGCGCAT	TGATGGGACC	TATTTCCGAT	TTAGTAGGAT	TTAAATGGAT	GTATCTAATT	10140
	TGTGGTATGT	TAGTCATTGT	AATAATGATT	ATGAGTTTCT	TGAAAAAGCC	AACACCACGT	10200
	CCAGCGAGTA	GTCTTTAATG	AAGTGAATTA	AAGCATATTA	AGTTAATGAA	TATTTAAATT	10260
50	TTAAAAGGTA	TATTGaGCAT	GGCGATTCAT	GTGCTTCATG	CTAGGACATG	AAACATTCTA	10320
	TATGGCTCGT	TTTAGAACG	ACAtATATCT	AAATAAAGCA	CGCTTAaAG	TGAGTTTTGA	10380

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	TTACATGAAA ATATGCAAAA CGAGTATAAC TGCTAATTGA TAGAAATAGC TCACCATAAA	10500
	ATTACGGTAT GATTTTAAAT ATAAGTAAGT CGCACTACCT GCTAGTATCA ATGCTGGAAT	10560
5	GAATTCACAC CATGTATTAA TGTATGGATA GTAGAACAGA GTTTCAGGA TAATGGACAA	10620
	TACTATTGTA ATCTTTAAAG GTATTAATCT GCTTAATTCT TGAATTAAAA TATGACGGAA	10680
	AATAAGTTGA CAAATCAAAG TATTTAATAT AATGGTTAAC GAAATATAG CTATTAACT	10740
10	GATGGAaCCA TACCCTTTAA TGAGCGGGTA AATGTCAAAG ACAGTAAAGG AATCTACATT	10800
	TAGTGCAGAA ATATTGAAAT GATTTAAAAG TAAAAAGAGT ACGACACTTA GTGTAAATGA	10860
	TATAAGAATA TGCCATTTAT ATTTAGCACT AGCAACGATT TGCGAACGTA TCATTGGAAT	10920
15	AAACGCATCT TCATGCATCA GACGAAAAAT AGCTAGTGAA ATAATACTG CGAGTAAATA	10980
	GCTAATGTTT ATTGAAATAG GAAAAGAGAA ACCCCACGGA GCTTGTGAG TGAATACAGC	11040
20	TACTAACCCA AAAGTTAAAA AGACGATAAT GATCGGCAAG ATGTTAACCA AAAATATGTA	11100
	AAGGAAAATA AATCCAATAT CACGTTTGAA AAAACGCGAT TGTTCGGTAG CGTATTCTTC	11160
	TTCTATGTAA TGTTTATTTG TATTTGACAT AGTATACCTC TTAAATAGTT GTATTATATA	11220
25	GATACTTAG CACATATTAC TTTGTATTGT ATGTTTATA CATTAAATTT TAAAATGAAA	11280
	AACATATCAT AAAATTGTTT TATAAAATGA AGCGCTTCCA TTGTGTTTTG TTTTGTAAGG	11340
	TGTATCATAA ATATTGAATT GAAATTTTGG GGGGAGGTAT TGTAATGACG TTTCTTACAG	11400
30	TCATGCAATT TATAGTTAAC ATTATCGTTG TAGGATTCAT GCTTACGGTT ATTGTTATCG	11460
	GGCTTATTTG GTTAATTAAA GATAAAAGAC AATCACAACA TAGTGTATTA AGGAATTATC	11520
	CTTTACTAGC ACGTATTAGA TATATTTTCTG AAAAAATGGG ACCGGAATTA CGTCAGTATT	11580
35	TATTTTCTGG GGATAATGAA GGGAAACCTT TTTCACGTAA TGATTATAAA AATATCGTTT	11640
	TGGCTGGAAA ATATAACTCT CGTATGACCA GCTTCGGTAC TACTAAAGAT TATCAAGACG	11700
	GCTTTTACAT ACAGAACACA ATGTTTCCGA TGCAACGTAA TGAGATTTCA GTAGATAATA	11760
40	CAACATTGTT ATCAACATTC ATTTATAAAA TCGCGAATGA GCGTTTATTT AGTCGTGAAG	11820
	AATATCGTGT GCCGACAAAG ATTGATCCGT ATTACTTAAG TGATGACCAT GCAATAAAAT	11880
45	TAGGTGAACA TTTAAACAT CCATTTATTT TAAAACGTAT CGTAGGACAA TCTGGTATGA	11940
	GTTATGGCGC TTTAGGAAAA AATGCCATTA CAGCTTTATC TAAAGGTCTA GCTAAAGCGG	12000
	GCACTGGAT GAATACAGGT GAAGGTGGCT TATCAGAATA TCATTTAAAA GGTAATGGGG	12060
50	ATATCATTTT CCAAATTGGT CCCGGTTTAT TTGGTGTTCG TGATAAAGAA GGTAATTTTA	12120
	GTGAAGGTTT ATTTAAAGAG GTTGCACAGT TATCTAACGT ACGCGCATTG GAGCTGAAGT	12180

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	TTGCTAAAAT CCGAAATGTT GAACCTTATA AAACAATCAA TTCACCTAAC CGTTACGAAT	12300
	TTATTTCATAA TGCTGAAGAT TTGATTTCGTT TCGTCGATCA GTTGCAGCAA TTAGGTCAAA	12360
5	AACCACTAGG ATTCAAAATT GTAGTAAGCA AAGTTTCAGA AATTGAAACA CTTGTACGTA	12420
	CGATGGTGGG ACTAGATAAG TATCCAAGCT TTATTACGAT TGATGGTGGT GAAGGTGGTA	12480
	CTGGTGCAAC ATTCCAAGAA TTACAAGATG GTGTTGGCTT ACCGCTATT ACAGCTCTAC	12540
10	CTATTGTGTC TGGCATGTTA GAAAAATATG GTATTTCGAGA TAAAGTGAAA TTGGCGGCAT	12600
	CTGGTAAGTT AGTGACACCA GATAAAATTG CGATTGCACT AGGTTTAGGT GCAGATTTTG	12660
	TAAATATCGC ACGTGGGATG ATGATTAGTG TCGGTTGTAT AATGAGTCAA CAATGTCACA	12720
15	TGAATACGTG TCCTGTAGGT GTTGCAACGA CAGATGCGAA GAAAGAAAAA GCATTGATTG	12780
	TTGGAGAAAA GCAATATCGT GTCACAAACT ATGTAACAAG TTTGCATGAA GGCTTATTCA	12840
20	ATATTGCAGC AGCTGTTGGC GTATCCAGTC CTACAGAAAT TACTGCTGAT CATATTGTAT	12900
	ATCGAAAAGT CGATGGTGAG TTACAAACGA TACATGATTA TAAATTAAAA CTCATTAGTT	12960
	AACTTAATTA TTTCCGGAAA TTGAAAGCAG CGGATTTTAG CGTTACTGCA AATAATTTTA	13020
25	TATTAGTAGT GGATGCTGGT CACACAAGAA CTTCAAATAT TAAAGCCCTC AGAATATGAA	13080
	TTAAGGTTTG TAACCTTAGT CTTATCTGAG GGCATTTTAA AGTTATAAAC TATTTGTCGT	13140
	CCATTTTATC TTTTCTTTT AAACCTCTGT GCTTTAATTG CTTTCAAGT TTTTCAAAAC	13200
30	TAATATCTTT ATTTTCTTTA GTCGAAACAC CAAGACGTTT ATTTAATTTT TTCATGTCAA	13260
	CTTCTGTGTA ATCTATGTCT AAGTGyTCAA TTGCTTTTTT ATCTTTATAG TCTACTTTGT	13320
	ATTTTACGCC TTTAAGGTCT TTGAAAATAC TTTCAGATTT GGCGAATAAC TTTTGGCTT	13380
35	CGTCTTTATC CATACTAGA TCGTCATATT TAATTGTGTT GATTGTAGAC TGTTTTAAAA	13440
	CTTTATCATC TTTATATGTG ATAGAAGTTA GTACATGTTT ACCACTAACA TCACCWTCAT	13500
	ATGTTTTGGT TTGTTCTTTA CCACAAGCTG ATAATGCAAT GATACAACT AATGCTACTA	13560
40	CAATTAATGA ACATAATTTT TTCAAAGTCA GTCGCCTTCT TTCGATATTT GTATTATAAA	13620
	GAAATTATAA CATTTACTAA AAAATGATGT TATTCAAAAA TTTAAATTTT GTCATTTTTT	13680
45	TTGAAGATAT GAGTTTTTTT AAGCGGATTC CTCACAAAAT TTTAAAAATA TTTAAGCCTk	13740
	AAAATGATAA AGCGkTAGGG AACGTTTTTC TGAAAGTTAG TGATACAATA GTTTTAAGTT	13800
	GAAATACAGG AGGATGAATA ACATGAATCA GTCAGTCAAA TTACTIONAAC ATTTAACAGA	13860
50	TGTAAACGGC ATTGCTGGTT ATGAAATGCA AGTTAAAGAA GCAATGCGTa ACTATATAGA	13920
	GCCTGTCACT GATCAAATTA TTGAAGATAA CTTGGGTGGC ATTTTGGAA AGAAAAATGC	13980

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